

Wed Aug 15 13:35:08 2001

us-09-372-036-29.ra1

Page 8

Search completed: August 15, 2001, 13:10:02
Job time: 39 sec

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-34

Query Match 61.4%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAPKA 8
|||||
DB 1 OOTAPKA 7

RESULT 14
US-08-482-847-34
Sequence 34, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:

APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482.847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-34

Query Match 61.4%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAPKA 8
|||||
DB 1 OOTAPKA 7

RESULT 15
US-08-456-670B-25
Sequence 25, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, Siegfried
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US

ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456.670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248

FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-25

Query Match 61.4%; Score 35; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 OOTAPKAPT 10
|||||
DB 1 OOTTKAPT 9

APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria innocua
US-08-456-670B-38

Query Match 68.4%; Score 39; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.55;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQTAPKAPT 11
:11111111:
Db 1 EQOTTAKAPT 11

RESULT 11
US-08-816-693A-51
Sequence 51, Application US/08816693A
Patent No. 5874241
GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S
APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawrence H
TITLE OF INVENTION: Clock Gene and Gene Product
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,693A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5874241thrup, Thomas E
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-816-693A-51

Query Match 64.9%; Score 37; DB 2; Length 747;

Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQTAPKAPT 10
:11111111:
Db 699 QOQPPQAPT 708

RESULT 12
US-08-885-291-51
Sequence 51, Application US/08885291A
Patent No. 6057125
GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
CURRENT APPLICATION NUMBER: US/08/885,291A
CURRENT FILING DATE: 1997-06-30
EARLIER APPLICATION NUMBER: 08/816,693
EARLIER FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 747
TYPE: PRT
ORGANISM: Mus musculus
US-08-885-291-51

Query Match 64.9%; Score 37; DB 3; Length 747;
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQTAPKAPT 10
:11111111:
Db 699 QOQPPQAPT 708

RESULT 13
US-08-127-499A-34
Sequence 34, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-26

Query Match 100.0%; Score 57; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OOOTAPKAPTE 11
|||||
Db 291 OOOTAPKAPTE 301

RESULT 9
US-08-456-670B-20
Sequence 20, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6533
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
SPRAIN: ECD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 17-23
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-20

Query Match 82.5%; Score 47; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 OOOTAPKAPT 10
|||||
Db 8 OOOTAPKAPT 16

RESULT 10
US-08-456-670B-38
Sequence 38, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: BGD
US-08-456-670B-40

Query Match 100.0%; Score 57; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 QOOTAPKAPTE 11
|||||
Db 291 QOOTAPKAPTE 301

RESULT 7
US-08-127-499A-26
Sequence 26, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-26

Query Match 100.0%; Score 57; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 QOOTAPKAPTE 11
|||||
Db 291 QOOTAPKAPTE 301

RESULT 8
US-08-482-847-26
Sequence 26, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

RESULT 4
US-08-482-847-33
; Sequence 33, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acid
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-482-847-33

Query Match 100.0%; Score 57; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 000TAPKAPTE 11
|||||
Db 7 000TAPKAPTE 17

RESULT 5
US-08-456-670B-39
; Sequence 39, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINKEWELER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: HUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 421911.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMELT-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
; US-08-456-670B-39

Query Match 100.0%; Score 57; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 000TAPKAPTE 11
|||||
Db 222 000TAPKAPTE 232

RESULT 6
US-08-456-670B-40
; Sequence 40, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINKEWELER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: HUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS

TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: SCD
US-08-456-670B-29

Query Match 100.0%; Score 57; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
Db 1 QOOTAPKAPTE 11

RESULT 2
US-08-456-670B-42
Sequence 42, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BUNGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUEBEL, ANDREAS
APPLICANT: GOEBEL, WERNER
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694DI

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-456-670B-42

Query Match 100.0%; Score 57; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
Db 2 QOOTAPKAPTE 12

RESULT 3
US-08-127-499A-33
Sequence 33, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-33

Query Match 100.0%; Score 57; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
Db 7 QOOTAPKAPTE 17

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 13:10:02 ; Search time 30.68 Seconds
(without alignments)
7.382 Million cell updates/sec

Title: US-09-372-036-29

Perfect score: 57

Sequence: 1 000TAPKAPTE 11

Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCtUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	11	2	US-08-456-670B-29
2	57	100.0	12	2	US-08-456-670B-42
3	57	100.0	21	1	US-08-127-459A-33
4	57	100.0	21	1	US-08-482-847-33
5	57	100.0	23	2	US-08-456-670B-39
6	57	100.0	478	2	US-08-456-670B-40
7	57	100.0	484	1	US-08-127-459A-26
8	57	100.0	484	1	US-08-482-847-26
9	47	82.5	23	2	US-08-456-670B-20
10	39	68.4	11	2	US-08-456-670B-38
11	37	64.9	747	2	US-08-816-693A-51
12	37	64.9	747	2	US-08-885-291-51
13	35	61.4	7	1	US-08-127-459A-34
14	35	61.4	7	1	US-08-482-847-34
15	35	61.4	9	2	US-08-456-670B-25
16	35	61.4	443	1	US-08-342-411A-4
17	34	59.6	405	5	PCT-US93-1140A-2
18	34	59.6	3457	2	US-08-416-603-4
19	33	57.9	21	2	US-08-934-915-72
20	32	56.1	73	3	US-09-041-889-12
21	32	56.1	73	3	US-08-837-058-12
22	32	56.1	220	3	US-09-041-889-2
23	32	56.1	220	3	US-08-837-058-2
24	32	56.1	298	4	US-08-961-083-24
25	32	56.1	459	4	US-09-118-319-6
26	32	56.1	459	4	US-09-286-691-2
27	32	56.1	459	4	US-09-687-147-2

28	32	56.1	605	2	US-08-687-956A-1	Sequence 1, Appl1
29	32	56.1	696	6	5262177-4	Patent No. 5262177
30	32	56.1	698	2	US-08-175-158A-2	Sequence 2, Appl1
31	32	56.1	788	2	US-08-918-914-4	Sequence 2, Appl1
32	32	56.1	903	2	US-08-853-310-2	Sequence 2, Appl1
33	32	56.1	1074	2	US-08-470-058-2	Sequence 2, Appl1
34	32	56.1	1074	3	US-09-037-188-2	Sequence 2, Appl1
35	32	56.1	1162	2	US-08-728-333A-2	Sequence 2, Appl1
36	32	56.1	1410	2	US-08-470-058-4	Sequence 4, Appl1
37	32	56.1	1410	3	US-09-037-188-4	Sequence 4, Appl1
38	32	56.1	1572	2	US-08-290-731C-5	Sequence 5, Appl1
39	32	56.1	1596	3	US-09-356-952-3	Sequence 3, Appl1
40	32	56.1	3118	2	US-08-457-273B-8	Sequence 8, Appl1
41	31	54.4	196	2	US-08-481-814A-9	Sequence 9, Appl1
42	31	54.4	339	1	US-08-248-629A-3	Sequence 3, Appl1
43	31	54.4	339	1	US-08-451-932-3	Sequence 3, Appl1
44	31	54.4	339	1	US-08-452-260-3	Sequence 3, Appl1
45	31	54.4	339	2	US-08-612-788-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-456-670B-29
Sequence 29, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, Siegfried
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, Winfried
APPLICANT: BURGER, Christa
APPLICANT: HOFMANN, Gottfried
APPLICANT: BOBERT, Andreas
APPLICANT: GOEBEL, Werner
APPLICANT: KOHLER, Stefan
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & ARANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456, 670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412, 227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075, 248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:

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```

DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
GN GLN OR SLR1756.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria: Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95244839; PubMed=7727755;
RA Reyes J.C., Florencio F.J.;
RT *Electron transport controls transcription of the glutamine
RT synthetase gene (glnA) from the cyanobacterium Synechocystis sp. PCC
RT 6803."
RL Plant Mol. Biol. 27:789-799(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Suglura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT *Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X69199; CAA49139.1; -
DR EMBL: D90903; BAA17055.1; -
DR HSSP: P06201; 2LGS.
DR InterPro: IPR001691; -
DR Pfam: PF00120; gln-synt; 1.
DR PROSITE: PS00180; GLN_1; 1.
DR PROSITE: PS00181; GLN_ATP; 1.
KW Ligase.
KW FT CONFLICT 115 115 V -> A (IN REF. 2).
KW FT CONFLICT 145 147 QTE -> PNG (IN REF. 1).
KW FT CONFLICT 180 180 O -> E (IN REF. 1).
KW FT CONFLICT 204 206 GLC -> ARG (IN REF. 2).
KW FT CONFLICT 230 230 K -> KFDK (IN REF. 1).
KW FT CONFLICT 239 239 M -> I (IN REF. 1).
KW FT CONFLICT 358 358 K -> N (IN REF. 1).
KW FT CONFLICT 378 379 ML -> IV (IN REF. 1).
KW FT CONFLICT 430 430 E -> O (IN REF. 1).
SO SEQUENCE 473 AA; 53026 MW; 75F8E28EB5EA9515 CRC64;

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Query Match 50.0%; Score 5; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PVAPT 5
   11111
DB 184 PVAPT 188

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Search completed: August 15, 2001, 12:43:06
Job time: 496 sec

Query Match 50.0%; Score 5; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAAPT 5
DB 374 PVAAPT 378

RESULT 48
REBA_VIBCH STANDARD; PRT; 465 AA.
AC 007024; Q9KVA6;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PUTATIVE MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE (GDP) (EC 2.7.7.22)
GN REBA OR VC0241.
OS *Vibrio cholerae*.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
OX NCBI_TaxId=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EL TOR 017 / SEROTYPE OGAWA;
RX MEDLINE-92212870; PubMed-1372980;
RA Stroehner U.H., Karageorgos L.E., Morona R., Manning P.A.;
RT "Serotype conversion in *Vibrio cholerae* O1."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2565-2570(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-EL TOR N16961 / SEROTYPE O1;
RX MEDLINE-20406833; PubMed-10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dreigol I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Niemman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*."
RL Nature 406:477-483(2000).
CC -1- CATALYTIC ACTIVITY: GDP + D-MANNOSE 1-PHOSPHATE = ORTHOPHOSPHATE + GDP-MANNOSE.
CC -1- PATHWAY: GDP-MANNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF MANNOSE-6-PHOSPHATE ISOMERASES.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X59554; CAA42134.1; ALT_FRAME.
DR EMBL: AE004113; AAF93417.1; .
DR PIR: S28468; S28468.
DR TIGR: VC0241; .
DR InterPro: IPR001538; .
DR InterPro: IPR001825; .
DR Pfam: PF01050; MannoseP_isomert; 1.
DR Pfam: PF00483; NTP_transferase; 1.
KW Lipopolysaccharide biosynthesis; Transferase; Kinase.
SEQUENCE 465 AA; 51916 MW; 7274A5A876F49268 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
DB 337 QEVKK 341

RESULT 49
GLNA_FREDI STANDARD; PRT; 470 AA.
ID GLNA_FREDI
AC P33035;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
GN GLNA.
OS *Fremyella diplosiphon* (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; *Fremyella*.
OX NCBI_TaxId=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93129187; PubMed-1362348;
RA Elmorjani K., Liotenberg S., Hounard J., de Marsac N.T.;
RT "Molecular characterization of the gene encoding glutamine synthetase in the cyanobacterium *Calothrix* sp. PCC 7601."
RL Biochem. Biophys. Res. Commun. 189:1296-1302(1992).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE + ORTHOPHOSPHATE.
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO HEXAGON.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L05609; AAA23288.1; .
DR PIR: JC1403; JC1403.
DR HSSP: P06201; ZLGS.
DR InterPro: IPR001637; .
DR InterPro: IPR001691; .
DR Pfam: PF00120; gln-synt; 1.
DR PROSITE: PS00180; GLNA_1; 1.
DR PROSITE: PS00181; GLNA_ATP; 1.
DR PROSITE: PS00182; GLNA_ADENYLYATION; 1.
KW Ligase.
FT INIT_MET 0 BY SIMILARITY.
SEQUENCE 470 AA; 52919 MW; ADD7B49A7789E832 CRC64;
Query Match 50.0%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAAPT 5
DB 181 PVAAPT 185

RESULT 50
GLNA_SYNT3 STANDARD; PRT; 473 AA.
ID GLNA_SYNT3
AC P77961; Q59981;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

CC -----
CC -1- SIMILARITY: TO YEAST YBR287W.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z88056; CAB10852.1; -.
CC Hypothetical protein; Transmembrane.
CC TRANSMEM 18 38 POTENTIAL.
CC TRANSMEM 81 101 POTENTIAL.
CC TRANSMEM 269 289 POTENTIAL.
CC TRANSMEM 317 337 POTENTIAL.
CC TRANSMEM 354 374 POTENTIAL.
CC TRANSMEM 390 410 POTENTIAL.
CC TRANSMEM 428 448 POTENTIAL.
CC SEQUENCE 452 AA; 49575 MW; 71B77EAS725C69A8 CRC64;
CC -----
CC Query Match 50.0%; Score 5; DB 1; Length 452;
CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC Oy 4 PROEV 8
CC 11111
CC Db 342 PROEV 346
CC -----
CC RESULT 46
CC GATA_HELPY STANDARD; PRT; 453 AA.
CC 092L13;
CC 30-MAY-2000 (Rel. 39, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC DE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADT
CC SUBUNIT A).
CC GATA OR JHP0769.
CC OS Helicobacter pylori J99 (Campylobacter pylori J99).
CC OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
CC Helicobacter.
CC NCBI_TaxID=85963;
CC OX
CC RN
CC SEQUENCE FROM N.A.
CC RX MEDLINE=99120557; PubMed=9923682;
CC RA Alm R.A., Ling L.-S.L., Molt D.T., King B.L., Brown E.D., Dolg P.C.,
CC RA Smith D.R., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,
CC RA Tummino P.J., Caruso A., Ulla-Nickelsen M., Mills D.M., Ives C.,
CC RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
CC RA Trust T.J.;
CC "Genomic sequence comparison of two unrelated isolates of the human
CC gastric pathogen Helicobacter pylori";
CC RT Nature 397:176-180(1999).
CC RL
CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC GLN-TRNA(GLN) THROUGH THE TRANSMUTATION OF MISACTYLATED GLU-
CC TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
CC REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
CC AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMINE - ADP
CC + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMATE.
CC -1- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

CC -----
CC EMBL: AE001507; AAD06348.1; -.
CC DR InterPro: IPR000120; -.
CC DR Pfam: PF01425; Amidase; 1.
CC DR PROSITE: PS00571; AMIDASES; 1.
CC DR Protein biosynthesis; Ligase.
CC SQ SEQUENCE 453 AA; 49749 MW; FD97731532E7397 CRC64;
CC -----
CC Query Match 50.0%; Score 5; DB 1; Length 453;
CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC Oy 1 PVAPT 5
CC 11111
CC Db 374 PVAPT 378
CC -----
CC RESULT 47
CC GATA_HELPY STANDARD; PRT; 453 AA.
CC AC P56114;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADT
CC SUBUNIT A).
CC GATA OR HP0830.
CC OS Helicobacter pylori (Campylobacter pylori).
CC OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
CC Helicobacter.
CC NCBI_TaxID=210;
CC OX
CC RN
CC SEQUENCE FROM N.A.
CC RP STRAIN=26695 / ATCC 700392;
CC RX MEDLINE=97394467; PubMed=9252185;
CC RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
CC RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
CC RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
CC RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
CC RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
CC RA Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
CC RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
CC RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
CC RA Venter J.C.;
CC "The complete genome sequence of the gastric pathogen Helicobacter
CC pylori";
CC RT Nature 388:539-547(1997).
CC RL
CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC GLN-TRNA(GLN) THROUGH THE TRANSMUTATION OF MISACTYLATED GLU-
CC TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
CC REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
CC AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMINE - ADP
CC + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMATE.
CC -1- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE000594; AAD07880.1; -.
CC DR TIGR: H00830; -.
CC DR InterPro: IPR000120; -.
CC DR Pfam: PF01425; Amidase; 1.
CC DR PROSITE: PS00571; AMIDASES; 1.
CC DR Protein biosynthesis; Ligase.
CC SQ SEQUENCE 453 AA; 49652 MW; A35814B32F1AE13A CRC64;
CC -----

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OC Bacteria: Proteobacteria: epsilon subdivision: Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Voyis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: GLUCOSAMINE 1-PHOSPHATE = GLUCOSAMINE 6-
CC PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE001446; AAD05654.1; -.
DR InterPro: IPR001485; -.
DR Pfam: PF00408; PGM_PMM; 1.
DR PRINTS: PR00509; PGM_PMM; 1.
DR PROSITE: PS00710; PGM_PMM; 1.
KM Isomerase; Phosphorylation.
FT ACT_SITE 99
FT SEQUENCE 445 AA; 49174 MW; 586DD2E161295667 CRC64;
SQ
Query Match 50.0%; Score 5; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 OEYKK 10
DB 228 OEYKK 232
RESULT 44
GLMM_HELPY
AC P25177; STANDARD; PRT; 445 AA.
DT 01-MAY-1992 (rel. 22, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 01-OCT-2000 (rel. 40, Last annotation update)
DE PHOSPHOGLUCOSAMINE MUTASE (EC 5.4.2.-).
GN GLMM OR UREC OR HP0075.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria: Proteobacteria: epsilon subdivision: Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85P;
RX MEDLINE=91161505; PubMed=2001995;
RA Labigne A., Cussac V., Courcoux P.;
RT "Shuttle cloning and nucleotide sequences of Helicobacter pylori
RT genes responsible for urease activity.";
RL J. Bacteriol. 173:1920-1931(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,

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RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khaliq H.G., Glodex A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
CC -1- CATALYTIC ACTIVITY: GLUCOSAMINE 1-PHOSPHATE = GLUCOSAMINE 6-
CC PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
CC -----
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CC -----
DR EMBL: M60398; AAA25018.1; -.
DR EMBL: AE000529; AAD07146.1; -.
DR PIR: C38537; C38537.
DR TIGR: HP0075; -.
DR InterPro: IPR001485; -.
DR Pfam: PF00408; PGM_PMM; 1.
DR PROSITE: PS00710; PGM_PMM; 1.
KM Isomerase; Phosphorylation.
FT ACT_SITE 99
FT SEQUENCE 445 AA; 49086 MW; C0A52D904FFDAF20 CRC64;
SQ
Query Match 50.0%; Score 5; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 OEYKK 10
DB 228 OEYKK 232
RESULT 45
IDQ4_SCHPO
ID YDQ4_SCHPO STANDARD; PRT; 452 AA.
AC 014197;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE HYPOTHEICAL 49.6 KDA PROTEIN C5D6.04 IN CHROMOSOME I.
GN SPAC5D6.04.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes;
OC Schizosaccharomycetales: Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX Skellon J., Church C.M., Wood V., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

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CC -----
DR EMBL: AB013466; BAA33429.1; -
DR EMBL: AB013467; BAA33430.1; -
DR EMBL: AB013469; BAA33431.1; -
DR EMBL: AB013469; BAA33432.1; -
DR EMBL: AF079971; AAC77924.1; -
DR EMBL: U03896; AAB41444.1; -
DR MGI: 1334255; Pscd2.
DR HSSP: Q09418; 1PBV.
DR InterPro: IPR000904; -
DR InterPro: IPR001849; -
DR Pfam: PF00169; PH; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
KM Guanine-nucleotide releasing factor: Coiled coil.
KM Alternative splicing.
FT DOMAIN 10 67 COILED COIL (POTENTIAL).
FT DOMAIN 72 201 SECT.
FT DOMAIN 259 376 PH.
FT VARSPLIC 1 16 MISSING (IN ISOFORM 3).
FT VARSPLIC 273 273 MISSING (IN ISOFORM 2).
SO SEQUENCE 400 AA; 46571 MW; 88F14DA22A331A89 CRC64;

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Query Match 50.0%; Score 5; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3 APTQE 7
Db 358 APTQE 362

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RESULT 41
YLN2_CAEEL STANDARD; PRT; 415 AA.
ID YLN2_CAEEL STANDARD; PRT; 415 AA.
AC Q18964;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 46.2 KDA TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN
DE CHROMOSOME II.
GN D2013.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Mortimore B.;
RU Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z47808; CAAB7770.1; -
DR WormRep: D2013.2; CE00928.
DR InterPro: IPR000306; -
DR InterPro: IPR001680; -
DR Pfam: PF00400; WD40; 5.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PROSITE: PS00678; WD_REPEATS_1; 2.
DR PROSITE: PS00082; WD_REPEATS_2; 2.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KM Hypothetical protein; Repeat; WD repeat.
FT REPEAT 71 103 WD 1.

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FT REPEAT 119 148 WD 2.
FT REPEAT 202 232 WD 3.
FT REPEAT 373 403 WD 4.
SO SEQUENCE 415 AA; 46239 MW; 8927612C040F5E43 CRC64;

```

```

Query Match 50.0%; Score 5; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 PVAPT 5
Db 75 PVAPT 79

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```

RESULT 42
SCK_HUMAN STANDARD; PRT; 428 AA.
ID SCK_HUMAN STANDARD; PRT; 428 AA.
AC P98077;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE PROTEIN SCK (FRAGMENT).
DE SCK.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95090462; PubMed=7527937;
RA Kavanaugh W.M., Williams L.T.;
RT "An alternative to SH2 domains for binding tyrosine-phosphorylated
RT proteins."
RU Science 266:1862-1865(1994).
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN LIVER, ALSO PRESENT IN BRAIN.
CC -1- SIMILARITY: CONTAINS 1 PID DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: TO SHC TRANSFORMING PROTEINS.
DE HSSP: P29353; IMIL.
DR InterPro: IPR000050; -
DR InterPro: IPR000980; -
DR Pfam: PF00640; PID; 1.
DR Pfam: PF00017; SH2; 1.
DR PROSITE: PS01179; PID; 1.
DR PROSITE: PS50001; SH2; 1.
KW SH2 domain.
FT NON_TER 1 1
FT DOMAIN 34 216 PID.
FT DOMAIN 374 >428 SH2.
FT NON_TER 428 428
SO SEQUENCE 428 AA; 46522 MW; D19A3FDECCB1BC6 CRC64;

```

```

Query Match 50.0%; Score 5; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 PVAPT 5
Db 361 PVAPT 365

```

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RESULT 43
GLM_HELPJ STANDARD; PRT; 445 AA.
ID GLM_HELPJ STANDARD; PRT; 445 AA.
AC Q92M22;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PHOSPHOGLYCOSAMINE MUTASE (EC 5.4.2.-).
GN GLM OR UREC OR JHP0070.
OS Helicobacter pylori J99 (Campylobacter pylori J99).

```

Db 180 PVAPT 184

RESULT 39

CYH2_HUMAN STANDARD; PRT; 400 AA.

AC 099418; 092958;

DT 15-JUL-1998 (Rel. 36, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CYTOSIN 2 (ARF NUCLEOTIDE-BINDING SITE OPENER) (ARNO PROTEIN) (ARF EXCHANGE FACTOR).

GN PSCD2 OR ARNO.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=97100951; PubMed=8945478;

RA Charlin P., Paris S., Antony B., Robineau S., Bernaud-Dufour S., Jackson C.L., Chabre M.;

RT "A human exchange factor for ARF contains Sec7 and pleckstrin-homology domains.";

RL Nature 384:481-484(1996).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.

RC TISSUE=Brain;

RX MEDLINE=98079021; PubMed=9417041;

RA Frank S.F., Uppender S.K., Hansen S.H., Casanova J.E.;

RT "ARNO is a guanine nucleotide exchange factor for ADP-ribosylation factor 6.";

RL J. Biol. Chem. 273:23-27(1998).

RN (3)

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 51-252.

RX MEDLINE=98135767; PubMed=9476900;

RA Mossesova E., Gubis J.M., Goldberg J.;

RT "Structure of the guanine nucleotide exchange factor Sec7 domain of human ARNO and analysis of the interaction with ARF GTPase.";

RL Cell 92:415-423(1998).

RN (4)

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 51-252.

RX MEDLINE=98169075; PubMed=9510256;

RA Cherfils J., Menetrey J., Mathieu M., Le Bras G., Robineau S., Bernaud-Dufour S., Antony B., Chardin P.;

RT "Structure of the Sec7 domain of the Arf exchange factor ARNO.";

RL Nature 392:101-105(1998).

CC -1- FUNCTION: PROMOTES GUANINE-NUCLEOTIDE EXCHANGE ON ARF1, ARF3 AND ARF6. PROMOTES THE ACTIVATION OF ARF THROUGH REPLACEMENT OF GDP WITH GTP.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: UBIQUITOUS.

CC -1- SIMILARITY: CONTRAINS 1 SEC7 DOMAIN.

CC -1- SIMILARITY: CONTRAINS 1 PH DOMAIN.

CC -----

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CC -----

DR EMBL: X99753; CAA6084.1; -

DR EMBL: U70728; AAB09591.1; -

DR PDB: 1PBV; 09-MAR-99.

DR MIM: 602488; -

DR InterPro: IPR000904; -

DR InterPro: IPR001849; -

DR Pfam: PF00169; Pf; 1.

DR Pfam: PF01369; Sec7; 1.

DR PROSITE: PS50003; PH_DOMAIN: 1.

KW Guanine-nucleotide releasing factor; Coiled coil;

KW Alternative splicing; 3D-structure.

FT DOMAIN 10 63 COILED COIL (POTENTIAL).

FT DOMAIN 72 201 SEC7.

FT DOMAIN 259 376 PH.

FT VARSPIC 272 272 MISSING (IN ISOFORM 2).

SO SEQUENCE 400 AA; 46546 MW; 70441A58483BDOEI CRC64;

Query Match 50.0%; Score 5; DB 1; Length 400;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 APPOE 7

Db 358 APPOE 362

RESULT 40

CYH2_MOUSE STANDARD; PRT; 400 AA.

AC P97695; 089099;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CYTOSIN 2 (ARF NUCLEOTIDE-BINDING SITE OPENER) (ARNO PROTEIN) (CLM2) (SEC7 HOMOLOG B) (MSEC7-2).

GN PSCD2 OR SEC7B.

OS Mus musculus (Mouse), and

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090, 10116;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).

RC SPECIES=Mouse; TISSUE=Brain;

RX MEDLINE=98416066; PubMed=9744817;

RA Kim H.-S., Chen Y., Lonal P.;

RT "Complex regulation of multiple cytohesin-like genes in murine tissues and cells.";

RL FEBS Lett. 433:312-316(1998).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC SPECIES=Mouse;

RX Liu D., Zhang H., Lu J.;

RT "cDNA cloning of mouse cytohesin-2 and demonstration of its association with the integrin beta2 subunit.";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RN (3)

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC SPECIES=Rat;

RX PubMed=9352219;

RA Telemakos I., Benschel F., Stenius K., Sudhof T.C., Brose N.;

RL Eur. J. Cell Biol. 74:143-149(1997).

CC -1- FUNCTION: PROMOTES GUANINE-NUCLEOTIDE EXCHANGE ON ARF1, ARF3 AND ARF6. PROMOTES THE ACTIVATION OF ARF THROUGH REPLACEMENT OF GDP WITH GTP.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1/CLM2-A (SHOWN HERE), 2 AND 3/CLM2-B; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: PRESENT IN ALL TISSUES TESTED, WITH HIGHEST PROTEIN LEVELS IN BRAIN AND ADRENAL.

CC -1- SIMILARITY: CONTRAINS 1 SEC7 DOMAIN.

CC -1- SIMILARITY: CONTRAINS 1 PH DOMAIN.

CC -----

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Query Match 50.0%; Score 5; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPTO 6
|||||
DB 67 VAPTO 71

RESULT 37
GAG_HV1W2 STANDARD; PRT: 388 AA.
ID GAG_HV1W2
AC P05889;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-FEB-1994 (rel. 28, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P17, P24, P2, P7, P1, P6]
DE (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11705;
RN [1]
RP MEDLINE=6635450; PubMed=3012778;
RX Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salhuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS".
RL Science 233:1548-1553(1986).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES; SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC
CC -----
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CC -----
CC
CC EMBL: K03457; AAB12988.1; -
CC HSSP: P05888; IAA.
CC HIV: K03457; GAGSWMJ2.
CC InterPro: IPR000071; -
CC InterPro: IPR000721; -
CC Pfam: PF00540; gag_p17; 1.
CC Pfam: PF00607; gag_p24; 1.
CC AIDS: Core protein; Polyprotein; Myristate; Phosphorylation;
CC Zinc-finger.
CC
CC INIT_MER 0 0
CC CHAIN 1 131 BY SIMILARITY.
CC CHAIN 132 362 CORE PROTEIN P17 (MATRIX PROTEIN).
CC CHAIN 363 376 CORE PROTEIN P24 (CORE ANTIGEN).
CC CHAIN 377 >388 CORE PROTEIN P2.
CC CHAIN 377 >388 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
CC LIPID 1 1 MYRISTATE (BY SIMILARITY).
CC NON_TER 388 388
CC SEQUENCE 388 AA; 43314 MW; EF885BE10ECF7804 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 TOEVK 9
|||||
DB 309 TOEVK 313

RESULT 38
THAB_PAROL STANDARD; PRT: 391 AA.
ID THAB_PAROL
AC Q91242;
DT 15-JUL-1999 (rel. 38, Created)
DT 15-JUL-1999 (rel. 38, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE THYROID HORMONE RECEPTOR ALPHA B (THR-ALPHA-B).
GN THRA2 OR NR1A1-B.
OS Parathyroid hormone-related protein (PTHrP).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthopterygii; Acanthopterygii; Perciformes; Pleuronectiformes;
OC Pleuronectidae; Bothidae; Paralichthys.
OX NCBI_Taxid=8235;
RN [1]
RP MEDLINE=95008408; PubMed=7923940;
RX Yamano K., Araki K., Sekikawa K., Inui Y.;
RT "Cloning of thyroid hormone receptor genes expressed in metamorphosing
RT flounder".
RL Dev. Genet. 15:378-382(1994).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR TRIIODOTHYRONINE.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
CC
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC
CC EMBL: D16463; BAA03929.1; -
CC InterPro: IPR000324; -
CC InterPro: IPR000536; -
CC InterPro: IPR001628; -
CC InterPro: IPR001723; -
CC InterPro: IPR001728; -
CC Pfam: PF00104; hormone_rec; 1.
CC Pfam: PF00105; zf-C4; 1.
CC PRINTS: PRO0047; STROIDFINGER.
CC PRINTS: PRO0350; VITAMINDR.
CC PRINTS: PRO0398; STPDHORMNR.
CC PRINTS: PRO0546; THYROIDHORMR.
CC PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Multigene family.
CC
CC DOMAIN 1 32 MODULATING.
CC DNA_BIND 33 100 NUCLEAR RECEPTOR-TYPE.
CC ZN_FING 33 53 CA-TYPE.
CC ZN_FING 71 95 CA-TYPE.
CC DOMAIN 150 391 LIGAND-BINDING.
CC SEQUENCE 391 AA; 45055 MW; 19FB8631EE63D022 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PVAPT 5
|||||

CC Viruses: dsRNA viruses; Recoviridae; Orthoreovirus.
OX NCBI_TaxID=10885;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88072071; PubMed=3686825;
RA Wiener J.R., Joklik W.K.;
RT "Comparison of the reovirus serotype 1, 2, and 3 S3 genome segments
encoding the nonstructural protein sigma NS.";
RL Virology 161:332-339(1987).
CC -1- FUNCTION: THIS PROTEIN HAS A POLY(C)-DEPENDENT POLY(C) POLYMERASE
ACTIVITY, AND BINDS SINGLE-STRANDED, BUT NOT DOUBLE-STRANDED, RNA.
CC -----
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CC -----
DR EMBL: M18390; AAA47282.1; -
DR PIR: B27401; MNXRT2.
DR InterPro: IPR002507; -
DR Pfam: PF01518; PolyG_pol; 1.
KW Core protein; RNA-binding; Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 366 AA; 41334 MW; EF9202C3A6FC5085 CRC64;

OY 1 PVAPT 5
| | | | |
DB 189 PVAPT 193

Query Match 50.0%; Score 5; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 35
RRPO_REOVL
ID RRPO_REOVL STANDARD; PRT; 366 AA.
AC P07940;
DT 01-AUG-1988 (rel. 08; Created)
DT 01-AUG-1988 (rel. 08; Last sequence update)
DT 15-JUL-1998 (rel. 36; Last annotation update)
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (SIGMA NS PROTEIN) (CORE
DE PROTEIN) (RNA-BINDING PROTEIN).
GN S3.
OS Reovirus (type 1 / strain Lang).
OC Viruses; dsRNA viruses; Recoviridae; Orthoreovirus.
OX NCBI_TaxID=10884;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87025802; PubMed=3767989;
RA George C.X., Atwater J.A., Samuel C.E.;
RT "Biosynthesis of reovirus-specified polypeptides. Molecular cDNA
cloning and nucleotide sequence of the reovirus serotype 1 Lang
strain S3 mRNA which encodes the nonstructural RNA-binding protein
sigma NS.";
RL Biochem. Biophys. Res. Commun. 139:845-851(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88072071; PubMed=3686825;
RA Wiener J.R., Joklik W.K.;
RT "Comparison of the reovirus serotype 1, 2, and 3 S3 genome segments
encoding the nonstructural protein sigma NS.";
RL Virology 161:332-339(1987).
CC -1- FUNCTION: THIS PROTEIN HAS A POLY(C)-DEPENDENT POLY(C) POLYMERASE
ACTIVITY, AND BINDS SINGLE-STRANDED, BUT NOT DOUBLE-STRANDED, RNA.
CC -----
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CC -----
DR EMBL: M14325; AAA47273.1; -
DR EMBL: M18389; AAA47281.1; -
DR PIR: A25068; MNXRT.
DR InterPro: IPR002507; -
DR Pfam: PF01518; PolyG_pol; 1.
KW Core protein; RNA-binding; Transferase; RNA-directed RNA polymerase.
FT CONFLICT 250 250 V -> I (IN REF. 2).
SQ SEQUENCE 366 AA; 41188 MW; B9172A6A9251CC9A CRC64;

OY 1 PVAPT 5
| | | | |
DB 189 PVAPT 193

Query Match 50.0%; Score 5; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 36
ND1M_PODAN
ID ND1M_PODAN STANDARD; PRT; 367 AA.
AC P19041;
DT 01-NOV-1990 (rel. 16; Created)
DT 01-JUL-1993 (rel. 26; Last sequence update)
DT 15-JUL-1999 (rel. 38; Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
GN ND1.
OS Podospora anserina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Podospora.
OX NCBI_TaxID=5145;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S, AND A;
RX MEDLINE=89063443; PubMed=3197134;
RA Cummings D.J., Domenico J.M., Michel F.;
RT "DNA sequence and organization of the mitochondrial ND1 gene from
Podospora anserina: analysis of alternate splice sites.";
RL Curr. Genet. 14:253-264(1988).
RN [2]
RP COMPLETE GENOME.
RC STRAIN-S;
RX MEDLINE=90291512; PubMed=2357736;
RA Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;
RT "The complete DNA sequence of the mitochondrial genome of Podospora
anserina.";
RL Curr. Genet. 17:375-402(1990).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC -----
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CC -----
DR EMBL: X55026; CA38809.1; -
DR EMBL: X13164; CA31563.1; ALT-SEQ.
DR PIR: S06058; S06058.
DR InterPro: IPR001694; -
DR Pfam: PF00146; NADHdh; 1.
DR PROSITE: PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE: PS00668; COMPLEX1_ND1_2; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 367 AA; 41079 MW; 3AFC9D186EB25C2C CRC64;

OY 1 PVAPT 5
 |||||
 Db 284 PVAPT 288

RESULT 32
 WNT2_CAEL STANDARD; PRT; 360 AA.
 ID WNT2_CAEL
 AC P34889;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE WNT-2 PROTEIN PRECURSOR.
 GN WNT-2 OR CWN-2 OR W01B6.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=93288400; PubMed=8510930;
 RA Shachleford G.M., Shivakumar S., Shue L., Mason J., Kenyon C.,
 RA Varmus H.E.;
 RT "Two wnt genes in Caenorhabditis elegans";
 RL Oncogene 8:1857-1864(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Coles L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
 CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
 CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
 CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
 CC EXTRACELLULAR MATRIX.
 CC -1- DEVELOPMENTAL STAGE: DETECTED IN ALL LARVAL FORMS AND ADULTS,
 CC BUT IS MOST ABUNDANT IN THE EMBRYONIC STAGE.
 CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
 CC -----
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 CC -----
 DR EMBL: X72943; CA51448.1; -;
 DR EMBL: Z68301; CA92624.1; -;
 DR PIR: S32695; S32695.
 DR WormBep: W01B6.1; CE03753.
 DR InterPro: IPR000970; -;
 DR Pfam: PF00110; Wnt; 1.
 DR PROSITE: PS00246; WNT1; 1.
 KM Developmental protein: Glycoprotein: Signal.
 FT SIGNAL 1 37
 FT CHAIN 1 360
 FT CARBOHYD 90 360
 FT CARBOHYD 352 360
 FT CONFLICT 73 73
 FT CONFLICT 186 186
 FT CONFLICT 221 221
 FT CONFLICT 229 230
 FT CONFLICT 333 335
 FT SEQUENCE 360 AA; 40551 MW; E4A6EAFB2A710E46 CRC64;
 OY 5 TOEVK 9

Db 328 TOEVK 332
 |||||

RESULT 33
 RRPO_REOV STANDARD; PRT; 366 AA.
 ID RRPO_REOV
 AC P03526;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (SIGMA NS PROTEIN) (CORE
 DE PROTEIN) (RNA-BINDING PROTEIN).
 GN S3.
 OS Reovirus (type 3 / strain Deering).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 OX NCBI_TaxID=10886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84015379; PubMed=6312421;
 RA Richardson M.A., Furutachi Y.;
 RT "Nucleotide sequence of reovirus genome segment S3, encoding non-
 RT structural protein sigma NS";
 RL Nucleic Acids Res. 11:6399-6408(1983).
 RN [2]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE=83017876; PubMed=6927854;
 RA Antczak J.B., Chmelo R.A., Pickup D.J., Joklik W.K.;
 RT "Sequence at both termini of the 10 genes of reovirus serotype 3
 RT (strain Deering).";
 RL Virology 121:307-319(1982).
 CC -1- FUNCTION: THIS PROTEIN HAS A POLY(C)-DEPENDENT POLY(G) POLYMERASE
 CC ACTIVITY, AND BINDS SINGLE-STRANDED, BUT NOT DOUBLE-STRANDED, RNA.
 CC -1- SIMILARITY: 86.3% SIMILARITY TO REOVIRUS SEROTYPE 2 SIGMA NS
 CC PROTEIN.
 CC -----
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 CC -----
 DR EMBL: X01627; CA25768.1; -;
 DR EMBL: J02330; AAA47280.1; -;
 DR PIR: A04126; MNXRS.
 DR InterPro: IPR002507; -;
 DR Pfam: PF01518; PolyG_Pol; 1.
 KM Core protein: RNA-binding: Transferase: RNA-directed RNA polymerase.
 SQ SEQUENCE 366 AA; 41056 MW; 201A6223C4290D7D CRC64;
 OY 1 PVAPT 5
 |||||
 Db 189 PVAPT 193

Query Match 50.0%; Score 5; DB 1; Length 366;
 Best Local Similarity 100.0%; Pred. No. 1, le=02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 34
 RRPO_REOV STANDARD; PRT; 366 AA.
 ID RRPO_REOV
 AC P12002;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (SIGMA NS PROTEIN) (CORE
 DE PROTEIN) (RNA-BINDING PROTEIN).
 GN S3.
 OS Reovirus (type 2 / strain D5/Jones).


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RT      "Purification of two thermostable components of messenger
RT      ribonucleoprotein particles (mrnp) from Xenopus laevis oocytes,
RT      belonging to a novel class of RNA-binding proteins."
RL      FEBS Lett. 282:110-114(1991).
CC      -1- FUNCTION: BINDS TO CCAAT-CONTAINING 5' BOX OF THE HSP70 GENES.
CC      SEEMS TO BE A NEGATIVE REGULATORY FACTOR. ALSO BINDS TO MRNA.
CC      -1- SUBUNIT: POSSIBLY FORMS A HETERODIMER WITH P54 IN THE 6S AND 15S
CC      MRNA-BINDING PARTICLES.
CC      -1- SUBCELLULAR LOCATION: CYTOPLASMIC, EITHER FREE OR ASSOCIATED WITH
CC      RIBONUCLEOPROTEIN PARTICLES.
CC      -1- TISSUE SPECIFICITY: TESTIS AND IMMATURE OOCYTES.
CC      -1- PTM: PHOSPHORYLATION ACTIVATES IN VITRO RNA-BINDING.
CC      -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
CC      -----
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CC      -----
DR      EMBL: M59454; AAA49716.1; -.
DR      PTR: B38274; B38274.
DR      HSSP: P33081; INMG.
DR      TRANSFAC: T00294; -.
DR      InterPro: IPR002059; -.
DR      Pfam: PF00313; CSD. 1.
DR      PRINTS: PR00050; COLDSHOCK.
DR      PROSITE: PS00352; COLD_SHOCK. 1.
DR      KMW: Transcription regulation; DNA-binding; Nuclear protein;
DR      RNA-binding; Phosphorylation.
FT      DOMAIN 44 108 CSD.
FT      COMPACT 254 254 A -> T (IN REF. 1).
SQ      SEQUENCE 336 AA; 37202 MW; 4AD5838769C6B84D CRC64;

Query Match          50.0%; Score 5; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 PVAPT 5
        |||||
Db      207 PVAPT 211

RESULT 30
TRPA_MAIZE          STANDARD;          PRT;          346 AA.
AC      P42390;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      TRYPTOPHAN SYNTHASE ALPHA CHAIN PRECURSOR (EC 4.2.1.20).
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
OC      Andropogoneae; Zea.
OX      NCBI_TaxID=4577;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. CG000237;
RX      MEDLINE=95284367; PubMed=7766899;
RA      Kramer V.C., Kozlowski M.G.;
RT      *Structure of a maize tryptophan synthase alpha subunit gene with
RT      pth enhanced expression.
RL      Plant Mol. Biol. 27:1183-1188(1995).
CC      -1- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE
CC      OF INDOLEGLYCEROL PHOSPHATE TO INDOLE AND GLYCERALDEHYDE 3-
CC      PHOSPHATE.
CC      -1- CATALYTIC ACTIVITY: L-SERINE + 1-(INDOL-3-YL)GLYCEROL 3-PHOSPHATE
CC      = L-TRYPTOPHAN + GLYCERALDEHYDE 3-PHOSPHATE + H(2)O.
CC      -1- PATHWAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

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CC      -1- SUBUNIT: Tetramer of two alpha and two beta chains.
CC      -1- SUBCELLULAR LOCATION: CHLOROPLAST (PROBABLE).
CC      -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC      -----
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CC      -----
DR      EMBL: X76713; CAA54131.1; -.
DR      HSSP: P00929; 2TSY.
DR      MAlzDB: 102199; -.
DR      InterPro: IPR002028; -.
DR      Pfam: PF00290; TRP-synta. 1.
DR      PROSITE: PS00167; TRP-SYNTHASE ALPHA; 1.
DR      TRYPTOPHAN biosynthesis; Lyase; Chloroplast; Transl. peptide.
FT      TRANSIT 1 346 ? CHLOROPLAST (POTENTIAL).
FT      CHAIN 1 346 TRYPTOPHAN SYNTHASE ALPHA CHAIN.
SQ      SEQUENCE 346 AA; 36967 MW; 05F8FC2635071F3E CRC64;

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Query Match          50.0%; Score 5; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 QEVKK 10
        |||||
Db      278 QEVKK 282

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RESULT 31
YMA3_MYCBO          STANDARD;          PRT;          354 AA.
ID      YMA3_MYCBO
AC      Q02279;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      HYPOTHETICAL 38.1 KDA PROTEIN IN MAS 3 REGION.
OS      Mycobacterium bovis.
OC      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX      NCBI_TaxID=1765;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BCG;
RX      MEDLINE=92406887; PubMed=1527058;
RA      Mathur M., Kolatukudy P.E.;
RT      *Molecular cloning and sequencing of the gene for mycocerosic acid
RT      synthase, a novel fatty acid elongating multifunctional enzyme, from
RT      Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guérin.
RL      J. Biol. Chem. 267:19388-19395(1992).
CC      -1- SIMILARITY: SOME, TO M.TUBERCULOSIS RV2285.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M95808; AAA25370.1; -.
DR      KMW: Hypothetical protein.
SQ      SEQUENCE 354 AA; 37956 MW; 2C77C1259BD3686A CRC64;

Query Match          50.0%; Score 5; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CC -1- SUBCELLULAR LOCATION: PEROXISOMAL.
CC -1- SIMILARITY: BELONGS TO THE URICASE FAMILY.
CC -----
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CC -----
DR EMBL: M10594; AAA3994.1; -.
DR EMBL: AB002807; BAA19670.1; -.
DR EMBL: AB002809; BAA19672.1; -.
DR Mendel: 16776; Glyma:1087; nm16776.
DR InterPro: IPR002042; -.
DR Pfam: PF01014; URICase; 1.
DR PRINTS: PR00093; URICASE.
DR PROSITE: PS00366; URICASE; 1.
DR PROSITE: PS00342; MICROBODIES_CTER; 1.
DR Oxidoreductase; Peroxisome; Purine metabolism.
FT CONFLICT 208 L->F (IN REF.1).
SQ SEQUENCE 309 AA: 35137 MW: 8188F8F7ACAA00A9 CRC64:

Query Match
Best Local Similarity 50.0%; Score 5; DB 1; Length 309;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
DB 215 QEVKK 219

RESULT 28
ENT2_MOUSE STANDARD; PRT; 327 AA.
AC 061672;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 2 (EQUILIBRATIVE
DE NITROBENZYLMECAPTOPURINE RIBOSIDE-INSENSITIVE NUCLEOSIDE TRANSPORTER)
DE (EQUILIBRATIVE NEMPR-INSENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE
DE TRANSPORTER, EI-TYPE) (36 KDA NUCLEOLAR PROTEIN HNP36) (HYDROPHOBIC
DE NUCLEOLAR PROTEIN, 36 KDA) (DELAYED-EARLY RESPONSE PROTEIN 12).
GN SLC29A2 OR ENT2 OR HNP36 OR DER12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Fibroblast;
RX MEDLINE=95367016; PubMed=7639753;
RA Williams J.B., Lanahan A.A.;
RT "A mammalian delayed-early response gene encodes HNP36, a novel,
RT conserved nucleolar protein."
RL Biochem. Biophys. Res. Commun. 213:325-333(1995).
CC -1- FUNCTION: MEDIATES EQUILIBRATIVE TRANSPORT OF PURINE AND
CC PYRIMIDINE NUCLEOSIDES, AND THE PURINE BASE HYPOXANTHINE.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR. INTEGRAL MEMBRANE
CC PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM AND A SHORT
CC FORM/HNP36 (SHOWN HERE); SEEMS TO BE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- INDUCTION: BY PLATELET DERIVED GROWTH FACTOR (PDGF) AND FIBROBLAST
CC GROWTH FACTOR (bFGF).
CC -1- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS.
CC -----
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CC -----
DR EMBL: X86682; CAA60381.1; -.
DR MGD: MGI:1345278; SLC29a2.
DR InterPro: IPR002259; -.
DR Pfam: PF01733; Nucleoside tran. 1.
DR PRINTS: PRO1130; DERENTRNSPT.
KW Nucleic protein; Transmembrane; Transport; Alternative splicing.
FT TRANSMEM 2
FT TRANSMEM 22 POTENTIAL.
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 194 214 POTENTIAL.
FT TRANSMEM 231 251 POTENTIAL.
FT TRANSMEM 267 287 POTENTIAL.
FT TRANSMEM 303 323 POTENTIAL.
SQ SEQUENCE 327 AA: 36113 MW: 5D2D3FF4BBD592B6 CRC64:

Query Match
Best Local Similarity 50.0%; Score 5; DB 1; Length 327;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 APQIE 7
DB 100 APQIE 104

RESULT 29
YB56_XENLA STANDARD; PRT; 336 AA.
ID YB56_XENLA
AC P21574;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CYTOPLASMIC RNA-BINDING PROTEIN p56 (Y BOX BINDING PROTEIN-2) (Y-BOX
DE TRANSCRIPTION FACTOR) (MRNP4).
GN FRG12.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91062413; PubMed=2247479;
RA Tafuri S.R., Wolffe A.P.;
RT "Xenopus Y-box transcription factors: molecular cloning, functional,
RT analysis and developmental regulation."
RL Proc. Natl. Acad. Sci. U.S.A. 87:9028-9032(1990).
RN [2]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=92107999; PubMed=1729676;
RA Murray M.T., Schiller D.L., Franke M.M.;
RT "Sequence analysis of cytoplasmic mRNA-binding proteins of Xenopus
RT oocytes identifies a family of RNA-binding proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 89:11-15(1992).
RN [3]
RP PARTIAL SEQUENCE.
RC TISSUE-Ovary;
RX MEDLINE=92332467; PubMed=1629179;
RA Deschamps S., Viel A., Garrigos M., Denis H., le Maire M.;
RT "MRNP4, a major mRNA-binding protein from Xenopus oocytes is
RT identical to transcription factor FRG Y2."
RL J. Biol. Chem. 267:13799-13802(1992).
RN [4]
RP PARTIAL SEQUENCE.
RC TISSUE-Ovary;
RX MEDLINE=91224309; PubMed=1902800;
RA Deschamps S., Viel A., Denis H., le Maire M.;

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FT CHAIN 64 255 MAJOR ENVELOPE PROTEIN E (POTENTIAL).
FT CHAIN 256 >309 NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 309 AA; 32922 MW; 6E858E9C3DDB9EA9 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
Db 113 PVAPT 117

RESULT 26
ID URIC_SOYBN STANDARD; PRT; 309 AA.
AC P04670; P34805; P93160; P93161; O04105;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE URICASE II ISOZYME 1 (EC 1.7.3.3) (URATE OXIDASE) (MODULIN 35) (N-35)
OS GLYCINE MAX (SOYBEAN).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_Taxid=3847;
ON 11
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PRIZE;
RA Suzuki H., Verma D.P.S.;
RT "Soybean node-specific uricase (nodulin-35) is expressed and
RT assembled into a functional tetrameric holoenzyme in Escherichia
RT coli."
RL Plant Physiol. 95:384-389(1991).
RN 12
RP SEQUENCE FROM N.A., AND SEQUENCE OF 245-262.
RC STRAIN=CV. PRIZE;
RA Nguyen T., Zelechowska M., Foster V., Bergmann H., Verma D.P.S.;
RT "Primary structure of the soybean nodulin-35 gene encoding uricase II
RT localized in the peroxisome of uninfected cells of nodules."
RL Proc. Natl. Acad. Sci. U.S.A. 82:5040-5044(1985).
RN 13
RP SEQUENCE FROM N.A.
RC STRAIN=CV. AKISENGOKU; TISSUE=Cotyledon, and Root nodules;
RA Takane K., Tanaka K., Tajima S., Okazaki K., Kouchi H.;
RT "Expression of uricase II gene (nodulin-35) in cotyledons of soybean
RT plants."
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN 14
RP SEQUENCE FROM N.A.
RC STRAIN=CV. AKISENGOKU; TISSUE=Root nodules;
RA Takane K., Tajima S., Kouchi H.;
RT "Two distinct uricase II (nodulin 35) genes are differentially
RT expressed in soybean plants."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS A SUBUNIT OF THE NODULE SPECIFIC URICASE.
CC -1- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O -> 5-HYDROXYISOURATE +
CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: PEROXISOMAL.
CC -1- INDUCTION: DURING NODULATION IN LEGUME ROOTS AFTER RHIZOBIUM
CC INFECTION.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.

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CC -1- SIMILARITY: BELONGS TO THE URICASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M63743; AAA33997.1; -
DR EMBL: M95400; AAA34019.1; -
DR EMBL: L00353; AAA33995.1; -
DR EMBL: D86929; BAA13184.1; -
DR EMBL: D86930; BAA13185.1; -
DR EMBL: AB002810; BAA19673.1; -
DR PIR: A25776; A25776.
DR Mendel; 13686; GLYMA;1087.1.
DR Mendel; 16777; GLYMA;1087;ma16777.
DR InterPro: IPR002042; -.
DR Pfam: PF01014; URICASE. 1.
DR PRINTS: PR00093; URICASE.
DR PROSITE: PS00366; URICASE. 1.
DR PROSITE: PS00342; MICROBODIES_CTER; 1.
KM Nodulation; Oxidoreductase; Peroxisome; Purine metabolism.
FT SITE 307 309 MICROBODY TARGETING SIGNAL (POTENTIAL).
FT VARIANT 3 3 O -> K (IN CV. AKISENGOKU).
FT VARIANT 235 235 S -> T.
FT CONFLICT 60 60 D -> E (IN REF. 2).
FT CONFLICT 195 195 Y -> C (IN REF. 4).
SQ SEQUENCE 309 AA; 35138 MW; 6FB2A758FBA9A982 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OEVRK 10
Db 215 OEVRK 219

RESULT 27
ID URID_SOYBN STANDARD; PRT; 309 AA.
AC O04104;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE URICASE II ISOZYME 2 (EC 1.7.3.3) (URATE OXIDASE) (MODULIN 35) (N-35)
OS GLYCINE MAX (SOYBEAN).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_Taxid=3847;
ON 11
RP SEQUENCE FROM N.A., AND SEQUENCE OF 245-262.
RC STRAIN=CV. DARE;
RA Nguyen T., Zelechowska M., Foster V., Bergmann H., Verma D.P.S.;
RT "Primary structure of the soybean nodulin-35 gene encoding uricase II
RT localized in the peroxisome of uninfected cells of nodules."
RL Proc. Natl. Acad. Sci. U.S.A. 82:5040-5044(1985).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=CV. AKISENGOKU; TISSUE=Root nodules;
RA Takane K., Tajima S., Kouchi H.;
RT "Two distinct uricase II (nodulin 35) genes are differentially
RT expressed in soybean plants."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O -> 5-HYDROXYISOURATE +
CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

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DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HYPOTHEICAL 33.5 KDA PROTEIN IN MRPS9-YSM1 INTERGENIC REGION.
 GN YBR147W OR YBR1124.
 OS Saccharomyces cerevisiae (baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 CC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C;
 RA Enlian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
 RA Nlegmann E., Schenk-Groeninger R., Servos J., Wehner E.,
 RA Wolter R., Brendel M., Bauer H., Braun H., Dern K., Duesterhus S.,
 RA Gruenbein R., Hedges D., Klesau P., Korol S., Krebs B., Proft M.,
 RA Slegers K., Baur A., Boles E., Miosga T.,
 RA Schaff-Gerstenschlaeger I., Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/Genbank/DBD databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: SOME, TO S.POMBE SPAC2E12.03C AND SPAC17C9.10.
 CC -----
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 CC -----
 CC EMBL: 236016; CAA85105.1; -
 DR PIR: S46018; S46018.
 DR SGD: S0000351; YBR147W.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 13 33 POTENTIAL.
 FT TRANSMEM 45 65 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 164 184 POTENTIAL.
 FT TRANSMEM 200 220 POTENTIAL.
 FT TRANSMEM 239 259 POTENTIAL.
 FT TRANSMEM 263 283 POTENTIAL.
 SQ SEQUENCE 296 AA: 33496 MW: 5065896a1BARB43 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 296;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYKK 10
 DB 103 OEYKK 107

RESULT 24
 LXD2_PHOLE STANDARD; PRT; 305 AA.
 AC Q06878;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ACYL TRANSFERASE (EC 2.3.1.-) (ACT) (MYRISTOYL-ACP-SPECIFIC
 DE THIOESTERASE).
 GN LUXD.
 OS Photobacterium leiognathl.
 CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
 CC Photobacterium.
 CC NCBI_TaxID=658;
 CC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=741;
 RX MEDLINE=9331531; PubMed=8472957;
 RA Chao Y.-F., Weng S.-F., Lin J.-W.;
 RT "Sequence of the luxD gene encoding acyltransferase of the lux operon
 RT from Photobacterium leiognathl.";
 RL Gene 126:155-156(1993).

CC -1- FUNCTION: ACYL TRANSFERASE IS PART OF THE FATTY ACID REDUCTASE
 CC SYSTEM REQUIRED FOR ALDEHYDE BIOSYNTHESIS. IT PRODUCES FATTY
 CC ACIDS FOR THE LUMINESCENT REACTION.
 CC -1- PATHWAY: FIRST STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
 CC COMPLEX.
 CC -----
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 CC -----
 CC EMBL: X65612; CAA46563.1; -
 DR PIR: JN0518; JN0518.
 DR HSP: P03521; ITHF.
 KW Luminescence; Transferase; Acyltransferase.
 SQ SEQUENCE 305 AA: 34384 MW: 0BDAA76D08913164 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 305;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYKK 10
 DB 219 OEYKK 223

RESULT 25
 POLG_HCVH7 STANDARD; PRT; 309 AA.
 AC P27955;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GENOME POLYPROTEIN (CONTAINS: MATRIX PROTEIN (ENVELOPE PROTEIN M);
 DE MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN NS1) (FRAGMENT).
 OS Hepatitis C virus (isolate HCV7) (HCV).
 OS Hepatitis C virus (isolate HCV7) (HCV).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 CC Hepacivirus.
 CC NCBI_TaxID=11109;
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91112009; PubMed=1846505;
 RA Weiner A.J., Brauer M.J., Rosenblatt J., Richman K.H., Tung J.,
 RA Crawford K., Bonino F., Saracco G., Choo Q.-L., Houghton M.,
 RA Han J.H.;
 RT "Variable and hypervariable domains are found in the regions of HCV
 RT pestivirus envelope glycoproteins";
 RT Virology 180:842-848(1991).
 RL -----
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 CC -----
 CC EMBL: X53133; CAA37293.1; -
 DR InterPro: IPR002519; -
 DR InterPro: IPR002521; -
 DR InterPro: IPR002531; -
 DR Pfam: PF01560; HCV_NSI; 1.
 DR Pfam: PF01542; HCV_Core; 1.
 DR Pfam: PF01539; HCV_Env; 1.
 KW Polyprotein; Glycoprotein; Coat protein; Envelope protein;
 KW Transmembrane; Nonstructural protein.
 FT NON_TER 1 63 MATRIX PROTEIN (POTENTIAL).
 FT CHAIN 1 63

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DR EMBL: U34816; AAC43647.1; -
DR EMBL: AE000017; AAB95803.1; -
KM Hypothetical protein.
SQ SEQUENCE 250 AA; 28662 MW; 4378A2834BBB7877 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 250;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OEYK 10
IIIIII
DB 24 OEYK 28

RESULT 21
CB24_ARATH STANDARD; PRT; 251 AA.
ID CS24_ARATH
AC P27521;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR (LHCI TYPE III CAB-4)
DE (LHCP).
DE CAB4 OR P1P2.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H., Hanley S., Goodman H.M.;
RT "Isolation, characterization and chromosomal location of a new cab
RT gene from Arabidopsis thaliana";
RL Plant Physiol. 96:1387-1388(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. COLUMBIA;
RA Chlajene N., Robert C., Brothier P., Catolico L.,
RA Chlajene F., Saurin W., Melsenbach J., Mewes H.-W., Lemcke K.,
RA Mayer K.F.X., Queller F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT
CC RECEPTOR. IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS
CC WITH WHICH IT IS CLOSELY ASSOCIATED. THE N-TERMINUS OF THE PROTEIN
CC EXTENDS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF
CC GRANUL MEMBRANES AND PHOTOREGULATED BY REVERSIBLE PHOSPHORYLATION
CC OF ITS THREONINE RESIDUES. BOTH ARE BELIEVED TO MEDIATE THE
CC DISTRIBUTION OF EXCITATION ENERGY BETWEEN PHOTOSYSTEMS I AND II.
CC -1- SUBUNIT: THE LHC COMPLEX CONSISTS OF CHLOROPHYLLS (A & B) AND
CC CHLOROPHYLL A-B BINDING PROTEINS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
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KM Transmembrane: Phosphorylation.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN 2 251 CHLOROPHYLL A-B BINDING PROTEIN 4.
FT TRANSMEM 211 227 POTENTIAL.
SQ SEQUENCE 251 AA; 27733 MW; DC8B390C2AED9D22 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTQE 7
IIIIII
DB 196 APTQE 200

RESULT 22
URED_SYNY3 STANDARD; PRT; 270 AA.
ID URED_SYNY3
AC P73047;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UREASE ACCESSORY PROTEIN URED.
DE URED OR SLI1639.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_Taxid=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions";
RL DNA Res. 3:109-136(1996)
CC -1- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.
CC -1- SIMILARITY: BELONGS TO THE URED FAMILY.
CC -----
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DR EMBL: D90903; BAA17068.1; ALT_INIT.
DR InterPro: IPR002669; -
DR Pfam: PF01774; Ured; 1.
KM Nickel.
SQ SEQUENCE 270 AA; 30522 MW; FAA820E257B69286 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEYK 9
IIIIII
DB 254 TOEYK 258

RESULT 23
YB27_YEAST STANDARD; PRT; 296 AA.
ID YB27_YEAST
AC P38278;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

RP SEQUENCE.
 RX MEDLINE=88000549; PubMed=3307909;
 RA Dunbar J.C., Bradshaw R.A.;
 RT "Amino acid sequence of guinea pig prostate kallikrein.";
 RL Biochemistry 26:3471-3478(1987).
 CC -1- FUNCTION: GLANDULAR KALLIKEINS CLEAVE MET-LYS AND ARG-SER BONDS
 CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-1-XAA BONDS IN
 CC SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE
 CC KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS OF
 CC MET-1-XAA OR LEU-1-XAA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY. KALLIKREIN SUBFAMILY.
 DR PIR: A27207; A27207.
 DR HSSP: P00757; 1SGF.
 DR MEROPS: S01.160; -.
 DR InterPro: IPR001254; -.
 DR InterPro: IPR001314; -.
 DR Pfam: PF000089; TRYPSIN_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PROSITE: PS00134; TRYPsin_HIS_1.
 DR PROSITE: PS00135; TRYPsin_SER_1.
 KM Hydrolyse; Serine protease; Kininogenase; Glycoprotein.
 FT ACT_SITE 41 41 CHARGE RELAY SYSTEM.
 FT ACT_SITE 96 96 CHARGE RELAY SYSTEM.
 FT ACT_SITE 191 191 CHARGE RELAY SYSTEM.
 FT CARBOHD 78 78 N-LINKED (GLCNAC. . .).
 FT CARBOHD 169 169 N-LINKED (GLCNAC. . .).
 FT DISULFD 7 151 BY SIMILARITY.
 FT DISULFD 26 42 BY SIMILARITY.
 FT DISULFD 128 197 BY SIMILARITY.
 FT DISULFD 162 176 BY SIMILARITY.
 FT DISULFD 187 212 BY SIMILARITY.
 FT VARIANT 50 50 K -> W.
 SQ SEQUENCE 239 AA: 25969 MW: 56DC81BC10D49A64 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PROEV 8
 DB 118 PROEV 122
 RESULT 19
 Y984_CAMJE STANDARD; PRT; 246 AA.
 AC P45491; G9PNV5;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL PROTEIN CJO984.
 GN CJO984.
 OS Campylobacter jejuni.
 CC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 CC Campylobacter.
 CC NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43431;
 RX MEDLINE=95247673; PubMed=7730270;
 RA Hani E.K., Chan V.L.;
 RT "Expression and characterization of Campylobacter jejuni
 RT benzoylglycine amidohydrolase (Hipuricase) gene in Escherichia
 RT coli.";
 RL J. Bacteriol. 177:2396-2402(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIC 11168;
 RX MEDLINE=20150912; PubMed=10688204;
 RA Parthill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

RA Basham D., Chillingworth T., Davies R.M., Felwell T., Holtroyd S.,
 RA Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vleet A.H.M.,
 RA Whitehead S., Barrett B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 CC -----
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 CC -----
 DR EMBL: Z6940; CAA85397.1; -.
 DR EMBL: AL139076; CAB73240.1; -.
 KM Hypothetical protein.
 FT CONFLICT 16 16 V -> T (IN REF. 1).
 FT CONFLICT 21 21 N -> D (IN REF. 1).
 FT CONFLICT 42 42 E -> G (IN REF. 1).
 FT CONFLICT 51 51 Q -> K (IN REF. 1).
 FT CONFLICT 118 118 I -> V (IN REF. 1).
 FT CONFLICT 160 160 E -> K (IN REF. 1).
 FT CONFLICT 212 212 V -> I (IN REF. 1).
 SQ SEQUENCE 246 AA: 28820 MW: 378876C1703D70CF CRC64;

Query Match 50.0%; Score 5; DB 1; Length 246;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 APTOE 7
 DB 75 APTOE 79
 RESULT 20
 YG87_MYCPN STANDARD; PRT; 250 AA.
 ID YG87_MYCPN
 AC Q50315;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL PROTEIN MPN687 (K05_ORF250).
 GN MPN687 OR MP155.
 OS Mycoplasma pneumoniae.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 CC Mycoplasmataceae; Mycoplasma.
 CC NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=96177562; PubMed=8604303;
 RA Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
 RT "Sequence analysis of 56 kb from the genome of the bacterium
 RT Mycoplasma pneumoniae comprising the dna region, the atp operon and a
 RT cluster of ribosomal protein genes.";
 RL Nucleic Acids Res. 24:628-639(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97103885; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
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RL Nucleic Acids Res. 18:3069-3069(1990).
RP [2]
RN SEQUENCE OF 203-217 FROM N.A.
RC STRAIN-TAK:
RX MEDLINE-89345113; PubMed-2762136;
RA Plenlazez N.J., Velarde J. Jr., Plenlazez D., Luftig R.B.;
RT "Nucleotide sequence of human enteric adenovirus type 41 hexon-
associated protein VIII precursor (pVIII) including the early region
E3 promoter."
RL Nucleic Acids Res. 17:5398-5398(1989).
-----
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CC -----
DR EMBL: X52532; CAB38632.1; -.
DR EMBL: X15137; CAA33236.1; -.
DR PIR: S04851; S04851.
DR PIR: S10212; S10212.
KM Late protein; Phosphorylation.
SQ SEQUENCE 217 AA; 24740 MW; B6ECDAB63C24EC3E CRC64;

Query Match 50.0%; Score 5; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
Db 118 PVAPT 122

RESULT 16
ID YD67_SCHPO STANDARD; PRT; 217 AA.
AC 010319;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 24.9 KDA PROTEIN C17G8.07 IN CHROMOSOME 1.
GN SPAC17G8.07.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO HUMAN AFG AND ENL AND YEAST TRANSCRIPTION
CC INITIATION FACTOR TFIIF SMALL SUBUNIT (TFG3/NC1).
CC -1- SIMILARITY: STRONG. TO YEAST YNL107M.
-----
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CC -----
DR EMBL: Z69795; CAA93690.1; -.
KM Hypothetical protein.
SQ SEQUENCE 217 AA; 24946 MW; A274C2AFB0620D7F CRC64;

Query Match 50.0%; Score 5; DB 1; Length 217;

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Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QEVKK 10
Db 191 QEVKK 195;

RESULT 17
ID TRKA_PYRHO STANDARD; PRT; 228 AA.
AC 057719;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKA HOMOLOG.
GN TRKA OR PH1984.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Pyrococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE-98344137; PubMed-9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kusida N., Oguchi A.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: PART OF A POTASSIUM TRANSPORT SYSTEM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRKA FAMILY.
-----
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CC -----
DR EMBL: AP000007; BAA3111.1; -.
KM Transport; Potassium transport; NAD.
FT NP_BIND 2 NAD (POTENTIAL).
SQ SEQUENCE 228 AA; 25323 MW; F64E2D1AEEF3FDD6 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QEVKK 10
Db 215 QEVKK 219

RESULT 18
ID KUK2_CAVPO STANDARD; PRT; 239 AA.
AC P12323;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GRANDULAR KALLIKREIN, PROSTATIC (EC 3.4.21.35) (TISSUE KALLIKREIN)
DE (PROSTATE ESTERASE).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]

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CC -----
CC EMBL: M13821; AAA8544.1; -
CC PIR: A24499; IMPSB; -
CC SEQUENCE 201 AA; 22087 MW; 25C0694D288FDAAB CRC64;
DR
SQ
Query Match
Best Local Similarity 100.0%; Score 5; DB 1; Length 201;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 PROEV 8
DB 156 PROEV 160
RESULT 13
VAD1_TREPA STANDARD; PRT; 206 AA.
ID VAD1_TREPA
AC 083443;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE V-TYPE ATP SYNTHASE SUBUNIT D 1 (EC 3.6.1.34) (V-TYPE ATPASE SUBUNIT D
DE 1).
GN ATPD1 OR TP0428.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
CC NCB1_TaxID=160;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Morris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardam J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Childsbaram M., Uterback T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete."
RL Science 281:375-388(1998).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE V-ATPASE D SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL: AE001220; AAC65414.1; -
CC TIGR: TP0428; -
DR InterPro: IPR002699; -
DR Pfam: PF01813; ATP-synt_D; 1.
KM Hydrolyase; ATP synthetase; Hydrogen ion transport.
SQ SEQUENCE 206 AA; 23803 MW; BC33C36FC5795483 CRC64;
Query Match
Best Local Similarity 100.0%; Score 5; DB 1; Length 206;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 6 OEYKK 10
DB 80 OEYKK 84
RESULT 14
VG40_BPPH8 STANDARD; PRT; 209 AA.
ID VG40_BPPH8
AC P14817; P14818;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PROTEINS 40A/40B.
GN 40.
OS Bacteriophage phi-80.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
OC Lambda phage group.
OX NCB1_TaxID=10713;
RN [1]
RX MEDLINE=89011978; PubMed=3172225;
RA Ogawa T., Ogawa H., Tomizawa J.;
RT "Organization of the early region of bacteriophage phi 80. Genes and
RT proteins."
RL J. Mol. Biol. 202:537-550(1988).
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CC -----
CC EMBL: X13065; CAA31470.1; -
CC EMBL: X13065; CAA31469.1; -
DR PIR: S04827; S04827.
DR PIR: S04826; S04826.
KM Early protein.
FT CHAIN 1 209 PROTEIN 40A.
FT CHAIN 1 209 PROTEIN 40B.
SQ SEQUENCE 209 AA; 22974 MW; DD399BA02E7643D CRC64;
Query Match
Best Local Similarity 100.0%; Score 5; DB 1; Length 209;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 TOEVK 9
DB 59 TOEVK 63
RESULT 15
V33P_ADEA1 STANDARD; PRT; 217 AA.
ID V33P_ADEA1
AC P19416; Q64818;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE 33 KDA PHOSPHOPROTEIN.
OS Human adenovirus type 41.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCB1_TaxID=10524;
RN [1]
RX MEDLINE=90272433; PubMed=2349115;
RA Siemenda S.B., Pieniazek N.J., Velarde J. Jr., Pieniazek D.,
RA Lufg R.B.;
RT "Nucleotide sequence of the region coding for 100K and 33K proteins
RT of human enteric adenovirus type 41 (Tak).";

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CC -----
DR EMBL: AE001604: AAD18337.1; -.
DR EMBL: AE002217: AAF8402.1; -.
DR EMBL: AP002545: BAA98394.1; -.
DR TIGR: CP0584; -.
DR InterPro: IPR001059; -.
DR Pfam: PF01132; EFP: 1.
DR PROSITE: PS01275; EFP: 1.
KM Protein biosynthesis; Elongation factor.
SQ SEQUENCE 185 AA; 20673 MW; 6C6432CFB70354A CRC64;

Query Match
Best Local Similarity 50.0%; Score 5; DB 1; Length 185;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QYEVK 9
    |||||
DB 57 QYEVK 61

RESULT 10
VGG_BPPHK STANDARD; PRT; 187 AA.
AC Q38042;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MAJOR SPIKE PROTEIN (G PROTEIN) (GPG).
G.
OS Bacteriophage phi-K.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10848;
RN [1]
RP SEQUENCE FROM N.A.
RA Kodaira K.-I., Tadokoro H., Suzuki K., Oki M., Manto S., Taketo A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: MAJOR SPIKE COMPONENT. INVOLVED IN THE ATTACHMENT TO
CC THE BACTERIAL HOST.
CC -1- SUBUNIT: THE VIRION IS COMPOSED OF 60 COPIES EACH OF THE P, G, AND
CC J PROTEINS, AND 12 COPIES OF THE H PROTEIN. THERE ARE 12 SPIKES
CC WHICH ARE EACH COMPOSED OF 5 G AND ONE H PROTEINS.
CC -----
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CC -----
DR EMBL: X60323: CAA42892.1; -.
DR HSSP: P03643; IAL0.
KM Coat protein.
SQ SEQUENCE 187 AA; 19569 MW; C5C5CEC891241701 CRC64;

Query Match
Best Local Similarity 50.0%; Score 5; DB 1; Length 187;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
    |||||
DB 26 PVAPT 30

RESULT 11

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RL29_MYCGE
ID RL29_MYCGE STANDARD; PRT; 200 AA.
AC P47405;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L29.
GN RPMC OR RPL29 OR MG159.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bolt K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
CC -1- SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: U39696; AAC71377.1; -.
DR TIGR: MG159; -.
DR InterPro: IPR001854; -.
DR Pfam: PF00831; Ribosomal_L29; 1.
DR PROSITE: PS00579; RIBOSOMAL_L29; 1.
KM Ribosomal protein.
SQ SEQUENCE 200 AA; 23258 MW; 5BC115E52AA5EA92 CRC64;

Query Match
Best Local Similarity 50.0%; Score 5; DB 1; Length 200;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QYVKK 10
    |||||
DB 170 QYVKK 174

RESULT 12
IMWU_BPSPB STANDARD; PRT; 201 AA.
ID IMWU_BPSPB
AC P06650;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE IMMUNITY PROTEIN.
GN D.
OS Bacteriophage SP-beta.
OC Viruses; ssDNA viruses; no RNA stage; Tailed phages; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=10722;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2;
RX MEDLINE=86304188; PubMed=3091583;
RA McLaughlin J.R., Wong H.C., Ting Y.E., van Arsdell J.N., Chang S.;
RT "Control of lysogeny and immunity of Bacillus subtilis temperate
RL bacteriophage SP-beta by its d gene.";

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RT      "Cloning, expression, and sequence conservation of
RT      pathogenesis-related gene transcripts of potato.";
RL      Mol. Plant Microbe Interact. 2:325-331(1989).
CC      -I- INDUCTION: BY WOUNDING AND ELICITOR TREATMENTS
CC      -I- SIMILARITY: BELONGS TO THE BETV1 FAMILY OF PATHOGENESIS-RELATED
CC      PROTEIN.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M25156; AAA03020.1; -
DR      EMBL; M29042; AAA02829.1; -
DR      PIR; S11869; S11869.
DR      HSSP; P15494; 1BTV.
DR      InterPro: IPR000916; -.
DR      Pfam: PF00407; Bet.v.I.1.
DR      PRINTS: PR00634; BETALLERGEN.
DR      PROSITE: PS00451; PATHOGENESIS_BETV1; 1.
DR      Pathogenesis-related protein; Multigene family.
KW      SEQUENCE 155 AA; 17200 MW; 02A78EE6D26A7CD9 CRC64;

Query Match          50.0%; Score 5; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 PVAPT 5
        |||||
DB      13 PVAPT 17

RESULT 8
RPC1_BPMU STANDARD; PRT; 174 AA.
AC      P06019;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      REPRESSOR PROTEIN Cl.
GN      Cl OR 1.
OS      Bacteriophage Mu.
OC      Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
OX      NCBI_TaxID=10677;
RN      [1]
RP      MEDLINE=83012203; PubMed=6214696;
RA      Priess H., Kamp D., Kahmann R., Brauer B., Delius H.;
RT      "Nucleotide sequence of the immunity region of bacteriophage Mu.";
RL      Mol. Gen. Genet. 186:315-321(1982).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Priess H., Brauer B., Schmidt C., Kamp D.;
RT      "Sequence of the left end of Mu.";
RL      (in) Symonds N., Toussaint A., van de Putte P., Howe M.M. (eds.);
RL      Phage Mu, pp. 277-296, Cold Spring Harbor Laboratory Press,
RL      New York (1987).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Morgan G., Hatfull G., Hendrix R.;
RT      "Genome of bacteriophage Mu and comparison with the Haemophilus
RT      influenzae Mu-like prophage fluMu.";
RL      Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
DR      EMBL; V01464; CA24711.1; -
DR      EMBL; M64097; AAA32376.1; -
DR      EMBL; AF083977; AAF01132.1; -
DR      PIR; S07291; S07291.
DR      HSSP; P07636; ITNS.
KW      Transcription regulation; Repressor; DNA-binding.
SQ      SEQUENCE 174 AA; 19213 MW; 11A4B3F5B5E49C5 CRC64;

Query Match          50.0%; Score 5; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 QEVKK 10
        |||||
DB      168 QEVKK 172

RESULT 9
EFP1_CHLPN STANDARD; PRT; 185 AA.
AC      Q92900; Q92906;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      ELONGATION FACTOR P 1 (EF-P 1).
GN      EFP1 OR CPN0184 OR CP0584.
OS      Chlamydia pneumoniae (Chlamydia pneumoniae).
OC      Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX      NCBI_TaxID=83558;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CWL029;
RC      MEDLINE=99206606; PubMed=10192388;
RA      Kalman S., Mitchell W., Marathe R., Lamme C., Fan J., Hyman R.W.,
RA      Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT      "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL      Nat. Genet. 21:385-389(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=AR39;
RC      MEDLINE=20150255; PubMed=10684935;
RA      Read T.D., Brunning R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA      White O., Hickey E.K., Peterson J., Umayam L.A., Ulteback T.,
RA      Berry K., Bass S., Linher K., Weidman J., Kouri H., Craven B.,
RA      Bowman C., Dodson R., Gwinn M., Nelson W., Deboy R., Kolonay J.,
RA      McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RT      "Genome sequences of Chlamydia trachomatis Morn and Chlamydia
RT      pneumoniae AR39.";
RL      Nucleic Acids Res. 28:1397-1406(2000).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=J138;
RC      MEDLINE=20330349; PubMed=10871362;
RA      Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA      Shiba T., Ishii K., Hatfort M., Kuhara S., Nakazawa T.;
RT      "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT      from Japan and CWL029 from USA.";
RL      Nucleic Acids Res. 28:2311-2314(2000).
CC      -----
CC      -I- FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATE EFFICIENT
CC      TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED
CC      70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING
CC      THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING
CC      THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE
CC      (BY SIMILARITY).
CC      -----
CC      -I- PATHWAY: PROTEIN BIOSYNTHESIS.
CC      -----
CC      -I- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC      -----
CC      -I- SIMILARITY: BELONGS TO THE ELONGATION FACTOR P FAMILY.
CC      -----
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Query Match 60.0%; Score 6; DB 1; Length 617;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10
|||||
DB 412 TOEVKK 417

RESULT 3

ENV_FOAMY STANDARD; PRT; 985 AA.

ID ENV_FOAMY
AC P14351:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ENV POLYPROTEIN (COAT POLYPROTEIN).
GN ENV.
OS Human spumaretrovirus (Foamy virus).
OC Viruses; Retroid viruses; Retroviridae; Spumaviruses.
OX NCBI_TaxID=11963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88004420; PubMed=2820721;
RA Fluegel R.M., Rethwalim A., Maurer B., Darai G.:
RT "Nucleotide sequence analysis of the env gene and its flanking
RL regions of the human spumaretrovirus reveals two novel genes.";
EMD J. 6:2077-2084(1987).
CC -----
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CC -----

DR EMBL: X05591; CAA29086.1; -
DR EMBL: M54578; AAA46123.1; -
DR PIR: C29685; VCLJSP.
KW Coat protein; Transmembrane; Polypeptide; Glycoprotein.
FT TRANSMEM 64 84
FT TRANSMEM 958 978
FT CARBOHYD 21 21
FT CARBOHYD 105 105
FT CARBOHYD 137 137
FT CARBOHYD 179 179
FT CARBOHYD 282 282
FT CARBOHYD 307 307
FT CARBOHYD 342 342
FT CARBOHYD 387 387
FT CARBOHYD 401 401
FT CARBOHYD 419 419
FT CARBOHYD 524 524
FT CARBOHYD 553 553
FT CARBOHYD 779 779
FT CARBOHYD 805 805
FT CARBOHYD 830 830
SQ SEQUENCE 985 AA; 113494 MW; 60F588EA931BE0AF CRC64;

Query Match 60.0%; Score 6; DB 1; Length 985;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10
|||||
DB 181 TOEVKK 186

RESULT 4

ATX9_TETTH STANDARD; PRT; 1133 AA.

ID ATX9_TETTH
AC Q95050:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROBABLE CATION-TRANSPORTING ATPASE 9 (EC 3.6.1.-).
GN TP9.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymena; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cu428;
RA Wang S., Takeyasu K.:
RT "The starvation-induced P-type ATPase in Tetrahymena thermophila."
RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O -> ADP + ORTHOPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES). SUBFAMILY V.
CC -----

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CC -----

DR EMBL: U41063; AAB08071.1; -
DR InterPro: IPR001757; -
DR Pfam: PF00122; E1-E2_ATPase; 4.
DR PROSITE: PS00154; ATPASE_E1-E2; 1.
KW Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.
FT DOMAIN 1 6
FT TRANSMEM 7 28
FT TRANSMEM 29 34
FT TRANSMEM 35 53
FT TRANSMEM 54 167
FT TRANSMEM 168 190
FT TRANSMEM 191 193
FT TRANSMEM 194 212
FT TRANSMEM 213 363
FT TRANSMEM 364 383
FT TRANSMEM 384 396
FT TRANSMEM 397 418
FT TRANSMEM 419 887
FT TRANSMEM 888 906
FT TRANSMEM 907 915
FT TRANSMEM 916 931
FT TRANSMEM 932 948
FT TRANSMEM 949 972
FT TRANSMEM 973 994
FT TRANSMEM 995 1018
FT TRANSMEM 1019 1030
FT TRANSMEM 1031 1050
FT TRANSMEM 1051 1101
FT TRANSMEM 1102 1124
FT TRANSMEM 1125 1133
FT MOD. RES 451 451
FT METAL 827 827
FT METAL 831 831
SQ SEQUENCE 1133 AA; 129669 MW; 6875FFB651BA027 CRC64;

Query Match 60.0%; Score 6; DB 1; Length 1133;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10
|||||

837	4	40.0	304	1	HEX1_HUMAN	Q9YJ33 homo sapien	910	4	40.0	323	1	MCH_METUA	Q50303 methanococc
838	4	40.0	304	1	META_THEMA	Q9WY23 thermotoga	911	4	40.0	323	1	OTX1_BRARE	Q91994 brachydanio
839	4	40.0	304	1	YONI_CAEL	Q09522 caenorhabdi	912	4	40.0	323	1	PF27_BRARE	P52775 mus musculi
840	4	40.0	305	1	BLAC_STRLA	P35193 streptomyce	913	4	40.0	323	1	YH8_MYCTU	O50668 mycobacteri
841	4	40.0	305	1	DDLB_ECOLI	P07862 escherichia	914	4	40.0	324	1	CAHC_HORVU	P40880 hordeum vul
842	4	40.0	305	1	FBR1_SCHPO	P35551 schizosacch	915	4	40.0	324	1	CBH_LACPL	Q06115 lactobacilli
843	4	40.0	305	1	MALM_SALTY	P26478 salmoneila	916	4	40.0	324	1	PTGA_BACST	P42015 bacillus st
844	4	40.0	305	1	MIAA_AQUAE	O67162 aquifex aeo	917	4	40.0	324	1	RADA_SULSO	O55075 sulfobius
845	4	40.0	305	1	ROAO_HUMAN	O13151 homo sapien	918	4	40.0	324	1	YC30_CVAPA	P48271 cyanophora
846	4	40.0	305	1	YORK_BACSU	P45927 bacillus su	919	4	40.0	325	1	MODD_MYCBO	O30620 mycobacteri
847	4	40.0	306	1	YOPD_YEREN	P37132 yeastina en	920	4	40.0	325	1	MODD_MYCTU	O50906 mycobacteri
848	4	40.0	307	1	ALF_HELPJ	Q9ZM96 helicobacte	921	4	40.0	325	1	WZB3_ECOLI	P33272 escherichia
849	4	40.0	307	1	ALF_HELPJ	P56109 helicobacte	922	4	40.0	325	1	WZB8_ECOLI	O33953 escherichia
850	4	40.0	307	1	CRTB_SYNP7	P37269 synecococc	923	4	40.0	325	1	WZB8_SHIFL	P37790 shigella dy
851	4	40.0	307	1	GP7D_CHLPS	O46257 chlamydia p	924	4	40.0	325	1	WZB8_SHIFL	P37792 shigella fl
852	4	40.0	307	1	V53_BPAPS	O92135 bacterioph	925	4	40.0	326	1	BLAA_STRCT	P33651 streptomyc
853	4	40.0	308	1	KDGD_BACSU	P42235 bacillus su	926	4	40.0	326	1	TG12_YEAST	P34857 saccharomyc
854	4	40.0	308	1	URIC_CANLI	P34798 canavalia s	927	4	40.0	326	1	VP40_EBOZM	Q05128 ebola virus
855	4	40.0	308	1	URIC_PHAVU	P53763 phaseolus v	928	4	40.0	326	1	VS09_ROTHT	P15051 human rotav
856	4	40.0	308	1	YL58_CAEL	P34438 caenorhabd	929	4	40.0	326	1	VS09_ROTHT	P15051 human rotav
857	4	40.0	309	1	HEWZ_AQUAE	O67083 aquifex aeo	930	4	40.0	326	1	VS09_ROTHT	P15051 human rotav
858	4	40.0	309	1	P2A_DROME	P23296 drosophila	931	4	40.0	326	1	WZB1_ECOLI	P76372 escherichia
859	4	40.0	309	1	TUS_ECOLI	P16525 escherichia	932	4	40.0	326	1	Y168_HUMAN	P50749 homo sapien
860	4	40.0	310	1	ATPG_SPIPL	P50006 spirulina p	933	4	40.0	327	1	CG65_HUMAN	O93375 homo sapien
861	4	40.0	310	1	PYDB_LACLC	P54322 lactococcus	934	4	40.0	327	1	FBR1_MOUSE	P33550 mus musculi
862	4	40.0	311	1	VORR_PYRHO	O58414 pyrococcus	935	4	40.0	327	1	GLSA_SYNY3	P73903 synecocyst
863	4	40.0	311	1	YBRU_BORBR	O06702 bordetella	936	4	40.0	327	1	OGA1_HUMAN	O95222 homo sapien
864	4	40.0	312	1	VP12_RDVA	O05054 rice dwarf	937	4	40.0	327	1	WZB8_SALTY	O04866 salmoneila
865	4	40.0	312	1	VP12_RDVF	O05443 rice dwarf	938	4	40.0	327	1	Y745_HELPJ	O94198 helicobacte
866	4	40.0	312	1	VP12_RDVO	O86480 rice dwarf	939	4	40.0	327	1	Y745_HELPJ	O94198 helicobacte
867	4	40.0	312	1	YCXX_CHLMO	P09754 chlamydomon	940	4	40.0	327	1	Y1G3_YEAST	O25441 helicobacte
868	4	40.0	313	1	CBBR_RHIME	P56885 rhizobium m	941	4	40.0	327	1	YN91_YEAST	P40517 saccharomyc
869	4	40.0	313	1	FWT_THEMA	O84928 thermotoga	942	4	40.0	328	1	COBP_PSEEM	P53779 saccharomyc
870	4	40.0	314	1	HEWZ_CHLTP	O84928 thermotoga	943	4	40.0	328	1	IBP2_HUMAN	P33375 pseudomonas
871	4	40.0	314	1	MDH_RICPR	Q926f3 rickettsia	944	4	40.0	328	1	IRL1_HUMAN	P10065 homo sapien
872	4	40.0	314	1	SIX3_CHICK	O42406 gallus gall	945	4	40.0	328	1	RPOA_MYCGE	Q01638 homo sapien
873	4	40.0	315	1	GBF1_ARATH	P42774 arabidopsis	946	4	40.0	328	1	T2EB_YEAST	P47423 mycoplasma
874	4	40.0	315	1	HYFC_ECOLI	P77658 escherichia	947	4	40.0	328	1	CGA1_YEAST	P36145 saccharomyc
875	4	40.0	315	1	MCH_METKA	P94954 methanopyru	948	4	40.0	329	1	Y493_MYCTU	P53208 saccharomyc
876	4	40.0	315	1	RPOA_CLOPE	O91BW9 clostridium	949	4	40.0	329	1	Y493_MYCTU	O86779 streptomyc
877	4	40.0	315	1	RSEB_TAEIN	P47492 haemophilus	950	4	40.0	330	1	HEW2_RAT	O11158 mycobacteri
878	4	40.0	316	1	MCH_ARCFU	O28344 archaeglob	951	4	40.0	330	1	SWR_RICPR	P06214 rattus norv
879	4	40.0	316	1	YB33_YEAST	P38298 saccharomyc	952	4	40.0	330	1	Y677_METUA	O50890 methanococc
880	4	40.0	317	1	LDH_BACCA	P10655 bacillus ca	953	4	40.0	331	1	FHR4_HUMAN	O92496 homo sapien
881	4	40.0	317	1	RSP4_URECA	P38981 urechis cau	954	4	40.0	331	1	LEU1_THERM	O56216 thermus aqu
882	4	40.0	317	1	Y187_AQUAE	O67728 aquifex aeo	955	4	40.0	331	1	MA2_MESAU	P56670 mesocricetu
883	4	40.0	317	1	Y207_AQUAE	O66402 aquifex aeo	956	4	40.0	331	1	Y244_METUA	Q06299 methanococc
884	4	40.0	318	1	NUIM_TAMTE	O78695 tamandua te	957	4	40.0	332	1	AXHA_ASPNG	P79019 aspergillus
885	4	40.0	318	1	PEX7_MOUSE	P97865 mus musculi	958	4	40.0	332	1	AXHA_ASPNG	P79021 aspergillus
886	4	40.0	319	1	HALL_RAT	P15978 rattus norv	959	4	40.0	332	1	LYNB_MYCLE	O95028 drosophila
887	4	40.0	319	1	LDH_BIFLO	P19869 bifidobacte	960	4	40.0	332	1	LYNB_MYCLE	O95028 drosophila
888	4	40.0	319	1	MCH_METTM	P51616 methanobact	961	4	40.0	332	1	SIX3_HUMAN	O93781 mycobacteri
889	4	40.0	319	1	MOCB_SYNP7	Q56208 synecococc	962	4	40.0	332	1	SR4_PHYPO	O93343 homo sapien
890	4	40.0	319	1	STRN_STRGR	P29784 streptomyce	963	4	40.0	332	1	YCJW_ECOLI	P11113 physarum po
891	4	40.0	319	1	YPP5_CAEL	P41883 caenorhabd	964	4	40.0	333	1	MOSA_RHIME	P77615 escherichia
892	4	40.0	320	1	CHIX_PEA	P36007 pisum sativ	965	4	40.0	333	1	SIX3_MOUSE	O67607 rhizobium m
893	4	40.0	320	1	GSMB_SYNY3	P73493 synecocyst	966	4	40.0	334	1	CHMU_ARATH	O62233 mus musculi
894	4	40.0	320	1	KHSE_ZYMMO	O69015 zymomonas m	967	4	40.0	334	1	DPOB_HUMAN	P43738 arabidopsis
895	4	40.0	320	1	MCH_METTH	O26667 methanobact	968	4	40.0	334	1	DPOB_HUMAN	P06746 homo sapien
896	4	40.0	320	1	THRR_MMYVQ	P03320 mouse mamma	969	4	40.0	334	1	FLA3_PYRHO	P06746 homo sapien
897	4	40.0	320	1	THRR_MMYVQ	P27477 synecococc	970	4	40.0	334	1	MDHM_YEAST	O58284 pyrococcus
898	4	40.0	321	1	FBR1_HUMAN	P22087 homo sapien	971	4	40.0	334	1	Y111_HALNI	P17505 saccharomyc
899	4	40.0	321	1	LIPA_ECOLI	P25845 escherichia	972	4	40.0	335	1	COLD_HUMAN	P23464 halobacteri
900	4	40.0	321	1	MCH_METBA	P94919 methanosarc	973	4	40.0	335	1	LYB1_MYCTU	P18813 homo sapien
901	4	40.0	321	1	SAPB_ECOLI	Q47623 escherichia	974	4	40.0	335	1	TRPD_HELPJ	O53458 mycobacteri
902	4	40.0	321	1	SAPB_SALTY	P36668 salmoneila	975	4	40.0	335	1	TRPD_HELPJ	O53458 mycobacteri
903	4	40.0	322	1	ARCI_YEAST	P05089 homo sapien	976	4	40.0	335	1	TWR8_CAEL	Q92J77 helicobacte
904	4	40.0	322	1	CCCL_YEAST	P47818 saccharomyc	977	4	40.0	336	1	DLDH_ACHLA	P34410 caenorhabd
905	4	40.0	322	1	HA10_MOUSE	P01898 mus musculi	978	4	40.0	336	1	Y625_METUA	P34484 achloplasm
906	4	40.0	322	1	HCR_ECOLI	P73824 escherichia	979	4	40.0	337	1	LEPB_HAESO	O58042 methanococc
907	4	40.0	322	1	SC13_HUMAN	P55735 homo sapien	980	4	40.0	337	1	F16Q_HUMAN	P36685 haemophilus
908	4	40.0	323	1	FBR1_XENLA	P22332 xenopus lae	981	4	40.0	339	1	KDGT_ERWCH	O00757 homo sapien
909	4	40.0	323	1	MCH_METEX	O85014 methyllobact	982	4	40.0	339	1	MURG_THEMA	P17501 erwinia chr

691	4	40.0	263	1	T2T8_THETH	P29748	thermus aqu	764	281	1	TRPA_METJA	Q60180	methanococ
692	4	40.0	263	1	TRPA_ANTSP	P31204	antilhamio	765	282	1	YC53_METJA	Q58650	methanococ
693	4	40.0	264	1	CXB1_XENIA	P08983	xenopus lae	766	283	1	Y43F_MYCPN	P75158	mycoplasma
694	4	40.0	264	1	DMPH_PSESP	P49156	pseudomonas	767	284	1	RP32_PROMI	P50509	proteus mir
695	4	40.0	264	1	IOD2_PNSCA	P49896	rana catesb	768	284	1	VDLC_HELPY	O05730	helicobacte
696	4	40.0	264	1	PUL1_HUMAN	P17947	homo sapien	769	285	1	TONB_HELPY	O25899	helicobacte
697	4	40.0	264	1	RCIT_BPp4	P13059	bacterioph	770	286	1	MCMI_YEAST	P11746	saccharomyc
698	4	40.0	264	1	RSP4_STRPU	P46771	strongyloce	771	287	1	MYOC_RAT	P20448	rattus norv
699	4	40.0	264	1	TRPA_SYNY3	P77960	synecocyst	772	287	1	RL3_MYCPN	P75580	mycoplasma
700	4	40.0	264	1	TRPC_LACLA	O01999	lactococcus	773	287	1	Y280_MYCPN	P75384	mycoplasma
701	4	40.0	265	1	APAL_PIG	P18648	sus scrofa	774	287	1	Y1CC_HAEIN	P44726	haemophilus
702	4	40.0	265	1	DH47_ARATH	P31168	arabidopsis	775	288	1	EPMO_HUMAN	P32856	homo sapien
703	4	40.0	265	1	IOD2_HUMAN	Q92813	homo sapien	776	288	1	FXE3_MOUSE	Q99Y14	mus musculus
704	4	40.0	265	1	REFAP_ECOLI	P25741	escherichia	777	288	1	HMXX_CHICK	P50232	gallus gall
705	4	40.0	265	1	TRPA_METTM	P26920	methanobact	778	288	1	STIA_MOUSE	O55223	gallus gall
706	4	40.0	265	1	YMI2_PARTE	P15613	paramectium	779	288	1	WTL_ALUMI	P50992	mus musculus
707	4	40.0	266	1	PUL1_MOUSE	P17433	mus musculus	780	288	1	Y940_MYCTU	F71369	mycobacteri
708	4	40.0	266	1	SURE_METJA	Q57979	methanococ	781	289	1	ATPG_HAEIN	P43716	haemophilus
709	4	40.0	266	1	UXUR_HAEIN	P44487	haemophilus	782	289	1	DAPA_METJA	O57695	methanococ
710	4	40.0	267	1	STO3_CAEEL	Q20657	caenorhabdi	783	289	1	FRAP_ANASP	P46017	anabaena sp
711	4	40.0	267	1	TRPA_BACSU	P07601	bacillus su	784	289	1	SYLE_AQUAE	O67646	aquifex aeo
712	4	40.0	267	1	Y412_METJA	O57855	methanococ	785	290	1	ATPG_BACSU	P37810	bacillus su
713	4	40.0	268	1	ENGA_SALTY	Q9XC18	salmonella	786	290	1	HXB8_HUMAN	P13378	homo sapien
714	4	40.0	268	1	KSGA_RICPR	O05952	r dimethyla	787	290	1	STX_APLCA	Q16932	aplysia cal
715	4	40.0	269	1	NUDC_VIBCH	Q9KX27	vibriho chol	788	290	1	TODE_PSEPU	P13453	pseudomonas
716	4	40.0	269	1	TRPA_BACST	P19867	bacillus st	789	291	1	YJBC_ECOLI	P32684	escherichia
717	4	40.0	270	1	HCE1_ORYLA	P31580	oryzias lat	790	291	1	C1LE_HAEIN	P44660	haemophilus
718	4	40.0	270	1	ILIA_MOUSE	P01582	mus musculus	791	291	1	GTH2_WHEAT	P30111	triticum ae
719	4	40.0	270	1	MOTB_BACSU	P28611	bacillus su	792	291	1	STXA_DROME	Q24517	drosophila
720	4	40.0	270	1	PANB_THEMA	Q9XZ31	thermotoga	793	292	1	COPE_CAEEL	O62246	caenorhabdi
721	4	40.0	270	1	PYRD_THEMA	Q9WY98	thermotoga	794	292	1	YVRE_BACSU	O34940	bacillus su
722	4	40.0	270	1	TRPA_METTH	O27697	methanobact	795	293	1	HMX1_MOUSE	P13297	mus musculus
723	4	40.0	270	1	YIDA_ECOLI	P09997	escherichia	796	293	1	META_CAMJE	Q9P142	campylobact
724	4	40.0	271	1	RL7A_ANGA	O76732	anopheles g	797	293	1	Y326_MYCPN	P75312	mycoplasma
725	4	40.0	271	1	VDLC_HELPY	Q9ZKX1	helicobacte	798	294	1	239F_HUMAN	O15777	homo sapien
726	4	40.0	271	1	Y228_TREPA	O83236	treponema p	799	294	1	DAPA_BUCAL	P57197	buchnera ap
727	4	40.0	271	1	YW34_MYCTU	O05879	mycobacteri	800	294	1	DAPA_THEMA	O9X1K9	thermotoga
728	4	40.0	272	1	VG67_HSVB	P28964	equine herp	801	295	1	FLAI_PYRKO	O9X2A1	pyrococcus
729	4	40.0	272	1	YIS2_SHISO	P16940	shigella so	802	295	1	CAC3_HABCO	P16233	haemonchus
730	4	40.0	273	1	GIAB_GIALA	P15518	giardia lam	803	295	1	DAPF_METJA	O58519	methanococ
731	4	40.0	273	1	TRPC_BRAJA	P94327	bradyrhizob	804	295	1	RL5B_XENLA	P15125	xenopus lae
732	4	40.0	274	1	PRCE_ARATH	O23717	arabidopsis	805	295	1	SUCD_PSEAE	P15166	xenopus lae
733	4	40.0	274	1	VGLE_HSV2	P13289	herpes simp	806	295	1	TRPC_SYNY3	O51567	pseudomonas
734	4	40.0	274	1	Y026_METJA	O60343	methanococ	807	295	1	YHOB_YEAST	O55508	synecocyst
735	4	40.0	275	1	FLA5_PYRKO	O9UWU0	schizosacch	808	295	1	110K_PLAKN	P13885	saccharomyc
736	4	40.0	275	1	VE39_NPYAC	P11042	autographa	809	296	1	CCO1_CAEEL	P08124	caenorhabdi
737	4	40.0	276	1	COAT_TNNA	P22959	tobacco nec	810	296	1	METF_AQUAE	O67442	aquifex aeo
738	4	40.0	276	1	LIP1_AQUAE	O67368	aquifex aeo	811	296	1	RL5_CHICK	P22451	gallus gall
739	4	40.0	276	1	PLPB_PASHA	O08869	pasteurella	812	296	1	RL5_HUMAN	P46777	homo sapien
740	4	40.0	276	1	RSP4_CAEEL	P46769	caenorhabdi	813	296	1	RL5_HUMAN	P09895	rattus norv
741	4	40.0	277	1	BHMT_PIG	O95332	sus scrofa	814	297	1	RL5_RAT	O02766	bos taurus
742	4	40.0	277	1	HXDB_NORVI	P31263	notophtalm	815	297	1	HMX1_BOVIN	P28360	homo sapien
743	4	40.0	277	1	TRPA_HALVO	P18284	halobacteri	816	297	1	OCCR_RHIME	F72284	rhizobium m
744	4	40.0	277	1	Y31K_SSV1	P20203	sulfolobus	817	297	1	YNFL_ECOLI	P77559	escherichia
745	4	40.0	278	1	FIXR_BRAJA	O27272	bradyrhizob	818	298	1	DAPA_HAEIN	P43797	haemophilus
746	4	40.0	278	1	T2D7_DROME	O27272	drosophila	819	298	1	OCCR_AGRTU	O04393	agrobacteri
747	4	40.0	278	1	T2N2_NEIGO	P24617	neisseria g	820	298	1	Y33K_HUMAN	O00679	homo sapien
748	4	40.0	278	1	WGLL_HCMV1	O68667	human cytom	821	299	1	ATPG_ACEMO	P50005	acetobacter
749	4	40.0	278	1	WGLL_HCMV2	O68668	human cytom	822	299	1	Y175_HELPY	O9ZM77	helicobacte
750	4	40.0	278	1	WGLL_HCMV3	O68669	human cytom	823	299	1	Y175_HELPY	P56112	helicobacte
751	4	40.0	278	1	WGLL_HCMV4	O68670	human cytom	824	299	1	YJH9_YEAST	P47032	saccharomyc
752	4	40.0	278	1	WGLL_HCMV5	O68671	human cytom	825	300	1	CEPM_BACHD	O9Z917	bacillus ha
753	4	40.0	278	1	WGLL_HCMV6	O68672	human cytom	826	301	1	CC21_TREBB	P38973	trypanosoma
754	4	40.0	278	1	WGLL_HCMV7	O68673	human cytom	827	301	1	FEAR_ECOLI	O47129	escherichia
755	4	40.0	278	1	WGLL_HCMV8	O68674	human cytom	828	301	1	NHAR_ECOLI	P10067	escherichia
756	4	40.0	278	1	WGLL_HCMV9	O68675	human cytom	829	301	1	YURD_CANLI	P34799	canavalia l
757	4	40.0	278	1	WGLL_HCMV10	O68676	human cytom	830	301	1	YMBI_BACSU	P39592	bacillus su
758	4	40.0	279	1	HCE2_ORYLA	P31581	oryzias lat	831	302	1	CASB_MACEU	P28550	macropus eu
759	4	40.0	281	1	DEGV_BACSU	P32436	bacillus su	832	302	1	C1LE_ECOLI	P77770	escherichia
760	4	40.0	281	1	HEMK_AQUAE	O66506	aquifex aeo	833	302	1	YEB6_MYCTU	P71766	mycobacteri
761	4	40.0	281	1	RM30_YEAST	P36528	saccharomyc	834	304	1	HEV1_CANFA	O13442	homo sapien
762	4	40.0	281	1	T2MT_METTE	P29565	methanobact	835	304	1		O9tsz2	canis fami
763	4	40.0	281	1				836	304	1			

545	4	40.0	231	1	PCRB_ARCFU	O29844	archaeoglob	618	4	40.0	249	1	PCNA_PYRAB	O9uyx8	pyrococcus
546	4	40.0	231	1	RSMB_MOUSE	P27048	mus musculu	619	4	40.0	249	1	PCNA_PYRFU	O73947	pyrococcus
547	4	40.0	232	1	CASB_PIG	P39037	sus scrofa	620	4	40.0	249	1	PCNA_PYRHO	O58369	pyrococcus
548	4	40.0	232	1	KUK_PIG	P00752	sus scrofa	621	4	40.0	249	1	REP2_ZYGBA	P13780	zygosacchar
549	4	40.0	233	1	BRAG_PSEAE	P21630	pseudomonas	622	4	40.0	249	1	REP2_ZYGBA	P13780	zygosacchar
550	4	40.0	233	1	PSMA_THEAC	P25156	thermoplasm	623	4	40.0	250	1	FR1_SOYBN	P43333	arabidopsis
551	4	40.0	233	1	RL1_THEMA	P29393	thermotoga	624	4	40.0	250	1	TRPC_BACSU	P19976	glycine max
552	4	40.0	233	1	SERA_ENTHI	P21138	thermoeoba h	625	4	40.0	250	1	Y627_PYRHO	P03964	baecillus su
553	4	40.0	234	1	GCHL_SYNY3	O55759	synechocyst	626	4	40.0	251	1	TPIS_LEIME	O58369	pyrococcus
554	4	40.0	234	1	RS3_ACTAC	P55827	actinobacil	627	4	40.0	251	1	TPIS_TYCR	P48499	leishmania
555	4	40.0	234	1	RS3_HAETN	P43372	haemophilus	628	4	40.0	252	1	DUT_HUMAN	P52270	typanosoma
556	4	40.0	234	1	SODM_CANAL	O13401	candida alb	629	4	40.0	252	1	GSC_HUMAN	P33316	homo sapien
557	4	40.0	235	1	AURB_CHLNU	P27197	chloroflexu	630	4	40.0	253	1	EBSD_ENTFA	P56915	homo sapien
558	4	40.0	235	1	YHHQ_HAETN	P44908	haemophilus	631	4	40.0	253	1	FRI_PEA	P36293	enterococcu
559	4	40.0	236	1	CD8A_RAT	P07725	rattus norv	632	4	40.0	253	1	HEMA_METH	P19975	plasm sativ
560	4	40.0	236	1	GAMT_HUMAN	O14353	homo sapien	633	4	40.0	253	1	KAD_CHLNU	O26266	methanobact
561	4	40.0	236	1	GAMT_MOUSE	O39969	mus musculu	634	4	40.0	253	1	KDSB_HAETN	O9pkx0	chlamydia m
562	4	40.0	236	1	YMI3_CAEBL	O21018	caenorhabdi	635	4	40.0	253	1	PMX2_HUMAN	O99811	homo sapien
563	4	40.0	237	1	COX2_TIRIU	O01556	trichophyto	636	4	40.0	253	1	RPSF_BACME	P35145	baecillus me
564	4	40.0	237	1	FLAI_PYRHO	O58281	pyrococcus	637	4	40.0	253	1	SQI_BACHD	O9K500	baecillus ha
565	4	40.0	237	1	GUN_ASPAC	P22669	aspergillus	638	4	40.0	253	1	SQI_BACSU	P37522	baecillus su
566	4	40.0	237	1	MTR4_METH	O27227	methanobact	639	4	40.0	253	1	TPIS_COPDA	P37522	baecillus su
567	4	40.0	237	1	MTR4_METH	P80184	methanobact	640	4	40.0	254	1	FRI_PHAVU	P18820	coplus japo
568	4	40.0	237	1	PSA5_SOYBN	O9m4t8	glycine max	641	4	40.0	254	1	TPIS_ARATH	P25699	phaseolus v
569	4	40.0	237	1	RL23_MYCPN	P75578	mycoplasma	642	4	40.0	254	1	TPIS_PETHY	P48491	arabidopsis
570	4	40.0	238	1	ERT3_HUMAN	P14138	homo sapien	643	4	40.0	254	1	YNO8_YEAST	P48495	petunia hyb
571	4	40.0	238	1	YT23_AGRVI	P70793	agrobacteri	644	4	40.0	254	1	FLA5_PYRHO	P53904	saccharomyc
572	4	40.0	239	1	RIM9_YEAST	O04734	saccharomyc	645	4	40.0	255	1	RL8A_YEAST	P17076	saccharomyc
573	4	40.0	239	1	UPPS_HAETN	P4938	haemophilus	646	4	40.0	255	1	RL8B_YEAST	P29453	saccharomyc
574	4	40.0	239	1	WT1_SMIMA	P49953	smilthopsis	647	4	40.0	255	1	RNH2_BACSU	O31744	baecillus su
575	4	40.0	240	1	BS12_TRYCR	P18270	trypanosoma	648	4	40.0	255	1	RPSF_BACLI	P26766	baecillus li
576	4	40.0	240	1	FARR_ECOLI	P13669	escherichia	649	4	40.0	255	1	RPSF_BACSU	P07860	baecillus su
577	4	40.0	240	1	HOL_SYNY3	P27849	synechocyst	650	4	40.0	255	1	TONB_YEREN	O05740	yersinia en
578	4	40.0	240	1	RSMB_CHICK	O9v94	gallus galli	651	4	40.0	255	1	TRPC_BACME	P70937	baecillus me
579	4	40.0	240	1	RSMB_ERIEU	O9v67	eritaceus e	652	4	40.0	255	1	YORE_PSECL	O03003	pseudomonas
580	4	40.0	240	1	RSMB_HUMAN	P14678	homo sapien	653	4	40.0	256	1	GLD2_RHOCA	P6981	rhodobacter
581	4	40.0	240	1	RSMB_MONDO	O9v66	monodelphis	654	4	40.0	256	1	GSC_MOUSE	O02591	mus musculu
582	4	40.0	240	1	RSMN_HUMAN	P14648	homo sapien	655	4	40.0	256	1	Y165_METJA	O57629	methanococc
583	4	40.0	241	1	GLTL_ECOLI	P41076	escherichia	656	4	40.0	257	1	CG1C_ORYSA	P93411	oryza sativ
584	4	40.0	241	1	RASH_MSVHA	P01115	harvey muri	657	4	40.0	257	1	HS70_LUPEO	P16121	lupinus pol
585	4	40.0	242	1	C17_HUMAN	P57077	homo sapien	658	4	40.0	257	1	KLKI_MACFA	P07276	macaca fasc
586	4	40.0	242	1	FLGH_CAOCR	P22606	caulobacter	659	4	40.0	257	1	TRPC_AOUAE	O67675	agulfex aeo
587	4	40.0	243	1	CAVT_BRALA	P05548	branchiosteo	660	4	40.0	258	1	HL_YEAST	P53551	saccharomyc
588	4	40.0	243	1	DENR_HUMAN	O43583	homo sapien	661	4	40.0	258	1	HB21_SPAEH	P15464	spalax leuc
589	4	40.0	243	1	GSCB_XENLA	P29454	xenopus lae	662	4	40.0	258	1	KLKI_PAPHA	O28773	papio hamad
590	4	40.0	243	1	MURE_HAETN	P53546	xenopus lae	663	4	40.0	258	1	YH33_THEMA	Q9x255	thermotoga
591	4	40.0	243	1	MURE_HAETN	P53186	haemophilus	664	4	40.0	259	1	GATR_ECOLI	P36930	haemophilus
592	4	40.0	243	1	TRUA_MYCPN	O50291	mycoplasma	665	4	40.0	259	1	NAD2_METJA	O68747	methanococc
593	4	40.0	244	1	HIO_CHITH	O07134	chironomus	666	4	40.0	259	1	RMS2_ARATH	P42814	arabidopsis
594	4	40.0	244	1	S40A_CHITE	O05018	chironomus	667	4	40.0	260	1	1433_LYCES	P33209	lycopersico
595	4	40.0	244	1	YK91_MYCTU	O10700	mycobacteri	668	4	40.0	260	1	143C_TORAC	P93343	nicotiana t
596	4	40.0	244	1	YR01_CAEBL	O10014	caenorhabdi	669	4	40.0	260	1	PSMA_THERK	O24733	thermococcu
597	4	40.0	245	1	KAD_CHLTR	O84130	chlamydia t	670	4	40.0	260	1	SHP_MOUSE	Q62227	mus musculu
598	4	40.0	245	1	UNG_MYCGE	P47343	mycoplasma	671	4	40.0	260	1	TRPC_LACCA	P17217	lactobacilli
599	4	40.0	245	1	YH77_ARCFU	O28497	archaeoglob	672	4	40.0	261	1	DHG2_BACME	P39483	baecillus me
600	4	40.0	246	1	DOG1_YEAST	P38774	saccharomyc	673	4	40.0	261	1	KLK2_HUMAN	P09151	homo sapien
601	4	40.0	246	1	KAD_ARATH	O82514	arabidopsis	674	4	40.0	261	1	KLK3_HUMAN	P07288	homo sapien
602	4	40.0	246	1	MCT2_SHEEP	P79204	ovis aries	675	4	40.0	261	1	MOTB_BACSU	P28612	baecillus su
603	4	40.0	246	1	RL4_HALMA	P12733	haloarcuula	676	4	40.0	261	1	TNF5_BOVIN	P51749	bos taurus
604	4	40.0	246	1	STX6_HUMAN	O95475	homo sapien	677	4	40.0	261	1	Y497_MYCLE	P54580	mycobacteri
605	4	40.0	247	1	GRAB_HUMAN	P10144	h granzyme	678	4	40.0	262	1	YOB4_CAEBL	O09257	caenorhabdi
606	4	40.0	247	1	MCT1_HUMAN	P23946	homo sapien	679	4	40.0	262	1	APAL_BRARE	O42363	brachydanio
607	4	40.0	247	1	MCT1_MACFA	P56445	macaca fasc	680	4	40.0	262	1	COR4_WHEAT	P46524	tritlicum ae
608	4	40.0	247	1	MCT1_PAPHA	P52195	papio hamad	681	4	40.0	262	1	IOD2_MOUSE	Q321Y9	mus musculu
609	4	40.0	247	1	MCT2_MERON	P50341	meriones un	682	4	40.0	262	1	IOD2_RAT	P70551	rattus norv
610	4	40.0	247	1	MCT3_RAT	P21844	mus musculu	683	4	40.0	262	1	KLKI_HUMAN	P22090	homo sapien
611	4	40.0	247	1	MCT5_MOUSE	PMX2_MOUSE	mus musculu	684	4	40.0	262	1	RS4_HUMAN	P47961	citricetus
612	4	40.0	248	1	RS3_CAEFL	O52633	caenorhabdi	685	4	40.0	262	1	RS4_CHICK	P12750	homo sapien
613	4	40.0	248	1	TPIS_CLOAB	P283206	lycopersico	686	4	40.0	262	1	THIM_ECOLI	P44733	haemophilus
614	4	40.0	249	1	HMX1_CHICK	P28361	gallus galli	687	4	40.0	263	1	MAZG_HAETN	P13728	dtrosophila
615	4	40.0	249	1	MCT1_CANFA	P218442	canis famli	688	4	40.0	263	1			
616	4	40.0	249	1				689	4	40.0	263	1			
617	4	40.0	249	1				690	4	40.0	263	1			

399	4	40.0	191	1	MLE1_RABIT	P02602	oryctolagus	472	4	40.0	212	1	RAB2_RAT	P05712	rattus norv
400	4	40.0	191	1	PGHD_CANFA	Q9x655	canis famil	473	4	40.0	212	1	RL14_HUMAN	P05014	homo sapien
401	4	40.0	192	1	GCH2_HELPJ	Q9z142	helicobacte	474	4	40.0	212	1	RL1_AERPE	O9y9w6	aeropyrum p
402	4	40.0	192	1	GCH2_HELPJ	008315	helicobacte	475	4	40.0	212	1	YTRB_ECOLI	P39310	escherichia
403	4	40.0	192	1	ZAK4_HUMAN	Q14206	homo sapien	476	4	40.0	213	1	RL14_RAT	063507	escherichia
404	4	40.0	193	1	H10_MOUSE	P10922	mus musculu	477	4	40.0	213	1	RL3_BACST	P28600	baecillus st
405	4	40.0	193	1	H10_MOUSE	P43378	rattus norv	478	4	40.0	213	1	UBC_ASPM2	P25659	african swi
406	4	40.0	194	1	H5B_XENLA	P22845	xenopus lae	479	4	40.0	213	1	YBL5_YEAST	P38121	saccharomyc
407	4	40.0	194	1	PGHD_HORSE	O97921	equus cabal	480	4	40.0	214	1	FLA4_PYROH	O58862	pyrococcus
408	4	40.0	194	1	RAS5_DICDI	P32254	dictyostell	481	4	40.0	214	1	NEUM_XENLA	P55860	xenopus lae
409	4	40.0	194	1	RS4_BOVIN	P79103	bos taurus	482	4	40.0	214	1	RL18_AERPE	O9y194	aeropyrum p
410	4	40.0	194	1	RS4_HORSE	P55832	equus cabal	483	4	40.0	214	1	RSMB_RAT	P17136	rattus norv
411	4	40.0	194	1	YO8R_CAEEL	P34655	caenorhabdi	484	4	40.0	214	1	SC14_SCHCO	P35795	schizophyll
412	4	40.0	195	1	HPEK_SYNY3	P72736	synecocyst	485	4	40.0	215	1	COAT_PMY	P16596	papaya mosa
413	4	40.0	195	1	TPIS_LACSA	P48493	lactuca sat	486	4	40.0	215	1	UBC_ASPB7	P27465	african swi
414	4	40.0	195	1	YV23_CAEEL	P50437	caenorhabdi	487	4	40.0	215	1	Y256_HAEIN	P43973	haemophilus
415	4	40.0	196	1	AMEL_MOUSE	P45559	mus musculu	488	4	40.0	215	1	YK2_YEAST	P53144	saccharomyc
416	4	40.0	196	1	NTPE_ENTHR	P43436	enterococcu	489	4	40.0	216	1	KCY_CHLPN	O9z7y5	chlamydia p
417	4	40.0	197	1	HAMI_YEAST	P47119	saccharomyc	490	4	40.0	216	1	Y726_METJA	O58130	methanococ
418	4	40.0	197	1	TRPC_METJA	O57690	methanococ	491	4	40.0	217	1	FLA2_METJA	O58302	methanococ
419	4	40.0	198	1	PR73_MMTVC	P03319	mouse mamma	492	4	40.0	217	1	SOMA_CEREL	P56437	cervus elap
420	4	40.0	198	1	TNFA_MOUSE	P43488	mus musculu	493	4	40.0	218	1	GTAL_CAVPO	P81706	cavia porce
421	4	40.0	198	1	YV14_YEAST	P47089	saccharomyc	494	4	40.0	218	1	MERB_BACSR	P16172	baecillus sp
422	4	40.0	199	1	NHAA_RHOSO	O53118	rhodococcus	495	4	40.0	218	1	MOGI_YEAST	P47123	saccharomyc
423	4	40.0	200	1	SSUE_PSEPU	O85762	pseudomonas	496	4	40.0	218	1	FLA4_PYRAB	O9y4w8	pyrococcus
424	4	40.0	201	1	COAT_LVX	P27334	lilly virus	497	4	40.0	219	1	FLA4_PYRKO	P06993	pyrococcus
425	4	40.0	201	1	LEUD_ECOLI	P30126	escherichia	498	4	40.0	219	1	H1B_XENLA	O28372	archaeoglob
426	4	40.0	201	1	PYRE_HELPJ	O9z1x0	helicobacte	499	4	40.0	219	1	RI8T_ARCFU	O28869	archaeoglob
427	4	40.0	201	1	PYRE_HELPJ	P56162	helicobacte	500	4	40.0	222	1	AMTB_SECE	P30771	secale cere
428	4	40.0	201	1	YPT1_PVTIN	O01690	phytophthor	501	4	40.0	222	1	KCY2_HAEIN	P43963	haemophilus
429	4	40.0	202	1	AMEL_MONDO	Q28462	monodelphis	502	4	40.0	222	1	RNS2_SOLTU	O01796	solanum tub
430	4	40.0	202	1	COAT_ELV	P35927	erysimum la	503	4	40.0	223	1	YDHC_BACSU	O05494	baecillus su
431	4	40.0	202	1	FTHC_HUMAN	P49914	homo sapien	504	4	40.0	224	1	ASR2_CRIGR	O60436	crictetulus
432	4	40.0	202	1	HR2A_TRIFL	P14530	trifluresuru	505	4	40.0	225	1	GP30_BRSP1	O38423	bacterioph
433	4	40.0	202	1	SDC4_RAT	P34901	rattus norv	506	4	40.0	225	1	RS3_LEPIN	O9x330	leptospira
434	4	40.0	204	1	BTB3_MOUSE	O64152	mus musculu	507	4	40.0	225	1	YB67_AERPE	O9yuc5	aeropyrum p
435	4	40.0	204	1	CLH5_CLAHE	P42059	cladosporiu	508	4	40.0	226	1	14P_HUMAN	O14530	homo sapien
436	4	40.0	205	1	DUT_RAT	P70583	rattus norv	509	4	40.0	226	1	ATP6_HELPJ	O9z115	helicobacte
437	4	40.0	205	1	HYFA_ECOLI	P23481	escherichia	510	4	40.0	226	1	ATP6_HELPJ	P56605	helicobacte
438	4	40.0	205	1	KAD_MICLU	P33107	micrococcus	511	4	40.0	226	1	HMMD_BRARE	O01704	brachydanio
439	4	40.0	205	1	RG84_HUMAN	P49798	homo sapien	512	4	40.0	226	1	LPOT_MYCTU	P96384	mycobacteri
440	4	40.0	205	1	RG84_MOUSE	O08899	mus musculu	513	4	40.0	226	1	OGGI_AOUAE	O66612	aquilex aeo
441	4	40.0	205	1	RG84_RAT	P49799	rattus norv	514	4	40.0	226	1	COX2_CANAD	O47657	canis adust
442	4	40.0	205	1	YNSO_YEAST	P42844	saccharomyc	515	4	40.0	227	1	COX2_CANAU	O47659	canis aureu
443	4	40.0	206	1	Y086_CAEEL	P34632	caenorhabdi	516	4	40.0	227	1	COX2_CANME	O47671	canis meson
444	4	40.0	207	1	FLA2_PYROH	O58283	pyrococcus	517	4	40.0	227	1	COX2_CANST	P98031	canis simen
445	4	40.0	207	1	IL6_MARMO	O35736	marmota mon	518	4	40.0	227	1	COX2_CHRR	O47670	chrysocyon
446	4	40.0	207	1	LEXA_AERHY	Q44069	aeromonas h	519	4	40.0	227	1	COX2_CUOAL	O47668	cuon alpinu
447	4	40.0	207	1	PLCR_PSEAE	P40695	pseudomonas	520	4	40.0	227	1	COX2_DUSTH	O47672	dusicyon th
448	4	40.0	208	1	CSF3_MOUSE	P09920	mus musculu	521	4	40.0	227	1	COX2_FELCA	P48890	felis silve
449	4	40.0	208	1	GCA3_HUMAN	O95843	homo sapien	522	4	40.0	227	1	COX2_HALGR	P38596	halichoerus
450	4	40.0	208	1	NOIY_RHISN	P55716	rhicobium s	523	4	40.0	227	1	COX2_LVCP1	O47674	lycaon pict
451	4	40.0	208	1	RS3A_SULSO	O9uxd4	sulfolobus	524	4	40.0	227	1	COX2_MACRO	P92662	macropus ro
452	4	40.0	208	1	SAOX_RHOCA	O52671	rhodobacter	525	4	40.0	227	1	COX2_NYCPR	O47675	nyctereutes
453	4	40.0	208	1	SPC3_STRPU	P16537	strongyloce	526	4	40.0	227	1	COX2_PHOVI	O00588	phoca vitul
454	4	40.0	209	1	RL3_BACSU	P42920	baecillus su	527	4	40.0	227	1	COX2_PSECP	O47676	pseudalopex
455	4	40.0	209	1	RPOC_BUCAP	P41185	buchnera ap	528	4	40.0	227	1	COX2_PSEEG	O47677	pseudalopex
456	4	40.0	209	1	YC02_KLECP	O48448	klebsiella	529	4	40.0	227	1	COX2_PSEBU	O47678	pseudalopex
457	4	40.0	209	1	YDGI_BACSU	P96707	baecillus su	530	4	40.0	227	1	COX2_SPEVE	O47679	vulpes macr
458	4	40.0	209	1	YLZ3_CAEEL	P34416	caenorhabdi	531	4	40.0	227	1	COX2_VULMA	O47680	vulpes vulp
459	4	40.0	210	1	RS7_HALHA	P15763	halobacteri	532	4	40.0	227	1	COX2_VULZU	O47681	vulpes zerd
460	4	40.0	210	1	TIR1_YEAST	P27654	saccharomyc	533	4	40.0	227	1	COX2_VULZE	O57811	pyrococcus
461	4	40.0	211	1	Y121_HUMAN	O14135	homo sapien	534	4	40.0	227	1	KCY_ECOLI	P23863	escherichia
462	4	40.0	211	1	DEDD_ECOLI	P09549	escherichia	535	4	40.0	227	1	SYL_PSESY	P52833	pseudomonas
463	4	40.0	211	1	GLP1_STNAL	P45854	sinapis alb	536	4	40.0	227	1	TZH2_HAEHA	P00643	haemophilus
464	4	40.0	211	1	IL6_MOUSE	P08505	mus musculu	537	4	40.0	228	1	CAPB_STRAU	P39851	staphylococ
465	4	40.0	211	1	SERB_METJA	O58989	methanococ	538	4	40.0	228	1	Y4MB_RHISN	P55661	rhicobium s
466	4	40.0	211	1	TX10_HUMAN	O75333	homo sapien	539	4	40.0	229	1	RT07_MARPO	P26667	marichantia
467	4	40.0	212	1	IFEA_CAEEL	O22888	caenorhabdi	540	4	40.0	230	1	YP2A_STRAU	P03866	staphylococ
468	4	40.0	212	1	RAB2_HUMAN	P08886	lymaea sta	541	4	40.0	231	1	FLUG_PSEPU	O52081	pseudomonas
469	4	40.0	212	1	RAB2_LYMS	O05975	lymaea sta	542	4	40.0	231	1	KCY1_HAEIN	P43892	haemophilus
470	4	40.0	212	1	RAB2_MOUSE	P53994	mus musculu	543	4	40.0	231	1			
471	4	40.0	212	1	RAB2_RABIT	O01971	oryctolagus	544	4	40.0	231	1			

253	4	40.0	142	1	HBAA_ANGAN	P80945	angullia an	326	4	40.0	163	1	ILVH_SALTY	P21622	salmonella
254	4	40.0	142	1	IL3_CALJA	Q28334	callitrich	327	4	40.0	163	1	SP17_PAPIA	O95230	papio hamad
255	4	40.0	142	1	IL3_SAGOE	P51445	sagunus oe	328	4	40.0	164	1	FLAV_HELPY	P94553	helicobacte
256	4	40.0	143	1	PER_DROPT	Q25206	dtrosophila	329	4	40.0	164	1	FLAV_HELPY	O25776	helicobacte
257	4	40.0	143	1	YS85_CAEEL	Q09623	caenorhabdi	330	4	40.0	164	1	IM17_SCHPO	P81130	schizosacch
258	4	40.0	144	1	CSF2_CEREL	P51748	cervus elap	331	4	40.0	164	1	OV17_ONCVO	P36991	onchocerca
259	4	40.0	144	1	CSF2_SHEEP	P28773	ovis aries	332	4	40.0	164	1	YOJ3_CAEEL	P36226	caenorhabdi
260	4	40.0	144	1	HEX9_ADEL2	P03284	human adeno	333	4	40.0	165	1	DEST_CHICK	P18359	gallus gall
261	4	40.0	144	1	RS14_TRYHB	P19800	trypanosoma	334	4	40.0	165	1	H1_TEMPY	P12305	tetrahymena
262	4	40.0	145	1	DH11_GOSHI	P09442	gossypium h	335	4	40.0	165	1	RS13_SULSO	P69896	sulfolobus
263	4	40.0	145	1	R19E_METTH	O27653	methanobact	336	4	40.0	165	1	RS41_MACPU	P79183	macaca tusc
264	4	40.0	145	1	YNR9_YEAST	P35880	saccharomyc	337	4	40.0	166	1	COF1_HUMAN	P23528	homo sapien
265	4	40.0	146	1	FLI3_BACSU	P20487	bacillus su	338	4	40.0	166	1	COF1_MOUSE	P18760	mus musculu
266	4	40.0	147	1	GLB_PAREP	P80721	paramphisto	339	4	40.0	166	1	COF1_PIG	P10668	sus scrofa
267	4	40.0	147	1	PHEB_BACSU	P21204	bacillus su	340	4	40.0	166	1	COF1_RAT	P45592	rattus norv
268	4	40.0	148	1	C552_THERH	P04164	thermus aqu	341	4	40.0	166	1	TPX_BACSU	P80864	bacillus su
269	4	40.0	148	1	CNRK_ALCEU	P37975	alcaligenes	342	4	40.0	167	1	QCR4_BACSU	P46911	bacillus su
270	4	40.0	148	1	YXIE_BACSU	P42297	bacillus su	343	4	40.0	167	1	YKG3_YEAST	P35125	saccharomyc
271	4	40.0	149	1	LRPB_BACSU	P96653	bacillus su	344	4	40.0	169	1	GP38_CANPA	O95163	methanococ
272	4	40.0	149	1	MLE3_MOUSE	P05978	mus musculu	345	4	40.0	169	1	YIST_BACSU	O07939	bacillus su
273	4	40.0	149	1	MLE3_RABIT	P02603	oryctolagus	346	4	40.0	170	1	FMF7_ECOLI	P25394	escherichia
274	4	40.0	149	1	MLE3_RAT	P02601	rattus norv	347	4	40.0	170	1	HEMX_PROXI	O51887	proteus mir
275	4	40.0	149	1	R19_HELPY	O921W3	helicobacte	348	4	40.0	171	1	ATPF_HELPY	O92K77	helicobacte
276	4	40.0	149	1	SP17_MOUSE	O62252	mus musculu	349	4	40.0	171	1	ATPF_HELPY	P36086	helicobacte
277	4	40.0	150	1	HS11_ORYSA	P27777	oryza sativ	350	4	40.0	171	1	IF3_LISMO	O53084	listeria mo
278	4	40.0	150	1	R19_HELPY	P56035	helicobacte	351	4	40.0	171	1	NUPM_BOVIN	P42029	bos taurus
279	4	40.0	150	1	RS13_METJA	P54019	methanococ	352	4	40.0	172	1	HS20_NIPER	O07160	nippostrong
280	4	40.0	151	1	HS11_WHEAT	P12810	tritlicum ae	353	4	40.0	172	1	RUB2_PSEOL	P00272	pseudomonas
281	4	40.0	151	1	SOD1_LYCES	P14830	lycopersico	354	4	40.0	173	1	Y150_METJA	O51613	methanococ
282	4	40.0	151	1	SP17_MACFA	O19021	macaca fasc	355	4	40.0	174	1	HSGB_BUCAI	P57659	buchnera ap
283	4	40.0	152	1	CORA_RAT	O63532	rattus norv	356	4	40.0	174	1	NEUJ_RAT	P12760	rattus norv
284	4	40.0	152	1	PYRI_PYRHO	O58452	pyrococcus	357	4	40.0	174	1	RBS1_WHEAT	P00871	tritlicum ae
285	4	40.0	152	1	R19_SYNY3	P42352	synecocyst	358	4	40.0	174	1	RBS_HORVU	O40004	hordeum vul
286	4	40.0	153	1	H2B1_CHLRE	P50565	chlamydomon	359	4	40.0	174	1	VC17_BPPEA	P08389	bacterioph
287	4	40.0	153	1	HS13_SOYBN	P04793	glycine max	360	4	40.0	174	1	YGT3_YEAST	P33102	saccharomyc
288	4	40.0	153	1	MYG_CARCR	P56208	caetelia car	361	4	40.0	175	1	RBS2_WHEAT	P26667	tritlicum ae
289	4	40.0	153	1	MYG_CHEMY	P02202	chelonla my	362	4	40.0	175	1	RBS_AEGSO	O38791	aegilops sq
290	4	40.0	153	1	MYG_GRAGE	P02201	grapeitmsy g	363	4	40.0	175	1	YGTG_YEAST	P53054	saccharomyc
291	4	40.0	153	1	VG17_BPPE5	P15850	bacterioph	364	4	40.0	176	1	IPYR_AERPE	O93454	aeropyrum p
292	4	40.0	153	1	YPR4_CHRYI	P45373	chromatium	365	4	40.0	176	1	ITRT_ACACO	P24924	acacia conf
293	4	40.0	154	1	HS11_LYCES	P30221	lycopersico	366	4	40.0	176	1	VEGP_HUMAN	P31023	homo sapien
294	4	40.0	154	1	HS14_SOYBN	P04794	glycine max	367	4	40.0	176	1	Y017_MYCCE	P47123	mycoplasma
295	4	40.0	154	1	HS15_SOYBN	P04795	glycine max	368	4	40.0	177	1	APT_MYCPN	P75348	mycoplasma
296	4	40.0	155	1	BCCP_HAEIN	P43874	haemophilus	369	4	40.0	177	1	CYSC_SYNY3	P73280	synecocyst
297	4	40.0	155	1	PRL_PHAVU	P25985	phaseolus v	370	4	40.0	179	1	14P_BOVIN	O18883	bos taurus
298	4	40.0	155	1	PR2_PHAVU	P25986	phaseolus v	371	4	40.0	179	1	RK27_TOBAC	P30155	nicotiana t
299	4	40.0	155	1	RNH_SALTY	P23329	salmonella	372	4	40.0	180	1	KCY_ARCFU	O23879	archaeoglob
300	4	40.0	156	1	CU55_ARADI	P80518	araneus dia	373	4	40.0	180	1	YC47_METJA	O95043	schistosoma
301	4	40.0	156	1	MAFK_HUMAN	O60675	homo sapien	374	4	40.0	181	1	NADD_CAMJE	O58644	methanococ
302	4	40.0	156	1	W723_METJA	O56133	methanococ	375	4	40.0	181	1	Y856_METJA	O98mg3	campylobact
303	4	40.0	157	1	HS2C_CHLRE	P18111	chlamydomon	376	4	40.0	183	1	RL17_PODCA	O58266	methanococ
304	4	40.0	157	1	PRFC_CANFA	Q28278	canis famli	377	4	40.0	183	1	STL_SULSO	P37380	podocoryne
305	4	40.0	157	1	VE6_HPV36	P50810	human papil	378	4	40.0	184	1	CAS3_MOUSE	O33768	sulfolobus
306	4	40.0	158	1	HS12_MEDSA	P27880	medicago sa	379	4	40.0	184	1	RL13_SCHMA	O20862	mus musculu
307	4	40.0	158	1	ILVH_BUCAP	O85294	buchnera ap	380	4	40.0	184	1	SM21_SCHMA	O95043	schistosoma
308	4	40.0	158	1	SAM2_SOYBN	P26987	glycine max	381	4	40.0	185	1	DP1_MOUSE	O60870	mus musculu
309	4	40.0	159	1	SH3B_DROME	O9nf05	drosophila	382	4	40.0	185	1	ERPL_CHLTR	O84124	chlamydia t
310	4	40.0	159	1	CU57_ARADI	P80519	araneus dia	383	4	40.0	185	1	SC6_SCHCO	O74300	schizophyll
311	4	40.0	159	1	DUT_ORFN2	P14597	orf virus (384	4	40.0	186	1	ARDH_LEIDO	O05883	leishmania
312	4	40.0	159	1	Y268_BORBU	O44756	borrella bu	385	4	40.0	186	1	IF3_BORBU	O51208	borrella bu
313	4	40.0	160	1	PETD_ODOSI	P49489	odontella s	386	4	40.0	186	1	W730_METJA	O56140	methanococ
314	4	40.0	160	1	RL10_METTH	O27191	methanobact	387	4	40.0	187	1	BNM2_PSEPU	P08085	pseudomonas
315	4	40.0	160	1	RL21_CAEEL	P34334	caenorhabdi	388	4	40.0	187	1	DCMB_MERSO	P08085	pseudomonas
316	4	40.0	161	1	HS16_SOYBN	P05478	glycine max	389	4	40.0	187	1	LEPU_BACSU	P24293	methanotri
317	4	40.0	161	1	ID4_MOUSE	P41139	mus musculu	390	4	40.0	187	1	MAVE_METEX	P42939	bacillus su
318	4	40.0	161	1	LE23_ARCFU	O29626	archaeoglob	391	4	40.0	187	1	MLEI_MOUSE	O49123	methylobact
319	4	40.0	161	1	VG41_HSVSA	O01027	herpesvirus	392	4	40.0	187	1	TOD2_PSEPU	P05977	mus musculu
320	4	40.0	162	1	MAFG_HUMAN	O15525	homo sapien	393	4	40.0	187	1	Y160_THEMA	P13454	pseudomonas
321	4	40.0	162	1	MAFG_MOUSE	O54790	mus musculu	394	4	40.0	188	1	MLEI_RAT	O93244	thermotoga
322	4	40.0	163	1	HL_TETTH	P10136	tetrahymena	395	4	40.0	189	1	TNAE_HUMAN	P02600	rattus norv
323	4	40.0	163	1	HMCS_DICDI	P54872	dicyostella	396	4	40.0	189	1	NCS2_CAEEL	P36609	caenorhabdi
324	4	40.0	163	1	ILVH_ECOLI	P00894	escherichia	397	4	40.0	189	1	PAAD_RICPR	O92d09	ricketsia
325	4	40.0	163	1	ILVH_HAEIN	P45260	haemophilus	398	4	40.0	190	1	YBAY_ECOLI	P77717	escherichia

107	5	50.0	1265	1	PIG2_RAT	P24135	rattus norv	180	4	40.0	105	1	YMO3_CAEEL	P34494	caenorhabdi
108	5	50.0	1290	1	XCPC_XENLA	P50532	xenopus lae	181	4	40.0	106	1	CYC3_DESSA	P00135	desulfotolivr
109	5	50.0	1337	1	P152_YEAST	P3685	saccharomyc	182	4	40.0	106	1	KACH_RABIT	P01393	oryctolagus
110	5	50.0	1472	1	A2MG_RAT	P06238	rattus norv	183	4	40.0	106	1	TBCA_YEAST	P48606	saccharomyc
111	5	50.0	1500	1	SSP5_STRGN	P16952	streptococc	184	4	40.0	107	1	U139_ARATH	Q95888	arabidopsis
112	5	50.0	1637	1	ADP1_MYCPN	P11311	mycoplasma	185	4	40.0	109	1	PRVA_MOUSE	P32488	mus musculu
113	5	50.0	1912	1	VITR1_CHICK	P87498	gallus galli	186	4	40.0	109	1	RBS_PROHO	P27569	prochlooth
114	5	50.0	1938	1	MYSL_YEAST	P08964	saccharomyc	187	4	40.0	110	1	RPOW_THECE	Q56254	thermococc
115	5	50.0	2208	1	POLN_MANCV	Q69014	manchester	188	4	40.0	110	1	RS6_AOUAE	Q66474	aquifex aeo
116	5	50.0	2476	1	ZAN_PIG	Q28983	sus scrofa	189	4	40.0	110	1	Y16F_BPT4	P22195	bacterioph
117	5	50.0	3133	1	HMCT_BOMMO	P98092	bombyx mori	190	4	40.0	111	1	CCR4_STNY3	P73407	synecocyst
118	4	40.0	21	1	CXGT_CONTU	P17684	conus tulip	191	4	40.0	112	1	CL33_DROMI	Q01774	drosophila
119	4	40.0	32	1	ATP7_SPIOL	P80088	spinnacia ol	192	4	40.0	113	1	HCCL_CRYCO	Q01239	cryptocodi
120	4	40.0	42	1	TFXA_RHLT	P42723	rhizobium l	193	4	40.0	113	1	RBS3_WHEAT	P02398	triticum ae
121	4	40.0	44	1	Y5K3_VACCV	P18379	vaccinia vl	194	4	40.0	113	1	RLAI_DICDI	P22684	dictyostell
122	4	40.0	49	1	R332_BACLI	P35870	bacillus l1	195	4	40.0	113	1	Y12K_BPPH	P23788	bacterioph
123	4	40.0	49	1	R332_BACLI	Q06798	bacillus su	196	4	40.0	114	1	CU05_ROMAM	P81389	homo sapien
124	4	40.0	50	1	ITR2_BOVIN	P56651	bos taurus	197	4	40.0	114	1	ET3_RABIT	P19998	oryctolagus
125	4	40.0	53	1	ADO_RABIT	P80456	oryctolagus	198	4	40.0	115	1	GUAN_RAT	P28902	rattus norv
126	4	40.0	56	1	Y546_METJA	Q57966	methanococc	199	4	40.0	116	1	GCAD_BACCL	P42817	bacillus ca
127	4	40.0	59	1	TAT2_AOUAE	Q66477	aquifex aeo	200	4	40.0	116	1	GUAN_MOUSE	P33680	mus musculu
128	4	40.0	62	1	UCRX_BOVIN	P00130	bos taurus	201	4	40.0	116	1	RM14_ACAP0	P34829	acanthamoeb
129	4	40.0	65	1	YHSB_CLOAB	Q04333	clostridium	202	4	40.0	116	1	SP21_BACCO	P70877	bacillus co
130	4	40.0	65	1	YNOL_RHLR	P33214	rhizobium f	203	4	40.0	117	1	HV1A_HUMAN	P01742	homo sapien
131	4	40.0	66	1	YGLR_STRCO	Q05954	streptomyce	204	4	40.0	117	1	HV1B_HUMAN	P01743	homo sapien
132	4	40.0	66	1	YYCD_BACSU	P37480	bacillus su	205	4	40.0	117	1	HV1G_HUMAN	P23083	homo sapien
133	4	40.0	67	1	HJAI_METJA	Q57632	methanococc	206	4	40.0	117	1	NLTS_ORYZA	Q65091	oryza sativ
134	4	40.0	67	1	HJAI_METJA	Q58342	methanococc	207	4	40.0	119	1	NLRP_SALTI	Q56131	salmonella
135	4	40.0	67	1	HJAI_METJA	Q58655	methanococc	208	4	40.0	119	1	RL24_LEPIN	Q9x435	leptospira
136	4	40.0	67	1	HJAI_METJA	Q60264	methanococc	209	4	40.0	120	1	CU19_ARADI	P80515	araneus dla
137	4	40.0	68	1	TRPC_BACPU	Q9wv88	streptococc	210	4	40.0	121	1	YHIT_AOUAE	Q66536	aquifex aeo
138	4	40.0	68	1	TRPC_BACPU	P18268	bacillus pu	211	4	40.0	121	1	RBS1_SPIOL	P00870	spinnacia ol
139	4	40.0	72	1	VG35_ARCFU	Q05245	mycobacteri	212	4	40.0	123	1	Y949_METJA	Q58359	methanococc
140	4	40.0	73	1	Y556_ARCFU	Q29695	archaeoglob	213	4	40.0	124	1	GC5H_THEMA	Q9w455	thermotoga
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143	4	40.0	77	1	KEA2_ECOLI	P31964	desulfotolivr	216	4	40.0	124	1	HV1E_HUMAN	P12940	hordium vul
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145	4	40.0	82	1	RS16_SALTY	Q9ze35	rickettsia	218	4	40.0	125	1	FAB2_AMBME	P81400	ambystoma m
146	4	40.0	82	1	TATA_VIRCH	P36242	salmonella	219	4	40.0	125	1	FLIO_CHICK	P80262	gallus gall
147	4	40.0	83	1	GVGI_HALNI	P57051	vibrio chol	220	4	40.0	125	1	HV1F_HUMAN	P54699	salmonella
148	4	40.0	88	1	Y67_BPT7	P24371	halobacteri	221	4	40.0	125	1	SDIS_COMTE	P06326	homo sapien
149	4	40.0	89	1	ACYP_ARCFU	P03801	archaeoglob	222	4	40.0	125	1	CU24_ARADI	P00947	comamonas t
150	4	40.0	90	1	LPPL_HUMAN	Q29440	archaeoglob	223	4	40.0	126	1	CU26_ARADI	P80516	araneus dla
151	4	40.0	90	1	RPOL_SULAC	Q95968	homo sapien	224	4	40.0	127	1	YFID_HAEIN	P44455	haemophilus
152	4	40.0	90	1	Y032_HELPJ	P46217	sulfolobus	225	4	40.0	127	1	RL7_TREPA	Q83268	treponema p
153	4	40.0	92	1	RL5_MOUSE	Q9zn32	helicobacte	226	4	40.0	129	1	RM14_ACACA	P46767	acanthamoeb
154	4	40.0	93	1	IM09_ARATH	Q9xg99	arabidopsis	227	4	40.0	130	1	NRD1_BACSU	P50618	bacillus su
155	4	40.0	93	1	VOIC_CAEEL	Q09283	caenorhabdi	228	4	40.0	130	1	SY28_MOUSE	Q9j112	mus musculu
156	4	40.0	94	1	NLPD_SALDU	P39780	caenorhabdi	229	4	40.0	130	1	Y390_METJA	Q57835	methanococc
157	4	40.0	94	1	YNGC_CLOPE	P26834	clostridium	230	4	40.0	130	1	Y614_METJA	Q58031	methanococc
158	4	40.0	96	1	SASG_BACME	P02961	bacillus me	231	4	40.0	130	1	Y056_MCTU	P71993	mycobacteri
159	4	40.0	96	1	YC4_TYLCU	P38612	tomato yell	232	4	40.0	132	1	HEX9_ADE40	P48312	human adeno
160	4	40.0	98	1	CYTB_MOUSE	Q62426	mus musculu	233	4	40.0	132	1	TF5A_METJA	Q58265	methanococc
161	4	40.0	98	1	NLPD_SALTY	P40827	salmonella	234	4	40.0	132	1	VG24_BPM15	Q05221	mycobacteri
162	4	40.0	98	1	YC4_TYLCU	P27272	tomato yell	235	4	40.0	133	1	CDD_SCHPO	C09190	schizosacch
163	4	40.0	98	1	YORR_PYRMO	Q48399	bacterioph	236	4	40.0	133	1	HEX9_ADE41	P32539	human adeno
164	4	40.0	99	1	Y13J_BPT4	P27085	methanobact	237	4	40.0	133	1	ITL4_FELCA	P55070	fells silve
165	4	40.0	99	1	Y13J_BPT4	P10623	methanococc	238	4	40.0	133	1	PROF_HELAN	Q81992	heliolantus
166	4	40.0	99	1	Y13J_BPT4	P39503	bacterioph	239	4	40.0	134	1	H2B_ENTIV	P40284	entamoeba 1
167	4	40.0	99	1	Y13J_BPT4	P20297	pyrococcus	240	4	40.0	134	1	NIFB_KLEBO	Q9ng84	homo sapien
168	4	40.0	100	1	REGN_BPP22	P04891	bacterioph	241	4	40.0	134	1	VG24_BPPD2	P64218	mycobacteri
169	4	40.0	101	1	RL5_RABIT	P19949	oryctolagus	242	4	40.0	135	1	YB76_YEAST	P31776	zea mays (m
170	4	40.0	102	1	SGP3_CHRVI	Q52055	chromatium	243	4	40.0	136	1	COX2_CANFA	P38322	saccharomyc
171	4	40.0	102	1	VE7_PAPVE	P11332	european el	244	4	40.0	137	1	NIFB_KLEBO	Q63855	canis famli
172	4	40.0	103	1	ACBP_ANAPL	P45882	anas platyr	245	4	40.0	137	1	GC5H_PYRAB	P56265	pyrococcus
173	4	40.0	103	1	LAC_CHICK	P20763	gallus galli	246	4	40.0	138	1	NEDR_MICVI	Q09091	pleurochrys
174	4	40.0	104	1	GAST_BOVIN	P01352	bos taurus	247	4	40.0	139	1	RBS_PLECA	Q08052	pleurochrys
175	4	40.0	104	1	GAST_SHEEP	P00266	ovis aries	248	4	40.0	139	1	RS6_BORBU	Q51142	borrella bu
176	4	40.0	105	1	YR7H_ECOLI	P21332	escherichia	249	4	40.0	140	1	YB60_HELPU	Q25775	helicobacte
177	4	40.0	105	1	LAC_HUMAN	P01842	homo sapien	250	4	40.0	141	1	YFE3_CLOPA	Q04655	clostridium
178	4	40.0	105	1	NDC1_BRAVA	P26024	bradyrhizob	251	4	40.0					
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:43:05 ; Search time 20.38 Seconds
(without alignments)
16.808 Million cell updates/sec

Title: US-09-372-036-31

Perfect score: 10

Sequence: 1 PVAPQTQEVKK 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 3425486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	6	60.0	617	1	ABP1_SACEX
3	6	60.0	985	1	ENV_FOAMV
4	6	60.0	1133	1	ATX3_TETTH
5	5	50.0	102	1	HCC2_CRVCO
6	5	50.0	103	1	KAC4_RABTT
7	5	50.0	153	1	PRS1_SOLTU
8	5	50.0	174	1	RPC1_BPMU
9	5	50.0	185	1	EPF1_CHLPN
10	5	50.0	187	1	VGG_BPPHK
11	5	50.0	200	1	RLZ9_MYCGE
12	5	50.0	201	1	IMMU_BPSPB
13	5	50.0	206	1	VAD1_TREPA
14	5	50.0	209	1	VG40_BPPH8
15	5	50.0	217	1	V33P_ADEA1
16	5	50.0	217	1	YD67_SCHBO
17	5	50.0	228	1	TRKA_PYRHO
18	5	50.0	239	1	KLK2_CAVPO
19	5	50.0	246	1	Y984_CAME
20	5	50.0	250	1	Y887_MYCPN
21	5	50.0	251	1	CB24_ARATH
22	5	50.0	270	1	URED_SYNY3
23	5	50.0	296	1	YB27_YEAST
24	5	50.0	305	1	LXD2_PHOLE
25	5	50.0	309	1	POLG_HCVH7
26	5	50.0	309	1	URIG_SOYBN
27	5	50.0	309	1	URID_SOYBN
28	5	50.0	327	1	ENT2_MOUSE
29	5	50.0	336	1	YB56_XENLA
30	5	50.0	346	1	TRPA_MAIZE
31	5	50.0	354	1	YMA3_MYCBO
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33	5	50.0	366	1	RRPO_REOVD

34	5	50.0	366	1	RRPO_REOVD	P12002 reovirus (t
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37	5	50.0	386	1	GAG_HY1W2	P05889 human immun
38	5	50.0	391	1	THAB_PAROL	P09124 parathichy
39	5	50.0	400	1	CYH2_MOUSE	P099418 homo sapien
40	5	50.0	400	1	CYH2_MOUSE	P97695 mus musculu
41	5	50.0	415	1	YLN2_CAEBL	Q18964 caenorhabdi
42	5	50.0	428	1	SOX_HUMAN	P98077 homo sapien
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45	5	50.0	452	1	YDQ4_SCHPO	O14197 schizosacch
46	5	50.0	453	1	GATA_HELPJ	O92113 helicobacte
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48	5	50.0	465	1	RPBA_VIBCH	O07024 vibrio chol
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50	5	50.0	473	1	GLNA_SYNY3	P77961 synechocyst
51	5	50.0	473	1	SYE_AQUAE	O67271 aquifex aeo
52	5	50.0	481	1	PEO_LISIN	O01836 listeria in
53	5	50.0	484	1	SCAT_ECOLI	P39301 escherichia
54	5	50.0	490	1	SUCP_LEIME	O59495 leuconostoc
55	5	50.0	498	1	YCUK_ECOLI	P78061 escherichia
56	5	50.0	501	1	YH92_CAEBL	Q23256 caenorhabdi
57	5	50.0	503	1	GAG_HY1JR	P20873 human immun
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61	5	50.0	509	1	PSBB_GUTHH	O78511 guillardi
62	5	50.0	519	1	CHX2_MOUSE	P30658 mus musculu
63	5	50.0	519	1	UVRC_AQUAE	O67887 aquifex aeo
64	5	50.0	572	1	GAG_IPHA	P04023 hamster int
65	5	50.0	572	1	PTL_STPAU	P51183 staphylococ
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73	5	50.0	642	1	HEMA_INCP1	P07968 influenza c
74	5	50.0	642	1	HEMA_INCP2	P07967 influenza c
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76	5	50.0	643	1	DP3X_ECOLI	P06710 escherichia
77	5	50.0	648	1	HEMA_INCPB	O67387 influenza c
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83	5	50.0	707	1	BMP1_XENLA	P98070 xenopus lae
84	5	50.0	713	1	ICAL_PIG	P12675 sus scrofa
85	5	50.0	723	1	ICAL_SHEEP	O95208 ovis aries
86	5	50.0	747	1	YHMA_CAEBL	P34478 caenorhabdi
87	5	50.0	752	1	HPRI_YEAST	P17629 saccharomyc
88	5	50.0	778	1	RG12_MOUSE	O61193 mus musculu
89	5	50.0	791	1	PPSA_ECOLI	P23538 escherichia
90	5	50.0	806	1	NNOG_MYCTU	P95175 mycopacteri
91	5	50.0	806	1	PFEB_DROME	O05192 drosophila
92	5	50.0	817	1	VRP1_YEAST	P37370 saccharomyc
93	5	50.0	909	1	CR1A_FUSO	P32958 fusarium so
94	5	50.0	925	1	UVRA_ZYMMO	O31151 zygomonas m
95	5	50.0	958	1	IF3A_TOBAC	Q40554 nicotiana t
96	5	50.0	980	1	PEX6_HUMAN	O13608 homo sapien
97	5	50.0	983	1	Y144_HUMAN	Q14157 homo sapien
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99	5	50.0	991	1	IF2P_YEAST	P98063 mus musculu
100	5	50.0	1002	1	MYPS_HUMAN	P39730 saccharomyc
101	5	50.0	1141	1	AB11_CAEBL	O00872 homo sapien
102	5	50.0	1196	1	AB11_CAEBL	P39945 caenorhabdi
103	5	50.0	1210	1	AF4_HUMAN	P51825 homo sapien
104	5	50.0	1233	1	YF16_YEAST	P33597 saccharomyc
105	5	50.0	1245	1	C5BA_BACTU	O45712 bacillus th
106	5	50.0	1252	1	PIG2_HUMAN	P16885 homo sapien

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 33 646.5
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FILING DATE: 22-OCT-1992
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APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
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APPLICATION NUMBER: DE P 43 18 186.4
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ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 05495-0001-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-471-770-59

Query Match 50.0%; Score 5; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TOEVK 9
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Db 309 TOEVK 313

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OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-470-202-59

Query Match 50.0%; Score 5; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEVR 9
|||||
DB 309 TOEVR 313

RESULT 49
US-08-470-202-60
Sequence 60, Application US/08470202
Patent No. 5759808
GENERAL INFORMATION:
APPLICANT: Guerlier, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and Its
TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,202
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael J. Blake
REGISTRATION NUMBER: 37,096
REFERENCE/DOCKET NUMBER: 05495-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-470-202-60

Query Match 50.0%; Score 5; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEVR 9
|||||
DB 309 TOEVR 313

RESULT 50
US-08-471-770-59
Sequence 59, Application US/08471770
Patent No. 5770427
GENERAL INFORMATION:
APPLICANT: Guerlier, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and Its
TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,770
FILING DATE: 06-JUN-1995

Query Match 50.0%; Score 5; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
Db 361 PVAPT 365

RESULT 45

US-09-071-709-12
Sequence 12, Application US/09071709
Patent No. 6171790
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,709
FILING DATE: Filed Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PP-0513 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-709-12

Query Match 50.0%; Score 5; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYK 9
Db 33 TOEYK 37

RESULT 46

US-08-889-841-8
Sequence 8, Application US/08889841B
Patent No. 6090392
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: US 60/676,737
EARLIER FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 486
TYPE: PRT
ORGANISM: HIV
US-08-889-841-8

OY 2 VAPTO 6
Db 457 VAPTO 461

Query Match 50.0%; Score 5; DB 3; Length 486;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPTO 6
Db 457 VAPTO 461

RESULT 47

US-08-889-841-10
Sequence 10, Application US/08889841B
Patent No. 6090392
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: US 60/676,737
EARLIER FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 491
TYPE: PRT
ORGANISM: HIV
US-08-889-841-10

Query Match 50.0%; Score 5; DB 3; Length 491;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPTO 6
Db 457 VAPTO 461

RESULT 48

US-08-470-202-59
Sequence 59, Application US/08470202
Patent No. 5759808
GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and Its
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

APPLICANT: Okada, Shigenori
APPLICANT: Adachi, Kenichi
TITLE OF INVENTION: BILE ACID SULFATASE GENE, PLASMID
TITLE OF INVENTION: CONTAINING SAID GENE AND METHOD OF PRODUCING BILE ACID
TITLE OF INVENTION: SULFATE SULFATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,104A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP PCT/JP93/00244
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: SAGE03.001AUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-140-104A-2

Query Match 50.0%; Score 5; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PTOEV 8
DB 431 PTOEV 435

RESULT 43
US-08-353-550-6
Sequence 6, Application US/08353550
Patent No. 5744313
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Cavanaugh, William M.
TITLE OF INVENTION: No. 5744313el Protein Domain which Binds
TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,550
FILING DATE: 09-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 02307K-057300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-550-6

Query Match 50.0%; Score 5; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
DB 361 PVAPT 365

RESULT 44
US-08-551-687-6
Sequence 6, Application US/08551687
Patent No. 5925547
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Cavanaugh, William M.
TITLE OF INVENTION: No. 5925547el Protein Domain which Binds
TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,687
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,550
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: P39,787
REFERENCE/DOCKET NUMBER: 2307K-5731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-687-6

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,550
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: P39,787
REFERENCE/DOCKET NUMBER: 2307K-5731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-687-1

Query Match 50.0%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
11111
Db 361 PVAPT 365

RESULT 40
US-08-807-342B-5
Sequence 5, Application US/08807342B
Patent No. 6077686
GENERAL INFORMATION:
APPLICANT: Dett, Channing
APPLICANT: O'Bryan, John P.
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: No. 6077686el SHC Proteins
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,342B
FILING DATE: 28-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,516
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: MTS2USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-08-807-342B-5

Query Match 50.0%; Score 5; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
11111
Db 364 PVAPT 368

RESULT 41
US-08-679-635A-3
Sequence 3, Application US/08679635A
Patent No. 5985643
GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,635A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-679-635A-3

Query Match 50.0%; Score 5; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYK 10
11111
Db 228 OEYK 232

RESULT 42
US-08-140-104A-2
Sequence 2, Application US/08140104A
Patent No. 5585255
GENERAL INFORMATION:
APPLICANT: Tsukada, Yogi
APPLICANT: Tazuke, Yasuhiko

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-581A-2

Query Match 50.0%; Score 5; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTOE 7
IIIIII
DB 357 APTOE 361

RESULT 37
US-09-023-591A-2
Sequence 2, Application US/09023591A
Patent No. 6210914
GENERAL INFORMATION:
APPLICANT: Staunton, Donald E.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding/Signalling
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,591A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,581
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/33886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-023-591A-2
Query Match 50.0%; Score 5; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 APTOE 7
IIIIII
DB 357 APTOE 361
RESULT 38
US-08-353-550-1
Sequence 1, Application US/08353550
Patent No. 5744313

GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: No. 5744313el Protein Domain Which Binds
TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,550
FILING DATE: 09-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 02307K-057300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-550-1

Query Match 50.0%; Score 5; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
IIIIII
DB 361 PVAPT 365

RESULT 39
US-08-551-687-1
Sequence 1, Application US/08551687
Patent No. 5925547
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: No. 5925547el Protein Domain Which Binds
TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,687
FILING DATE: 01-NOV-1995

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-504B-19

Query Match 50.0%; Score 5; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OEYK 10
DB 278 OEYK 282

RESULT 35
US-08-459-444-19
Sequence 19, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalin M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evoila, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-JUN-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/PI/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-459-444-19

Query Match 50.0%; Score 5; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OEYK 10
DB 278 OEYK 282

RESULT 36
US-08-839-581A-2
Sequence 2, Application US/08839581A
Patent No. 5938705
GENERAL INFORMATION:
APPLICANT: Staunton, Donald E.
Lipsky, Brian P.
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
Binding/Signaling
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,581A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/33886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids

STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-448A-19

Query Match 50.0%; Score 5; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 2,6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
|1111
DB 278 QEVKK 282

RESULT 33
US-08-459-595A-19
Sequence 19, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains

STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-595A-19

Query Match 50.0%; Score 5; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 2,6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
|1111
DB 278 QEVKK 282

RESULT 34
US-08-459-504B-19
Sequence 19, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park

GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Ruten, William J.
TITLE OF INVENTION: NANV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hardin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human 27
US-08-444-818-156

Query Match 50.0%; Score 5; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAFT 5
11111
Db 113 PVAFT 117

RESULT 31
US-07-951-715A-19
Sequence 19, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CCG 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-951-715A-19

Query Match 50.0%; Score 5; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QEVK 10
11111
Db 278 QEVK 282

RESULT 32
US-08-459-448A-19
Sequence 19, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation

SUSAN D., POPE, SHARON H., STRAUSBERG, SUSAN L., RUFF, MICHAEL D.,
; AUGUSTINE, PATRICIA C., DANFORTH, HARRY D.
; TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
; ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,432
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 581,693
; FILING DATE: 12-SEP-1990
; APPLICATION NUMBER: 215,162
; FILING DATE: 05-JUL-1989
; APPLICATION NUMBER: 746,520
; FILING DATE: 19-JUN-1985
; APPLICATION NUMBER: 627,811
; FILING DATE: 05-JUL-1984
; SEQ ID NO: 2:
; LENGTH: 242
5482709-2

Query Match 50.0%; Score 5; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PTOEV 8
; | | | | |
Db 36 PTOEV 40

RESULT 28
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5869102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; NUMBER OF INVENTIONS: THEREOF
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 50.0%; Score 5; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 APTOE 7
; | | | | |
Db 239 APTOE 243

RESULT 29
US-08-444-818-152
; Sequence 152, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Ruter, William J.
; TITLE OF INVENTION: NANV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Ailsa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110,002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-444-818-152

Query Match 50.0%; Score 5; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
; | | | | |
Db 113 PVAPT 117

RESULT 30
US-08-444-818-156
; Sequence 156, Application US/08444818
; Patent No. 6150087

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosaipiens
INDIVIDUAL ISOLATE: S18
PCT-US95-10398-57

Query Match 50.0%; Score 5; DB 5; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
11111
DB 50 PVAPT 54

RESULT 25
US-08-969-721-8
Sequence 8, Application US/08969721
Patent No. 5972339
GENERAL INFORMATION:
APPLICANT: Walker, Bruce D.
TITLE OF INVENTION: METHODS OF ELICITING ANTI-HIV-1
TITLE OF INVENTION: HELPER T CELL RESPONSES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,721
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/732001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-969-721-8

Query Match 50.0%; Score 5; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEYK 9
11111
DB 178 TOEYK 182

RESULT 26
5273901-3
Patent No. 5273901
APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
SPOROZOITE 21.5 KB ANTIGEN, AC-6B
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/581,693
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
SEQ ID NO: 3
LENGTH: 242
5273901-3

Query Match 50.0%; Score 5; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PTOEV 8
11111
DB 36 PTOEV 40

RESULT 27
5482709-2
Patent No. 5482709
APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
US-08-468-570-57

Query Match 50.0%; Score 5; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVAPT 5
|1111
Db 50 PVAPT 54

RESULT 22
US-08-290-665A-57
Sequence 57, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
US-08-290-665A-57

Query Match 50.0%; Score 5; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVAPT 5
|1111
Db 50 PVAPT 54

RESULT 23
US-08-444-818-167
Sequence 167, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutler, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Ailsa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110,002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: JH27
US-08-444-818-167

Query Match 50.0%; Score 5; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVAPT 5
|1111
Db 125 PVAPT 129

RESULT 24
PCT-US95-10398-57
Sequence 57, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

US-08-231-368-44
; Sequence 44, Application US/08231368
; Patent No. 5756312
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-368-44

Query Match 50.0%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
|||||
Db 50 PVAPT 54

RESULT 20
US-08-440-210-44
; Sequence 44, Application US/08440210
; Patent No. 5766845
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,210
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-210-44

Query Match 50.0%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
|||||
Db 50 PVAPT 54

RESULT 21
US-08-468-570-57
; Sequence 57, Application US/08468570
; Patent No. 5871962
; GENERAL INFORMATION:
; APPLICANT: BURK, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,570
; FILING DATE: 6-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/086.428B
;; FILING DATE: 29-JUN-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: RICHARD W. BORK
;; REGISTRATION NUMBER: 36,459
;; REFERENCE/DOCKET NUMBER: 2026-4070
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;;
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 57:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 192 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; ORIGINAL SOURCE:
;; ORGANISM: homosapiens
;; INDIVIDUAL ISOLATE: S18
;;
US-08-086-428B-57
;
Query Match 50.0%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 PVAPT 5
11111
DB 50 PVAPT 54
;
RESULT 17
US-08-440-103-44
;; Sequence 44, Application US/08440103
;; Patent No. 5670152
;; GENERAL INFORMATION:
;; APPLICANT: Weiner, Amy J.
;; APPLICANT: Houghton, Michael
;; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Chiron Corporation
;; STREET: 4560 Horton Street
;; CITY: Emeryville
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94608
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/440.103
;; FILING DATE: 12-MAY-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231.368
;; FILING DATE:
;; APPLICATION NUMBER: US/07/759.575
;; FILING DATE: 13-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McClung, Barbara G.
;; REGISTRATION NUMBER: 33,113
;; REFERENCE/DOCKET NUMBER: 0205.001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 601-2708
;; TELEFAX: (510) 655-3542
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 192 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-440-103-44
;
Query Match 50.0%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 PVAPT 5
11111
DB 50 PVAPT 54
;
RESULT 18
US-08-440-542-44
;; Sequence 44, Application US/08440542
;; Patent No. 5670153
;; GENERAL INFORMATION:
;; APPLICANT: Weiner, Amy J.
;; APPLICANT: Houghton, Michael
;; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Chiron Corporation
;; STREET: 4560 Horton Street
;; CITY: Emeryville
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94608
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/440.542
;; FILING DATE: 12-MAY-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231.368
;; FILING DATE:
;; APPLICATION NUMBER: US/07/759.575
;; FILING DATE: 13-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McClung, Barbara G.
;; REGISTRATION NUMBER: 33,113
;; REFERENCE/DOCKET NUMBER: 0205.001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 601-2708
;; TELEFAX: (510) 655-3542
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 192 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-440-542-44
;
Query Match 50.0%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 PVAPT 5
11111
DB 50 PVAPT 54
;
RESULT 19

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RESULT 14
US-08-810-572A-4
; Sequence 4, Application US/08010572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-810-572A-4

Query Match          50.0%; Score 5; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 APTQE 7
      |||||
Db      .53 APTQE 57

RESULT 15
US-08-497-025-10
; Sequence 10, Application US/08497025
; Patent No. 5646251
; GENERAL INFORMATION:
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Rivas, Alberto
; APPLICANT: Laus, Reiner
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: ALLOREACTION-ASSOCIATED ANTIGEN (ARA9):
; TITLE OF INVENTION: A NOVEL MEMBER OF THE IMMUNOGLOBULIN GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
```

```
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,025
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,212
; FILING DATE: 05-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..118
; OTHER INFORMATION:
; OTHER INFORMATION: Immunoglobulin-type domain of ARA9-h-1.*
;
US-08-497-025-10

Query Match          50.0%; Score 5; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      4 PTOEV 8
      |||||
Db      43 PTOEV 47

RESULT 16
US-08-086-428B-57
; Sequence 57, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BURK, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
```

APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14-20
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-17

Query Match 60.0%; Score 6; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTO 6
DB 8 PVAPTO 13

RESULT 13
US-08-456-670B-35
Sequence 35; Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKELEIR, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria innocua
US-08-456-670B-35

Query Match 50.0%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QEVKK 10
DB 7 QEVKK 11

OY 4 PTOEVKK 10
| | | | |
Db 1 PTOEVKK 7

RESULT 10

US-08-482-847-28
; Sequence 28, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-482-847-28

Query Match 70.0%; Score 7; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PTOEVKK 10
| | | | |
Db 1 PTOEVKK 7

RESULT 11

US-08-456-670B-26
; Sequence 26, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, Siegfried
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINXWETTER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED

APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-26

Query Match 60.0%; Score 6; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPQ 6
| | | | |
Db 4 PVAPQ 9

RESULT 12

US-08-456-670B-17
; Sequence 17, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, Siegfried
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINXWETTER, WINFRIED
; APPLICANT: BURGER, CHRISTA

APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-26

Query Match 100.0%; Score 10; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PVAPTOEVKK 10
|||||
Db 148 PVAPTOEVKK 157

RESULT 8
US-08-482-847-26
Sequence 26, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-26

Query Match 100.0%; Score 10; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PVAPTOEVKK 10
|||||
Db 148 PVAPTOEVKK 157

RESULT 9
US-08-127-499A-28
Sequence 28, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-28

Query Match 70.0%; Score 7; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ. ID NO.: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-39

Query Match 100.0%; Score 10; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTOEVRK 10
| | | | | | | | | |
Db 79 PVAPTOEVRK 88
RESULT 6
US-08-456-670B-40
; Sequence 40, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED

APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ. ID NO.: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-40

Query Match 100.0%; Score 10; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTOEVRK 10
| | | | | | | | | |
Db 148 PVAPTOEVRK 157
RESULT 7
US-08-127-499A-26
; Sequence 26, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane

APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: *Listeria monocytogenes*
STRAIN: EGD
US-08-456-670B-30

Query Match 100.0%; Score 10; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 PVAPTOEVKK 10
Db 3 PVAPTOEVKK 12

RESULT 3
US-08-127-499A-27
Sequence 27, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-27

Query Match 100.0%; Score 10; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PVAPTOEVKK 10
Db 5 PVAPTOEVKK 14

RESULT 4
US-08-482-847-27
Sequence 27, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-27

Query Match 100.0%; Score 10; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 PVAPTOEVKK 10
Db 5 PVAPTOEVKK 14

RESULT 5
US-08-456-670B-39
Sequence 39, Application US/08456670B
Patent No. 5532415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA

977 4 40.0 300 3 US-08-705-875A-6 Sequence 6, Appl1
978 4 40.0 300 4 US-09-220-731-21 Sequence 21, Appl1
979 4 40.0 300 4 US-08-439-992A-5 Sequence 5, Appl1
980 4 40.0 301 3 US-09-002-298-3 Sequence 3, Appl1
981 4 40.0 302 1 US-07-640-029-6 Sequence 6, Appl1
982 4 40.0 302 1 US-07-921-807B-7 Sequence 7, Appl1
983 4 40.0 302 1 US-07-921-807B-8 Sequence 8, Appl1
984 4 40.0 302 1 US-08-441-944A-7 Sequence 7, Appl1
985 4 40.0 302 4 US-08-441-944A-8 Sequence 8, Appl1
986 4 40.0 302 1 US-08-439-992A-6 Sequence 6, Appl1
987 4 40.0 303 1 US-07-917-111-2 Sequence 2, Appl1
988 4 40.0 303 1 US-07-917-111-3 Sequence 3, Appl1
989 4 40.0 303 1 US-08-479-638-2 Sequence 2, Appl1
990 4 40.0 303 1 US-08-479-638-3 Sequence 3, Appl1
991 4 40.0 303 2 US-08-294-871A-2 Sequence 4, Appl1
992 4 40.0 303 2 US-08-294-871A-4 Sequence 6, Appl1
993 4 40.0 303 2 US-08-294-871A-6 Sequence 8, Appl1
994 4 40.0 303 2 US-08-294-871A-8 Sequence 10, Appl1
995 4 40.0 303 2 US-08-294-871A-10 Sequence 12, Appl1
996 4 40.0 303 2 US-08-294-871A-12 Sequence 14, Appl1
997 4 40.0 303 2 US-08-294-871A-14 Sequence 16, Appl1
998 4 40.0 303 2 US-08-294-871A-16 Sequence 18, Appl1
999 4 40.0 303 2 US-08-294-871A-18 Sequence 20, Appl1
1000 4 40.0 303 2 US-08-294-871A-18 Sequence 20, Appl1

ALIGNMENTS

FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1
US-08-456-670B-31
Sequence 31, Application US/08456670B
Patent No. 5932415

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4

RESULT 2

US-08-456-670B-30
Sequence 30, Application US/08456670B
Patent No. 5932415

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:

831	4	40.0	232	2	US-08-615-271-8	Sequence 8, Appl	904	4	40.0	255	3	US-08-841-089-106	Sequence 106, App
832	4	40.0	232	3	US-09-074-660-8	Sequence 8, Appl	905	4	40.0	255	5	PCT-US95-04570-106	Sequence 106, App
833	4	40.0	232	3	US-09-074-659-8	Sequence 8, Appl	906	4	40.0	255	5	PCT-US95-04589-106	Sequence 106, App
834	4	40.0	232	3	US-09-106-468-8	Sequence 8, Appl	907	4	40.0	255	5	PCT-US96-01314-57	Sequence 57, Appl
835	4	40.0	232	4	US-09-106-466A-8	Sequence 8, Appl	908	4	40.0	257	6	5204259-5	Patent No. 5204259
836	4	40.0	232	4	US-09-106-467-8	Sequence 8, Appl	909	4	40.0	258	1	US-08-744-026-3	Sequence 3, Appl
837	4	40.0	232	6	5204259-1	Patent No. 5204259	910	4	40.0	258	2	US-09-102-732-3	Sequence 3, Appl
838	4	40.0	233	4	US-08-523-894-6	Sequence 6, Appl	911	4	40.0	258	4	US-08-961-083-00	Sequence 90, Appl
839	4	40.0	234	1	US-08-287-959-10	Sequence 10, Appl	912	4	40.0	258	4	US-09-261-767-3	Sequence 3, Appl
840	4	40.0	234	1	US-08-487-550-2	Sequence 2, Appl	913	4	40.0	258	6	5204259-3	Patent No. 5204259
841	4	40.0	235	1	US-08-458-516-23	Sequence 23, Appl	914	4	40.0	259	4	US-09-216-295-5	Sequence 5, Appl
842	4	40.0	235	2	US-08-378-939-12	Sequence 12, Appl	915	4	40.0	261	1	US-08-744-026-5	Sequence 5, Appl
843	4	40.0	235	4	US-09-049-672A-10	Sequence 10, Appl	916	4	40.0	261	2	US-09-102-732-5	Sequence 5, Appl
844	4	40.0	235	4	US-09-049-672A-12	Sequence 12, Appl	917	4	40.0	261	3	US-08-768-859A-6	Sequence 6, Appl
845	4	40.0	236	3	US-08-487-550-10	Sequence 10, Appl	918	4	40.0	261	3	US-08-768-859A-19	Sequence 19, Appl
846	4	40.0	236	3	US-08-493-071-15	Sequence 15, Appl	919	4	40.0	261	3	US-09-083-531-6	Sequence 6, Appl
847	4	40.0	236	4	US-09-049-672A-7	Sequence 7, Appl	920	4	40.0	261	3	US-08-767-820A-6	Sequence 6, Appl
848	4	40.0	236	4	US-08-961-083-96	Sequence 96, Appl	921	4	40.0	261	3	US-08-767-820A-19	Sequence 19, Appl
849	4	40.0	236	4	US-08-096-946-10	Sequence 10, Appl	922	4	40.0	261	3	US-08-622-046B-3	Sequence 3, Appl
850	4	40.0	237	1	US-08-096-946-10	Sequence 10, Appl	923	4	40.0	261	3	US-08-622-046B-14	Sequence 14, Appl
851	4	40.0	237	1	US-08-096-946-11	Sequence 11, Appl	924	4	40.0	261	4	US-09-261-767-5	Sequence 5, Appl
852	4	40.0	237	2	US-08-672-564-3	Sequence 3, Appl	925	4	40.0	261	4	US-09-100-264-7	Sequence 7, Appl
853	4	40.0	237	2	US-08-844-024-2	Sequence 2, Appl	926	4	40.0	261	5	PCT-US95-06157-6	Sequence 6, Appl
854	4	40.0	237	2	US-08-718-547-2	Sequence 2, Appl	927	4	40.0	262	1	US-08-106-981-6	Sequence 6, Appl
855	4	40.0	237	2	US-08-768-859A-1	Sequence 1, Appl	928	4	40.0	262	1	US-08-744-026-4	Sequence 4, Appl
856	4	40.0	237	3	US-08-768-859A-16	Sequence 16, Appl	929	4	40.0	262	2	US-08-790-137-1	Sequence 1, Appl
857	4	40.0	237	3	US-08-767-820A-1	Sequence 21, Appl	930	4	40.0	262	2	US-08-790-137-3	Sequence 3, Appl
858	4	40.0	237	3	US-08-767-820A-16	Sequence 16, Appl	931	4	40.0	262	2	US-08-681-151-4	Sequence 4, Appl
859	4	40.0	237	3	US-08-767-820A-21	Sequence 21, Appl	932	4	40.0	262	2	US-09-102-732-4	Sequence 4, Appl
860	4	40.0	237	3	US-08-622-046B-1	Sequence 1, Appl	933	4	40.0	262	2	US-08-824-874-4	Sequence 4, Appl
861	4	40.0	237	3	US-08-622-046B-7	Sequence 7, Appl	934	4	40.0	262	3	US-08-807-151-4	Sequence 4, Appl
862	4	40.0	237	3	US-08-622-046B-12	Sequence 12, Appl	935	4	40.0	262	3	US-09-025-059-4	Sequence 4, Appl
863	4	40.0	237	3	US-08-944-483-37	Sequence 37, Appl	936	4	40.0	262	4	US-09-261-767-4	Sequence 4, Appl
864	4	40.0	237	4	US-08-944-483-38	Sequence 38, Appl	937	4	40.0	262	4	US-09-210-084-4	Sequence 4, Appl
865	4	40.0	237	4	US-09-100-264-1	Sequence 1, Appl	938	4	40.0	266	2	US-07-808-457-3	Sequence 3, Appl
866	4	40.0	237	4	US-09-100-264-3	Sequence 3, Appl	939	4	40.0	266	2	US-07-808-457-5	Sequence 5, Appl
867	4	40.0	237	4	US-09-100-264-3	Sequence 3, Appl	940	4	40.0	266	2	US-08-845-161A-33	Sequence 33, Appl
868	4	40.0	237	5	PCT-US94-07329-12	Sequence 12, Appl	941	4	40.0	266	4	US-09-270-751-33	Sequence 33, Appl
869	4	40.0	237	5	PCT-US94-07329-11	Sequence 11, Appl	942	4	40.0	266	5	PCT-US92-10178-3	Sequence 3, Appl
870	4	40.0	237	5	PCT-US95-06157-11	Sequence 11, Appl	943	4	40.0	266	5	PCT-US92-10178-5	Sequence 5, Appl
871	4	40.0	237	5	PCT-US95-06157-16	Sequence 16, Appl	944	4	40.0	269	4	US-08-646-265A-109	Sequence 109, App
872	4	40.0	238	3	US-08-768-859A-8	Sequence 8, Appl	945	4	40.0	270	4	US-09-038-305-16	Sequence 16, Appl
873	4	40.0	238	3	US-08-767-820A-8	Sequence 8, Appl	946	4	40.0	272	2	US-08-160-527A-7	Sequence 7, Appl
874	4	40.0	238	3	US-08-944-483-39	Sequence 39, Appl	947	4	40.0	272	2	US-08-492-027A-4	Sequence 4, Appl
875	4	40.0	238	4	US-09-216-295-12	Sequence 12, Appl	948	4	40.0	275	1	US-08-589-446-4	Sequence 4, Appl
876	4	40.0	238	4	US-09-216-295-12	Sequence 12, Appl	949	4	40.0	275	1	US-08-444-882-4	Sequence 4, Appl
877	4	40.0	238	5	PCT-US95-06157-8	Sequence 8, Appl	950	4	40.0	275	2	US-08-389-459A-4	Sequence 4, Appl
878	4	40.0	239	4	US-09-306-881-4	Sequence 4, Appl	951	4	40.0	275	3	US-08-987-867A-4	Sequence 4, Appl
879	4	40.0	240	1	US-08-472-228A-1	Sequence 1, Appl	952	4	40.0	277	1	US-08-690-457-5	Sequence 5, Appl
880	4	40.0	240	4	US-09-049-672A-11	Sequence 11, Appl	953	4	40.0	277	2	US-08-628-187-5	Sequence 5, Appl
881	4	40.0	240	5	PCT-US96-09303-1	Sequence 1, Appl	954	4	40.0	277	3	US-08-493-071-3	Sequence 3, Appl
882	4	40.0	240	6	5204445-2	Patent No. 5204445	955	4	40.0	278	1	US-07-921-807B-10	Sequence 10, Appl
883	4	40.0	244	3	US-08-768-859A-10	Sequence 10, Appl	956	4	40.0	278	1	US-08-188-382-9	Sequence 9, Appl
884	4	40.0	244	3	US-08-767-820A-10	Sequence 10, Appl	957	4	40.0	278	1	US-08-646-715-9	Sequence 9, Appl
885	4	40.0	244	3	US-08-622-046B-5	Sequence 5, Appl	958	4	40.0	278	1	US-08-641-356-3	Sequence 3, Appl
886	4	40.0	244	3	US-08-622-046B-16	Sequence 16, Appl	959	4	40.0	279	1	US-08-441-944A-10	Sequence 10, Appl
887	4	40.0	244	4	US-09-100-264-5	Sequence 5, Appl	960	4	40.0	282	5	US-08-397-411-13	Sequence 13, Appl
888	4	40.0	244	5	PCT-US95-06157-10	Sequence 10, Appl	961	4	40.0	283	6	PCT-US95-13335-1	Sequence 1, Appl
889	4	40.0	245	2	US-08-912-129A-48	Sequence 48, Appl	962	4	40.0	284	2	US-08-767-096-3	Sequence 3, Appl
890	4	40.0	247	2	US-08-851-974-1	Sequence 4, Appl	963	4	40.0	286	1	US-08-382-184-3	Sequence 3, Appl
891	4	40.0	247	2	US-08-851-974-4	Sequence 4, Appl	964	4	40.0	286	2	US-08-641-356-3	Sequence 3, Appl
892	4	40.0	247	2	US-09-213-390-1	Sequence 1, Appl	965	4	40.0	286	4	US-09-132-528-4	Sequence 4, Appl
893	4	40.0	247	2	US-09-213-390-4	Sequence 1, Appl	966	4	40.0	286	4	US-08-875-484-3	Sequence 3, Appl
894	4	40.0	249	2	US-08-991-946A-1	Sequence 1, Appl	967	4	40.0	287	1	US-08-690-457-4	Sequence 4, Appl
895	4	40.0	249	4	US-09-446-504-1	Sequence 1, Appl	968	4	40.0	287	2	US-08-628-187-4	Sequence 4, Appl
896	4	40.0	251	4	US-08-944-483-28	Sequence 28, Appl	969	4	40.0	287	3	US-08-493-071-2	Sequence 2, Appl
897	4	40.0	252	1	US-08-253-877C-6	Sequence 6, Appl	970	4	40.0	288	1	US-08-690-457-3	Sequence 3, Appl
898	4	40.0	252	2	US-08-452-164A-6	Sequence 6, Appl	971	4	40.0	288	2	US-08-628-187-3	Sequence 3, Appl
899	4	40.0	252	2	US-08-824-405-4	Sequence 4, Appl	972	4	40.0	288	3	US-08-493-071-1	Sequence 1, Appl
900	4	40.0	253	1	US-08-622-353-8	Sequence 8, Appl	973	4	40.0	299	2	US-08-923-856-1	Sequence 1, Appl
901	4	40.0	253	1	US-08-622-352A-10	Sequence 10, Appl	974	4	40.0	299	3	US-09-216-294-1	Sequence 1, Appl
902	4	40.0	255	2	US-08-310-912A-106	Sequence 106, App	975	4	40.0	300	1	US-07-640-029-5	Sequence 5, Appl
903	4	40.0	255	3	US-08-826-390-10	Sequence 10, Appl	976	4	40.0	300	3	US-08-705-875A-4	Sequence 4, Appl

685	4	40.0	140	4	US-08-569-147-82	Sequence 82, Appl	758	4	40.0	185	2	US-08-865-336-3	Sequence 3, Appl1
686	4	40.0	140	4	US-08-579-378A-12	Sequence 12, Appl	759	4	40.0	186	1	US-08-928-443-3	Sequence 3, Appl1
687	4	40.0	140	5	PCT-US93-11612-12	Sequence 12, Appl	760	4	40.0	186	3	US-09-129-055-3	Sequence 3, Appl1
688	4	40.0	141	1	US-08-461-284-4	Sequence 4, Appl1	761	4	40.0	188	3	US-09-122-443-14	Sequence 14, Appl
689	4	40.0	141	1	US-08-462-939-4	Sequence 4, Appl1	762	4	40.0	189	4	US-08-026-758-18	Sequence 18, Appl
690	4	40.0	141	1	US-08-453-877C-4	Sequence 4, Appl1	763	4	40.0	190	4	US-09-271-970-14	Sequence 14, Appl
691	4	40.0	141	2	US-08-452-164A-4	Sequence 4, Appl1	764	4	40.0	192	1	US-08-086-428B-53	Sequence 53, Appl
692	4	40.0	142	2	US-08-561-521-17	Sequence 17, Appl	765	4	40.0	192	1	US-08-086-428B-58	Sequence 58, Appl
693	4	40.0	142	2	US-08-476-176B-12	Sequence 12, Appl	766	4	40.0	192	1	US-08-086-428B-85	Sequence 85, Appl
694	4	40.0	142	2	US-08-476-176B-14	Sequence 14, Appl	767	4	40.0	192	2	US-08-468-570-53	Sequence 53, Appl
695	4	40.0	142	2	US-08-476-176B-16	Sequence 16, Appl	768	4	40.0	192	2	US-08-468-570-58	Sequence 58, Appl
696	4	40.0	142	2	US-08-476-176B-18	Sequence 18, Appl	769	4	40.0	192	2	US-08-468-570-85	Sequence 85, Appl
697	4	40.0	142	3	US-08-127-721A-12	Sequence 12, Appl	770	4	40.0	192	2	US-08-468-570-85	Sequence 85, Appl
698	4	40.0	142	3	US-08-127-721A-14	Sequence 14, Appl	771	4	40.0	192	2	US-08-290-665A-58	Sequence 58, Appl
699	4	40.0	142	3	US-08-127-721A-16	Sequence 16, Appl	772	4	40.0	192	2	US-08-290-665A-85	Sequence 85, Appl
700	4	40.0	142	3	US-08-127-721A-18	Sequence 18, Appl	773	4	40.0	192	5	PCT-US94-05795-3	Sequence 3, Appl1
701	4	40.0	142	3	US-08-485-246A-12	Sequence 12, Appl	774	4	40.0	192	5	PCT-US95-10398-53	Sequence 53, Appl
702	4	40.0	142	3	US-08-485-246A-14	Sequence 14, Appl	775	4	40.0	192	5	PCT-US95-10398-58	Sequence 58, Appl
703	4	40.0	142	3	US-08-485-246A-16	Sequence 16, Appl	776	4	40.0	192	5	PCT-US95-10398-85	Sequence 85, Appl
704	4	40.0	142	3	US-08-485-246A-18	Sequence 18, Appl	777	4	40.0	194	2	US-08-621-803-255	Sequence 255, App
705	4	40.0	142	5	PCT-US95-01219-17	Sequence 17, Appl	778	4	40.0	194	3	US-09-032-372-13	Sequence 13, Appl
706	4	40.0	144	3	US-08-545-809A-100	Sequence 100, App	779	4	40.0	194	3	US-09-078-317-12	Sequence 12, Appl
707	4	40.0	146	1	US-08-276-852-155	Sequence 155, App	780	4	40.0	195	2	US-08-621-803-263	Sequence 263, App
708	4	40.0	146	1	US-08-899-575-155	Sequence 155, App	781	4	40.0	196	4	US-09-383-586-11	Sequence 11, Appl
709	4	40.0	146	1	US-08-899-575-155	Sequence 155, App	782	4	40.0	198	1	US-08-097-827-2	Sequence 2, Appl1
710	4	40.0	146	5	PCT-US95-08743-155	Sequence 155, App	783	4	40.0	198	1	US-08-494-574-2	Sequence 2, Appl1
711	4	40.0	147	1	US-08-217-918A-4	Sequence 4, Appl1	784	4	40.0	205	2	US-08-829-110-6	Sequence 6, Appl1
712	4	40.0	147	1	US-08-259-372A-8	Sequence 8, Appl1	785	4	40.0	205	2	US-08-748-483-5	Sequence 5, Appl1
713	4	40.0	147	1	US-08-468-671-8	Sequence 8, Appl1	786	4	40.0	207	2	US-09-022-940-1	Sequence 1, Appl1
714	4	40.0	147	2	US-08-824-405-12	Sequence 12, Appl	787	4	40.0	207	3	US-08-996-338-23	Sequence 23, Appl
715	4	40.0	148	1	US-08-166-195A-51	Sequence 51, Appl	788	4	40.0	207	3	US-09-216-386-1	Sequence 1, Appl1
716	4	40.0	148	2	US-08-436-772-51	Sequence 51, Appl	789	4	40.0	208	2	US-08-531-525-15	Sequence 15, Appl
717	4	40.0	148	2	US-08-436-772A-51	Sequence 51, Appl	790	4	40.0	208	2	US-08-531-525-17	Sequence 17, Appl
718	4	40.0	151	2	US-08-722-050-8	Sequence 8, Appl1	791	4	40.0	208	2	US-08-844-120-1	Sequence 1, Appl1
719	4	40.0	156	1	US-07-766-682A-3	Sequence 3, Appl1	792	4	40.0	208	2	US-08-718-270A-15	Sequence 15, Appl
720	4	40.0	156	4	US-08-928-941D-4	Sequence 4, Appl1	793	4	40.0	208	2	US-08-718-270A-17	Sequence 17, Appl
721	4	40.0	156	4	US-08-928-941D-36	Sequence 36, Appl1	794	4	40.0	208	4	US-08-097-869-6	Sequence 6, Appl1
722	4	40.0	161	2	US-08-621-803-249	Sequence 249, App	795	4	40.0	210	1	US-07-667-276A-2	Sequence 2, Appl1
723	4	40.0	161	3	US-09-045-764A-4	Sequence 4, Appl1	796	4	40.0	211	4	US-08-097-869-8	Sequence 8, Appl1
724	4	40.0	161	4	US-09-271-970-2	Sequence 2, Appl1	797	4	40.0	212	2	US-08-531-525-18	Sequence 18, Appl
725	4	40.0	162	3	US-08-983-045-2	Sequence 2, Appl1	798	4	40.0	212	2	US-08-718-270A-18	Sequence 18, Appl
726	4	40.0	164	1	US-08-033-857A-8	Sequence 8, Appl1	799	4	40.0	212	4	US-08-973-462-25	Sequence 25, Appl
727	4	40.0	164	1	US-08-374-983A-8	Sequence 8, Appl1	800	4	40.0	215	2	US-08-912-129A-58	Sequence 58, Appl
728	4	40.0	164	2	US-08-824-405-2	Sequence 2, Appl1	801	4	40.0	215	2	US-08-929-418-2	Sequence 2, Appl1
729	4	40.0	166	2	US-08-483-695-3	Sequence 3, Appl1	802	4	40.0	219	2	US-08-902-516-2	Sequence 2, Appl1
730	4	40.0	166	2	US-07-965-285-3	Sequence 3, Appl1	803	4	40.0	221	1	US-08-032-848C-13	Sequence 13, Appl
731	4	40.0	166	2	US-08-487-231-3	Sequence 3, Appl1	804	4	40.0	222	1	US-08-458-516-22	Sequence 22, Appl
732	4	40.0	166	2	US-09-201-912-3	Sequence 3, Appl1	805	4	40.0	225	2	US-09-074-512-3	Sequence 3, Appl1
733	4	40.0	166	4	US-08-631-328-55	Sequence 55, Appl	806	4	40.0	225	2	US-07-929-198-2	Sequence 2, Appl1
734	4	40.0	169	1	US-07-841-646-9	Sequence 9, Appl1	807	4	40.0	226	1	US-07-929-198-4	Sequence 4, Appl1
735	4	40.0	169	1	US-08-147-023-9	Sequence 9, Appl1	808	4	40.0	226	1	US-08-557-146-15	Sequence 15, Appl
736	4	40.0	169	1	US-08-447-570-9	Sequence 9, Appl1	809	4	40.0	226	2	US-08-557-146-15	Sequence 15, Appl
737	4	40.0	169	2	US-08-449-700-9	Sequence 9, Appl1	810	4	40.0	226	2	US-09-154-344-15	Sequence 15, Appl
738	4	40.0	169	2	US-08-449-699A-9	Sequence 9, Appl1	811	4	40.0	226	4	US-08-944-483-43	Sequence 43, Appl
739	4	40.0	173	3	US-09-188-579-87	Sequence 87, Appl	812	4	40.0	227	4	US-08-944-483-40	Sequence 40, Appl
740	4	40.0	173	4	US-09-315-444-87	Sequence 87, Appl	813	4	40.0	229	4	US-08-751-359-22	Sequence 22, Appl
741	4	40.0	174	2	US-08-683-262B-45	Sequence 45, Appl	814	4	40.0	230	1	US-08-118-469A-3	Sequence 3, Appl1
742	4	40.0	174	2	US-08-683-262B-48	Sequence 48, Appl	815	4	40.0	230	1	US-08-909-119-3	Sequence 3, Appl1
743	4	40.0	176	3	US-09-130-663-29	Sequence 29, Appl	816	4	40.0	230	2	US-08-844-120-3	Sequence 3, Appl1
744	4	40.0	176	3	US-08-392-794A-8	Sequence 8, Appl1	817	4	40.0	230	2	US-09-022-940-3	Sequence 3, Appl1
745	4	40.0	176	3	US-09-432-335-29	Sequence 29, Appl	818	4	40.0	230	2	US-09-022-940-5	Sequence 5, Appl1
746	4	40.0	178	3	US-09-081-180-2	Sequence 2, Appl1	819	4	40.0	230	3	US-09-216-001-3	Sequence 3, Appl1
747	4	40.0	178	3	US-09-040-786-2	Sequence 2, Appl1	820	4	40.0	230	3	US-09-216-386-3	Sequence 3, Appl1
748	4	40.0	178	3	US-08-705-875A-8	Sequence 8, Appl1	821	4	40.0	230	3	US-09-216-386-5	Sequence 5, Appl1
749	4	40.0	178	3	US-09-122-443-9	Sequence 9, Appl1	822	4	40.0	230	4	US-08-878-862-3	Sequence 3, Appl1
750	4	40.0	178	4	US-09-147-928-4	Sequence 4, Appl1	823	4	40.0	232	1	US-08-278-091-8	Sequence 8, Appl1
751	4	40.0	178	4	US-09-220-731-23	Sequence 23, Appl	824	4	40.0	232	1	US-08-483-859-8	Sequence 8, Appl1
752	4	40.0	178	4	US-09-220-731-24	Sequence 24, Appl	825	4	40.0	232	1	US-08-472-173-8	Sequence 8, Appl1
753	4	40.0	179	2	US-09-271-970-8	Sequence 8, Appl1	826	4	40.0	232	2	US-08-487-167-8	Sequence 8, Appl1
754	4	40.0	179	2	US-08-621-803-257	Sequence 257, App	827	4	40.0	232	2	US-08-487-816-8	Sequence 8, Appl1
755	4	40.0	180	3	US-08-621-803-261	Sequence 261, App	828	4	40.0	232	2	US-08-296-149-8	Sequence 8, Appl1
756	4	40.0	180	3	US-09-038-909-4	Sequence 4, Appl1	829	4	40.0	232	2	US-08-801-499-8	Sequence 8, Appl1
757	4	40.0	181	4	US-08-961-083-114	Sequence 114, App	830	4	40.0	232	2	US-08-978-404B-45	Sequence 45, Appl

539	4	40.0	124	1	US-08-899-575-130	Sequence 130, App	612	4	40.0	136	5	PCT-US93-11611-11	Sequence 11, Appl
540	4	40.0	124	1	US-08-899-575-131	Sequence 131, App	613	4	40.0	137	1	US-08-477-877B-96	Sequence 96, Appl
541	4	40.0	124	1	US-08-899-575-132	Sequence 132, App	614	4	40.0	137	2	US-08-472-281A-96	Sequence 96, Appl
542	4	40.0	124	1	US-08-899-575-66	Sequence 66, Appl	615	4	40.0	137	2	US-08-477-989B-96	Sequence 96, Appl
543	4	40.0	124	1	US-08-899-575-68	Sequence 67, Appl	616	4	40.0	137	3	US-08-513-96B-98	Sequence 38, Appl
544	4	40.0	124	1	US-08-899-575-68	Sequence 68, Appl	617	4	40.0	138	3	US-08-513-96B-48	Sequence 44, Appl
545	4	40.0	124	1	US-08-899-575-125	Sequence 125, App	618	4	40.0	139	1	US-07-718-274A-10	Sequence 2, Appl
546	4	40.0	124	1	US-08-899-575-126	Sequence 126, App	619	4	40.0	139	1	US-08-163-877-10	Sequence 10, Appl
547	4	40.0	124	1	US-08-899-575-127	Sequence 127, App	620	4	40.0	139	1	US-08-149-106-2	Sequence 2, Appl
548	4	40.0	124	1	US-08-899-575-130	Sequence 130, App	621	4	40.0	139	1	US-08-298-021-2	Sequence 2, Appl
549	4	40.0	124	1	US-08-899-575-131	Sequence 131, App	622	4	40.0	139	1	US-08-278-729A-5	Sequence 5, Appl
550	4	40.0	124	1	US-08-899-575-132	Sequence 132, App	623	4	40.0	139	1	US-08-278-729A-6	Sequence 6, Appl
551	4	40.0	124	5	PCT-US95-08743-66	Sequence 66, Appl	624	4	40.0	139	1	US-08-155-343A-5	Sequence 5, Appl
552	4	40.0	124	5	PCT-US95-08743-67	Sequence 67, Appl	625	4	40.0	139	1	US-08-105-343A-6	Sequence 6, Appl
553	4	40.0	124	5	PCT-US95-08743-68	Sequence 68, Appl	626	4	40.0	139	1	US-08-406-672-5	Sequence 5, Appl
554	4	40.0	124	5	PCT-US95-08743-125	Sequence 125, App	627	4	40.0	139	1	US-08-406-672-6	Sequence 6, Appl
555	4	40.0	124	5	PCT-US95-08743-126	Sequence 126, App	628	4	40.0	139	1	US-08-643-553A-5	Sequence 5, Appl
556	4	40.0	124	5	PCT-US95-08743-127	Sequence 127, App	629	4	40.0	139	1	US-08-643-553A-6	Sequence 6, Appl
557	4	40.0	124	5	PCT-US95-08743-130	Sequence 130, App	630	4	40.0	139	1	US-08-643-763A-5	Sequence 5, Appl
558	4	40.0	124	5	PCT-US95-08743-131	Sequence 131, App	631	4	40.0	139	1	US-08-643-763A-6	Sequence 6, Appl
559	4	40.0	124	5	PCT-US95-08743-132	Sequence 132, App	632	4	40.0	139	1	US-08-462-623-5	Sequence 5, Appl
560	4	40.0	125	1	US-08-276-852-124	Sequence 124, App	633	4	40.0	139	1	US-08-462-623-6	Sequence 6, Appl
561	4	40.0	125	1	US-08-276-852-128	Sequence 128, App	634	4	40.0	139	1	US-08-451-953A-5	Sequence 5, Appl
562	4	40.0	125	1	US-08-276-852-129	Sequence 129, App	635	4	40.0	139	1	US-08-451-953A-6	Sequence 6, Appl
563	4	40.0	125	1	US-08-899-575-124	Sequence 124, App	636	4	40.0	139	1	US-08-360-914B-10	Sequence 10, Appl
564	4	40.0	125	1	US-08-899-575-128	Sequence 128, App	637	4	40.0	139	1	US-08-253-877C-19	Sequence 19, Appl
565	4	40.0	125	1	US-08-899-575-129	Sequence 129, App	638	4	40.0	139	1	US-08-202-047-7	Sequence 7, Appl
566	4	40.0	125	1	US-08-899-575-124	Sequence 124, App	639	4	40.0	139	1	US-08-202-047-9	Sequence 9, Appl
567	4	40.0	125	1	US-08-899-575-128	Sequence 128, App	640	4	40.0	139	1	US-08-202-047-11	Sequence 11, Appl
568	4	40.0	125	1	US-08-899-575-129	Sequence 129, App	641	4	40.0	139	1	US-08-741-589A-10	Sequence 10, Appl
569	4	40.0	125	2	US-08-665-202-56	Sequence 56, Appl	642	4	40.0	139	2	US-08-656-586-8	Sequence 8, Appl
570	4	40.0	125	2	US-08-665-202-58	Sequence 58, Appl	643	4	40.0	139	2	US-08-445-468A-5	Sequence 5, Appl
571	4	40.0	125	2	US-08-665-202-59	Sequence 59, Appl	644	4	40.0	139	2	US-08-445-468A-6	Sequence 6, Appl
572	4	40.0	125	4	US-09-199-149-3	Sequence 3, Appl	645	4	40.0	139	2	US-08-452-164A-19	Sequence 19, Appl
573	4	40.0	125	5	PCT-US95-08743-124	Sequence 124, App	646	4	40.0	139	2	US-08-461-357A-5	Sequence 5, Appl
574	4	40.0	125	5	PCT-US95-08743-128	Sequence 128, App	647	4	40.0	139	2	US-08-461-357A-6	Sequence 6, Appl
575	4	40.0	125	5	PCT-US95-08743-129	Sequence 129, App	648	4	40.0	139	2	US-08-912-088-6	Sequence 6, Appl
576	4	40.0	126	1	US-08-276-852-123	Sequence 123, App	649	4	40.0	139	2	US-08-912-088-6	Sequence 6, Appl
577	4	40.0	126	1	US-08-899-575-123	Sequence 123, App	650	4	40.0	139	3	US-08-603-024-18	Sequence 18, Appl
578	4	40.0	126	1	US-08-899-575-123	Sequence 123, App	651	4	40.0	139	3	US-08-278-720A-5	Sequence 5, Appl
579	4	40.0	126	5	PCT-US95-08743-123	Sequence 123, App	652	4	40.0	139	3	US-08-278-720A-6	Sequence 6, Appl
580	4	40.0	128	1	US-08-276-852-56	Sequence 56, Appl	653	4	40.0	139	3	US-08-964-690-7	Sequence 7, Appl
581	4	40.0	128	1	US-08-276-852-58	Sequence 58, Appl	654	4	40.0	139	3	US-08-964-690-9	Sequence 9, Appl
582	4	40.0	128	1	US-08-478-039-63	Sequence 63, Appl	655	4	40.0	139	3	US-08-964-690-11	Sequence 11, Appl
583	4	40.0	128	1	US-08-476-349A-63	Sequence 63, Appl	656	4	40.0	139	3	US-08-445-467-5	Sequence 5, Appl
584	4	40.0	128	1	US-08-899-575-56	Sequence 56, Appl	657	4	40.0	139	3	US-08-445-467-6	Sequence 6, Appl
585	4	40.0	128	1	US-08-899-575-58	Sequence 58, Appl	658	4	40.0	139	3	US-08-443-676-1	Sequence 1, Appl
586	4	40.0	128	1	US-08-202-047-22	Sequence 22, Appl	659	4	40.0	139	3	US-08-480-515A-5	Sequence 5, Appl
587	4	40.0	128	1	US-08-899-575-56	Sequence 56, Appl	660	4	40.0	139	3	US-08-480-515A-6	Sequence 6, Appl
588	4	40.0	128	3	US-08-899-575-58	Sequence 58, Appl	661	4	40.0	139	3	US-08-933-983-21	Sequence 21, Appl
589	4	40.0	128	3	US-08-964-690-22	Sequence 22, Appl	662	4	40.0	139	4	US-08-414-033A-5	Sequence 5, Appl
590	4	40.0	128	4	US-09-199-149-12	Sequence 12, Appl	663	4	40.0	139	4	US-08-414-033A-6	Sequence 6, Appl
591	4	40.0	128	5	PCT-US95-08743-56	Sequence 56, Appl	664	4	40.0	139	4	US-08-271-556A-3	Sequence 3, Appl
592	4	40.0	128	5	PCT-US95-08743-58	Sequence 58, Appl	665	4	40.0	139	4	US-08-271-556A-4	Sequence 4, Appl
593	4	40.0	129	1	US-08-313-075A-52	Sequence 52, Appl	666	4	40.0	139	4	US-08-905-223-49	Sequence 49, App
594	4	40.0	129	2	US-08-561-521-45	Sequence 45, Appl	667	4	40.0	139	5	PCT-US92-01968-5	Sequence 5, Appl
595	4	40.0	129	5	PCT-US95-01219-45	Sequence 45, Appl	668	4	40.0	139	5	PCT-US92-01968-6	Sequence 6, Appl
596	4	40.0	133	4	US-08-718-333A-8	Sequence 8, Appl	669	4	40.0	139	5	PCT-US93-07190-5	Sequence 5, Appl
597	4	40.0	133	4	US-07-634-278-19	Sequence 19, Appl	670	4	40.0	139	5	PCT-US93-07190-6	Sequence 6, Appl
598	4	40.0	135	1	US-08-477-728-19	Sequence 19, Appl	671	4	40.0	139	5	PCT-US93-07231-5	Sequence 5, Appl
599	4	40.0	135	1	US-08-474-040-19	Sequence 19, Appl	672	4	40.0	139	5	PCT-US93-07231-6	Sequence 6, Appl
600	4	40.0	135	1	US-08-487-200-19	Sequence 19, Appl	673	4	40.0	139	5	PCT-US93-08742-5	Sequence 5, Appl
601	4	40.0	135	1	US-08-137-117D-100	Sequence 100, App	674	4	40.0	139	5	PCT-US93-08742-6	Sequence 6, Appl
602	4	40.0	135	1	US-08-137-117D-102	Sequence 102, App	675	4	40.0	139	5	PCT-US93-08808-5	Sequence 5, Appl
603	4	40.0	135	2	US-08-137-117D-112	Sequence 112, App	676	4	40.0	139	5	PCT-US93-08808-6	Sequence 6, Appl
604	4	40.0	135	2	US-08-436-717-100	Sequence 100, App	677	4	40.0	139	5	PCT-US93-08885-5	Sequence 5, Appl
605	4	40.0	135	2	US-08-436-717-102	Sequence 102, App	678	4	40.0	139	5	PCT-US93-08885-6	Sequence 6, Appl
606	4	40.0	135	2	US-08-303-569B-31	Sequence 31, App	679	4	40.0	139	5	PCT-US94-13181-10	Sequence 10, Appl
607	4	40.0	135	2	US-08-621-751A-16	Sequence 16, App	680	4	40.0	140	1	US-07-946-421-28	Sequence 28, Appl
608	4	40.0	135	2	US-08-484-537-19	Sequence 19, Appl	681	4	40.0	140	3	US-08-836-561-63	Sequence 63, Appl
609	4	40.0	135	4	US-08-649-100-41	Sequence 41, Appl	682	4	40.0	140	3	US-08-836-561-78	Sequence 78, Appl
610	4	40.0	136	3	US-08-646-265A-99	Sequence 99, Appl	683	4	40.0	140	3	US-08-836-561-83	Sequence 83, Appl
611	4	40.0	136	4	US-08-646-265A-99	Sequence 99, Appl	684	4	40.0	140	3	US-08-836-561-83	Sequence 83, Appl

393	4	40.0	117	4	US-09-042-353-232	Sequence 232, App	466	4	40.0	120	3	US-08-397-411-10	Sequence 10, App1
394	4	40.0	117	5	PCT-US93-11611-6	Sequence 7, App1	467	4	40.0	120	5	PCT-US93-10555-12	Sequence 12, App1
395	4	40.0	117	5	PCT-US93-11611-7	Sequence 6, App1	468	4	40.0	120	5	PCT-US93-10555-13	Sequence 13, App1
396	4	40.0	117	5	PCT-US95-10053-14	Sequence 14, App1	469	4	40.0	121	1	US-07-634-278-53	Sequence 53, App1
397	4	40.0	117	5	PCT-US96-09448-17	Sequence 17, App1	470	4	40.0	121	1	US-08-477-728-53	Sequence 53, App1
398	4	40.0	118	1	US-08-300-386A-64	Sequence 64, App1	471	4	40.0	121	1	US-08-264-093-3	Sequence 3, App1
399	4	40.0	118	1	US-08-477-877B-93	Sequence 93, App1	472	4	40.0	121	1	US-08-478-039-64	Sequence 64, App1
400	4	40.0	118	1	US-08-491-845-14	Sequence 14, App1	473	4	40.0	121	1	US-08-478-040-53	Sequence 53, App1
401	4	40.0	118	1	US-08-481-371-12	Sequence 12, App1	474	4	40.0	121	1	US-08-478-200-95	Sequence 53, App1
402	4	40.0	118	2	US-08-472-281A-93	Sequence 93, App1	475	4	40.0	121	1	US-08-476-349A-64	Sequence 64, App1
403	4	40.0	118	2	US-08-491-835-10	Sequence 10, App1	476	4	40.0	121	1	US-08-202-047-23	Sequence 23, App1
404	4	40.0	118	2	US-08-428-257A-78	Sequence 78, App1	477	4	40.0	121	1	US-08-420-235B-23	Sequence 23, App1
405	4	40.0	118	2	US-08-232-081B-8	Sequence 8, App1	478	4	40.0	121	2	US-08-232-081B-41	Sequence 41, App1
406	4	40.0	118	2	US-08-477-989B-93	Sequence 93, App1	479	4	40.0	121	2	US-08-428-197-14	Sequence 14, App1
407	4	40.0	118	3	US-08-392-794A-4	Sequence 4, App1	480	4	40.0	121	3	US-08-964-690-23	Sequence 23, App1
408	4	40.0	118	3	US-09-153-733A-12	Sequence 12, App1	481	4	40.0	121	4	US-08-983-607-20	Sequence 20, App1
409	4	40.0	118	3	US-08-946-092A-10	Sequence 10, App1	482	4	40.0	121	4	US-08-793-624-23	Sequence 23, App1
410	4	40.0	118	3	US-08-931-645-64	Sequence 64, App1	483	4	40.0	121	4	US-08-484-537-53	Sequence 53, App1
411	4	40.0	118	3	US-08-513-96B-80	Sequence 80, App1	484	4	40.0	121	4	US-08-579-378A-8	Sequence 8, App1
412	4	40.0	118	3	US-08-983-607-24	Sequence 24, App1	485	4	40.0	121	5	PCT-US93-10555-14	Sequence 14, App1
413	4	40.0	118	4	US-09-199-149-5	Sequence 5, App1	486	4	40.0	121	5	PCT-US93-11612-8	Sequence 8, App1
414	4	40.0	118	4	US-09-172-062-10	Sequence 10, App1	487	4	40.0	121	5	PCT-US95-10194-23	Sequence 23, App1
415	4	40.0	118	4	US-07-587-264-60	Sequence 60, App1	488	4	40.0	121	5	PCT-US95-1365B-4	Sequence 4, App1
416	4	40.0	118	5	PCT-US94-00666-12	Sequence 12, App1	489	4	40.0	122	1	US-07-634-278-88	Sequence 88, App1
417	4	40.0	118	5	PCT-US94-00685-10	Sequence 10, App1	490	4	40.0	122	1	US-08-477-728-88	Sequence 88, App1
418	4	40.0	118	5	PCT-US95-11235-64	Sequence 64, App1	491	4	40.0	122	1	US-08-474-040-88	Sequence 88, App1
419	4	40.0	119	1	US-07-634-278-65	Sequence 65, App1	492	4	40.0	122	1	US-08-487-200-88	Sequence 88, App1
420	4	40.0	119	1	US-07-634-278-89	Sequence 89, App1	493	4	40.0	122	4	US-08-484-537-88	Sequence 88, App1
421	4	40.0	119	1	US-08-477-728-65	Sequence 65, App1	494	4	40.0	122	5	PCT-US95-00067-2	Sequence 2, App1
422	4	40.0	119	1	US-08-477-728-89	Sequence 89, App1	495	4	40.0	122	6	5304466-3	Patent No. 5304466
423	4	40.0	119	1	US-08-300-386A-65	Sequence 65, App1	496	4	40.0	123	1	US-08-497-312-17	Sequence 17, App1
424	4	40.0	119	1	US-08-478-039-65	Sequence 65, App1	497	4	40.0	123	1	US-08-477-877B-94	Sequence 94, App1
425	4	40.0	119	1	US-08-474-040-65	Sequence 65, App1	498	4	40.0	123	1	US-08-482-882-53	Sequence 53, App1
426	4	40.0	119	1	US-08-474-040-89	Sequence 89, App1	499	4	40.0	123	1	US-08-482-882-86	Sequence 86, App1
427	4	40.0	119	1	US-08-487-200-65	Sequence 65, App1	500	4	40.0	123	2	US-08-483-389-53	Sequence 53, App1
428	4	40.0	119	1	US-08-487-200-89	Sequence 89, App1	501	4	40.0	123	2	US-08-483-389-86	Sequence 86, App1
429	4	40.0	119	1	US-08-488-113B-160	Sequence 160, App1	502	4	40.0	123	2	US-08-472-281A-94	Sequence 94, App1
430	4	40.0	119	1	US-08-476-349A-65	Sequence 65, App1	503	4	40.0	123	2	US-08-487-113B-53	Sequence 53, App1
431	4	40.0	119	1	US-08-477-484B-160	Sequence 160, App1	504	4	40.0	123	2	US-08-487-113B-86	Sequence 86, App1
432	4	40.0	119	1	US-08-107-669B-24	Sequence 24, App1	505	4	40.0	123	2	US-08-561-521-11	Sequence 11, App1
433	4	40.0	119	1	US-08-472-788A-24	Sequence 24, App1	506	4	40.0	123	2	US-08-473-503-53	Sequence 53, App1
434	4	40.0	119	1	US-08-581-529B-12	Sequence 12, App1	507	4	40.0	123	2	US-08-473-503-86	Sequence 86, App1
435	4	40.0	119	1	US-08-491-845-10	Sequence 10, App1	508	4	40.0	123	2	US-08-652-816A-6	Sequence 6, App1
436	4	40.0	119	1	US-08-458-516-10	Sequence 10, App1	509	4	40.0	123	2	US-08-652-816A-16	Sequence 16, App1
437	4	40.0	119	1	US-08-455-559-18	Sequence 18, App1	510	4	40.0	123	2	US-08-652-816A-7	Sequence 7, App1
438	4	40.0	119	2	US-08-475-531B-24	Sequence 24, App1	511	4	40.0	123	2	US-08-652-816A-8	Sequence 8, App1
439	4	40.0	119	2	US-08-525-596B-22	Sequence 22, App1	512	4	40.0	123	2	US-08-652-816A-9	Sequence 9, App1
440	4	40.0	119	2	US-08-546-360-160	Sequence 160, App1	513	4	40.0	123	2	US-08-483-932-53	Sequence 53, App1
441	4	40.0	119	2	US-08-561-521-10	Sequence 10, App1	514	4	40.0	123	2	US-08-483-932-86	Sequence 86, App1
442	4	40.0	119	2	US-08-561-521-12	Sequence 12, App1	515	4	40.0	123	2	US-08-477-989B-94	Sequence 94, App1
443	4	40.0	119	2	US-08-561-521-13	Sequence 13, App1	516	4	40.0	123	2	US-08-720-420A-53	Sequence 53, App1
444	4	40.0	119	2	US-08-082-842A-24	Sequence 24, App1	517	4	40.0	123	2	US-08-720-420A-86	Sequence 86, App1
445	4	40.0	119	2	US-08-581-528A-12	Sequence 12, App1	518	4	40.0	123	3	US-08-714-017-53	Sequence 53, App1
446	4	40.0	119	3	US-09-097-616-12	Sequence 12, App1	519	4	40.0	123	3	US-08-714-017-86	Sequence 86, App1
447	4	40.0	119	3	US-09-177-860A-22	Sequence 22, App1	520	4	40.0	123	3	US-08-475-680-53	Sequence 53, App1
448	4	40.0	119	3	US-08-931-645-65	Sequence 65, App1	521	4	40.0	123	3	US-08-475-680-86	Sequence 86, App1
449	4	40.0	119	4	US-08-983-607-50	Sequence 50, App1	522	4	40.0	123	4	US-09-102-528-22	Sequence 22, App1
450	4	40.0	119	4	US-08-839-765-160	Sequence 160, App1	523	4	40.0	123	5	PCT-US95-01219-11	Sequence 11, App1
451	4	40.0	119	4	US-09-136-389-160	Sequence 160, App1	524	4	40.0	124	1	US-08-276-852-66	Sequence 66, App1
452	4	40.0	119	4	US-08-484-537-65	Sequence 65, App1	525	4	40.0	124	1	US-08-276-852-67	Sequence 67, App1
453	4	40.0	119	4	US-08-484-537-89	Sequence 89, App1	526	4	40.0	124	1	US-08-276-852-66	Sequence 68, App1
454	4	40.0	119	4	US-08-624-635-13	Sequence 13, App1	527	4	40.0	124	1	US-08-276-852-125	Sequence 125, App1
455	4	40.0	119	4	US-09-145-060-18	Sequence 18, App1	528	4	40.0	124	1	US-08-276-852-127	Sequence 127, App1
456	4	40.0	119	5	PCT-US94-00657-18	Sequence 18, App1	529	4	40.0	124	1	US-08-276-852-130	Sequence 130, App1
457	4	40.0	119	5	PCT-US94-07762-12	Sequence 12, App1	530	4	40.0	124	1	US-08-276-852-131	Sequence 131, App1
458	4	40.0	119	5	PCT-US94-07799-12	Sequence 12, App1	531	4	40.0	124	1	US-08-276-852-132	Sequence 132, App1
459	4	40.0	119	5	PCT-US95-01219-10	Sequence 10, App1	532	4	40.0	124	1	US-08-899-575-66	Sequence 66, App1
460	4	40.0	119	5	PCT-US95-01219-12	Sequence 12, App1	533	4	40.0	124	1	US-08-899-575-67	Sequence 67, App1
461	4	40.0	119	5	PCT-US95-01219-13	Sequence 13, App1	534	4	40.0	124	1	US-08-899-575-68	Sequence 68, App1
462	4	40.0	119	5	PCT-US95-11235-65	Sequence 65, App1	535	4	40.0	124	1	US-08-899-575-125	Sequence 125, App1
463	4	40.0	120	2	US-08-652-816A-19	Sequence 19, App1	536	4	40.0	124	1	US-08-899-575-126	Sequence 126, App1
464	4	40.0	120	2	US-08-428-197-12	Sequence 12, App1	537	4	40.0	124	1	US-08-899-575-127	Sequence 127, App1
465	4	40.0	120	2	US-08-428-197-13	Sequence 13, App1	538	4	40.0	124	1		

247	4	40.0	94	1	US-08-167-035-23	Sequence 23, Appl	320	4	40.0	116	1	US-08-487-200-57	Sequence 57, Appl
248	4	40.0	94	1	US-08-208-887A-23	Sequence 23, Appl	321	4	40.0	116	1	US-08-487-200-73	Sequence 73, Appl
249	4	40.0	94	2	US-08-539-005-23	Sequence 23, Appl	322	4	40.0	116	1	US-08-488-113B-169	Sequence 169, App
250	4	40.0	97	2	US-08-290-592E-16	Sequence 16, Appl	323	4	40.0	116	1	US-08-477-444B-169	Sequence 169, App
251	4	40.0	97	5	PCT-US95-10053-13	Sequence 13, Appl	324	4	40.0	116	1	US-08-107-669D-55	Sequence 55, Appl
252	4	40.0	97	5	PCT-US96-09448-16	Sequence 16, Appl	325	4	40.0	116	1	US-08-472-788A-86	Sequence 86, Appl
253	4	40.0	98	1	US-08-211-202-130	Sequence 130, App	326	4	40.0	116	1	US-08-690-102A-8	Sequence 8, Appl
254	4	40.0	98	1	US-08-211-202-140	Sequence 140, App	327	4	40.0	116	1	US-08-690-102A-9	Sequence 9, Appl
255	4	40.0	98	1	US-08-478-039-81	Sequence 81, Appl	328	4	40.0	116	2	US-08-477-531B-55	Sequence 55, Appl
256	4	40.0	98	1	US-08-475-349A-81	Sequence 81, Appl	329	4	40.0	116	2	US-08-646-380-169	Sequence 169, App
257	4	40.0	98	2	US-08-428-197-17	Sequence 17, Appl	330	4	40.0	116	2	US-08-561-521-41	Sequence 41, Appl
258	4	40.0	98	2	US-08-665-202-33	Sequence 33, Appl	331	4	40.0	116	2	US-08-082-842A-86	Sequence 86, Appl
259	4	40.0	98	5	PCT-US93-10555-17	Sequence 17, Appl	332	4	40.0	116	3	US-08-934-841-1	Sequence 1, Appl
260	4	40.0	100	3	US-09-034-916-13	Sequence 13, Appl	333	4	40.0	116	3	US-08-545-809A-104	Sequence 104, App
261	4	40.0	100	4	US-08-973-462-11	Sequence 11, Appl	334	4	40.0	116	3	US-09-393-409-1	Sequence 1, Appl
262	4	40.0	102	1	US-07-834-539A-55	Sequence 55, Appl	335	4	40.0	116	4	US-08-839-765-169	Sequence 169, App
263	4	40.0	102	1	US-08-033-131-63	Sequence 63, Appl	336	4	40.0	116	4	US-09-136-369-169	Sequence 169, App
264	4	40.0	102	1	US-08-335-583C-47	Sequence 47, Appl	337	4	40.0	116	4	US-08-484-537-6	Sequence 6, Appl
265	4	40.0	102	1	US-08-645-641-63	Sequence 63, Appl	338	4	40.0	116	4	US-08-484-537-7	Sequence 7, Appl
266	4	40.0	102	1	US-07-853-408B-63	Sequence 63, Appl	339	4	40.0	116	4	US-08-484-537-73	Sequence 73, Appl
267	4	40.0	102	2	US-08-096-762-63	Sequence 63, Appl	340	4	40.0	116	4	US-09-127-902-8	Sequence 8, Appl
268	4	40.0	102	2	US-08-800-353-55	Sequence 55, Appl	341	4	40.0	116	4	US-09-127-902-9	Sequence 9, Appl
269	4	40.0	102	2	US-08-308-865-65	Sequence 65, Appl	342	4	40.0	116	4	US-09-127-902-9	Sequence 9, Appl
270	4	40.0	102	2	US-08-288-508C-18	Sequence 18, Appl	343	4	40.0	116	4	US-09-155-107-8	Sequence 8, Appl
271	4	40.0	102	2	US-08-478-097A-16	Sequence 16, Appl	344	4	40.0	116	4	US-09-155-107-21	Sequence 21, Appl
272	4	40.0	102	3	US-08-289-222E-27	Sequence 27, Appl	345	4	40.0	116	5	PCT-US95-01219-41	Sequence 41, Appl
273	4	40.0	102	4	US-09-054-526B-27	Sequence 27, Appl	346	4	40.0	116	5	PCT-US95-09641-8	Sequence 8, Appl
274	4	40.0	102	4	US-08-931-858E-161	Sequence 161, App	347	4	40.0	116	5	PCT-US95-09641-9	Sequence 9, Appl
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276	4	40.0	102	5	PCT-US92-06185-55	Sequence 55, Appl	349	4	40.0	117	1	US-07-634-278-15	Sequence 15, Appl
277	4	40.0	102	5	PCT-US92-10983-63	Sequence 63, Appl	350	4	40.0	117	1	US-07-634-278-72	Sequence 72, Appl
278	4	40.0	104	1	US-07-764-731B-8	Sequence 8, Appl	351	4	40.0	117	1	US-07-634-278-104	Sequence 104, App
279	4	40.0	104	3	US-08-894-173-71	Sequence 71, Appl	352	4	40.0	117	1	US-07-634-278-105	Sequence 105, App
280	4	40.0	104	4	US-09-398-193-71	Sequence 71, Appl	353	4	40.0	117	1	US-08-477-728-4	Sequence 4, Appl
281	4	40.0	105	1	US-08-422-101-9	Sequence 9, Appl	354	4	40.0	117	1	US-08-477-728-15	Sequence 15, Appl
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295	4	40.0	110	4	US-08-469-617-23	Sequence 23, Appl	368	4	40.0	117	1	US-08-488-113B-166	Sequence 166, App
296	4	40.0	110	4	US-08-469-617-25	Sequence 25, Appl	369	4	40.0	117	1	US-08-477-484B-156	Sequence 156, App
297	4	40.0	112	3	US-08-545-809A-113	Sequence 113, App	370	4	40.0	117	1	US-08-107-669D-52	Sequence 52, Appl
298	4	40.0	113	4	US-08-836-075A-70	Sequence 70, Appl	371	4	40.0	117	1	US-08-472-788A-52	Sequence 52, Appl
299	4	40.0	113	4	US-08-836-075A-72	Sequence 72, Appl	372	4	40.0	117	2	US-08-477-531B-52	Sequence 52, Appl
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301	4	40.0	113	4	US-08-836-075A-78	Sequence 78, Appl	374	4	40.0	117	2	US-08-646-360-166	Sequence 166, App
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309	4	40.0	116	1	US-07-634-278-73	Sequence 73, Appl	382	4	40.0	117	3	US-08-545-809A-128	Sequence 128, App
310	4	40.0	116	1	US-08-477-728-5	Sequence 5, Appl	383	4	40.0	117	3	US-08-545-809A-133	Sequence 133, App
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313	4	40.0	116	1	US-08-477-728-73	Sequence 73, Appl	386	4	40.0	117	4	US-09-136-389-166	Sequence 166, App
314	4	40.0	116	1	US-08-474-040-5	Sequence 5, Appl	387	4	40.0	117	4	US-08-484-537-4	Sequence 4, Appl
315	4	40.0	116	1	US-08-474-040-6	Sequence 6, Appl	388	4	40.0	117	4	US-08-484-537-15	Sequence 15, Appl
316	4	40.0	116	1	US-08-474-040-57	Sequence 57, Appl	389	4	40.0	117	4	US-08-484-537-72	Sequence 72, Appl
317	4	40.0	116	1	US-08-474-040-73	Sequence 73, Appl	390	4	40.0	117	4	US-08-484-537-104	Sequence 104, App
318	4	40.0	116	1	US-08-487-200-5	Sequence 5, Appl	391	4	40.0	117	4	US-08-484-537-105	Sequence 105, App
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118	4	40.0	13	4	US-09-001-984C-25	Sequence 25, Appl	191	4	40.0	30	4	US-08-646-265A-146	Sequence 146, App
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122	4	40.0	15	2	US-08-687-956A-6	Sequence 6, Appl	195	4	40.0	31	1	US-08-023-980B-30	Sequence 30, Appl
123	4	40.0	15	4	US-08-595-945-11	Sequence 11, Appl	196	4	40.0	31	2	US-08-486-953A-25	Sequence 25, Appl
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128	4	40.0	16	1	US-08-466-763-13	Sequence 13, Appl	201	4	40.0	33	2	US-08-290-665A-241	Sequence 241, App
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130	4	40.0	16	2	US-08-102-385C-35	Sequence 35, Appl	203	4	40.0	35	4	US-09-001-984C-11	Sequence 11, Appl
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OM protein - protein search, using sw model

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Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 197339 seqs, 20590346 residues

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	100.0	12	2	US-08-456-670B-30	Sequence 30, Appl
3	100.0	21	1	US-08-127-499A-27	Sequence 27, Appl
4	100.0	21	1	US-08-482-847-27	Sequence 27, Appl
5	100.0	232	2	US-08-456-670B-39	Sequence 39, Appl
6	100.0	478	2	US-08-456-670B-40	Sequence 40, Appl
7	100.0	484	1	US-08-127-499A-26	Sequence 26, Appl
8	100.0	484	1	US-08-482-847-26	Sequence 26, Appl
9	70.0	7	1	US-08-127-499A-28	Sequence 28, Appl
10	70.0	9	2	US-08-482-847-28	Sequence 28, Appl
11	60.0	9	2	US-08-456-670B-26	Sequence 26, Appl
12	60.0	20	2	US-08-456-670B-17	Sequence 17, Appl
13	50.0	11	2	US-08-456-670B-35	Sequence 35, Appl
14	50.0	107	2	US-08-810-572A-4	Sequence 4, Appl
15	50.0	118	1	US-08-497-025-10	Sequence 10, Appl
16	50.0	192	1	US-08-086-428B-57	Sequence 57, Appl
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18	50.0	192	1	US-08-440-542-44	Sequence 44, Appl
19	50.0	192	1	US-08-231-366-44	Sequence 44, Appl
20	50.0	192	1	US-08-440-210-44	Sequence 44, Appl
21	50.0	192	2	US-08-468-570-57	Sequence 57, Appl
22	50.0	192	2	US-08-290-665A-57	Sequence 57, Appl
23	50.0	192	4	US-08-444-818-167	Sequence 167, App
24	50.0	192	5	PCT-US95-10398-57	Sequence 57, Appl
25	50.0	231	2	US-08-969-721-8	Sequence 8, Appl
26	50.0	242	6	5273901-3	Patent No. 5273901
27	50.0	242	6	5482709-2	Patent No. 5482709

28	50.0	293	2	US-08-810-572A-2	Sequence 2, Appl
29	50.0	339	4	US-08-444-818-152	Sequence 152, App
30	50.0	339	4	US-08-444-818-156	Sequence 156, App
31	50.0	346	1	US-07-951-715A-19	Sequence 19, Appl
32	50.0	346	2	US-08-459-448A-19	Sequence 19, Appl
33	50.0	346	3	US-08-459-504B-19	Sequence 19, Appl
34	50.0	346	3	US-08-459-504B-19	Sequence 19, Appl
35	50.0	346	3	US-08-459-444-19	Sequence 19, Appl
36	50.0	399	2	US-08-839-581A-2	Sequence 2, Appl
37	50.0	399	4	US-09-023-591A-2	Sequence 2, Appl
38	50.0	428	1	US-08-353-550-1	Sequence 1, Appl
39	50.0	428	2	US-08-551-687-1	Sequence 1, Appl
40	50.0	431	3	US-08-807-342B-5	Sequence 5, Appl
41	50.0	445	2	US-08-679-635A-3	Sequence 3, Appl
42	50.0	467	1	US-08-140-104A-2	Sequence 2, Appl
43	50.0	469	1	US-08-353-550-6	Sequence 6, Appl
44	50.0	469	2	US-08-551-687-6	Sequence 6, Appl
45	50.0	470	4	US-09-071-709-12	Sequence 12, Appl
46	50.0	486	3	US-08-889-841-8	Sequence 8, Appl
47	50.0	491	3	US-08-889-841-10	Sequence 10, Appl
48	50.0	498	1	US-08-470-202-59	Sequence 59, Appl
49	50.0	498	1	US-08-470-202-60	Sequence 60, Appl
50	50.0	498	1	US-08-471-770-59	Sequence 59, Appl
51	50.0	498	1	US-08-471-770-60	Sequence 60, Appl
52	50.0	498	2	US-08-468-059-59	Sequence 59, Appl
53	50.0	498	2	US-08-468-059-60	Sequence 60, Appl
54	50.0	591	3	US-08-991-408-4	Sequence 4, Appl
55	50.0	605	2	US-08-687-956A-1	Sequence 1, Appl
56	50.0	655	1	US-07-736-178C-2	Sequence 2, Appl
57	50.0	670	2	US-08-366-547-2	Sequence 2, Appl
58	50.0	739	3	US-09-035-648-24	Sequence 24, Appl
59	50.0	739	4	US-09-001-951-24	Sequence 24, Appl
60	50.0	762	2	US-08-907-166-10	Sequence 10, Appl
61	50.0	788	1	US-08-572-225-1	Sequence 1, Appl
62	50.0	1013	2	US-08-866-650-5	Sequence 5, Appl
63	50.0	1013	3	US-09-021-287-5	Sequence 5, Appl
64	50.0	1013	2	US-08-991-408-2	Sequence 2, Appl
65	50.0	1021	1	US-08-497-025-3	Sequence 3, Appl
66	50.0	1187	1	US-08-320-559-28	Sequence 28, Appl
67	50.0	1187	3	US-08-545-860D-28	Sequence 28, Appl
68	50.0	1187	5	PCT-US94-04496-28	Sequence 28, Appl
69	50.0	1210	1	US-08-320-559-26	Sequence 26, Appl
70	50.0	1210	3	US-08-545-860D-26	Sequence 26, Appl
71	50.0	1210	5	PCT-US94-04496-26	Sequence 26, Appl
72	50.0	1222	2	US-08-680-517-15	Sequence 15, Appl
73	50.0	1245	1	US-08-158-232-8	Sequence 8, Appl
74	50.0	1245	1	US-08-304-628-8	Sequence 8, Appl
75	50.0	1245	3	US-08-611-928-8	Sequence 8, Appl
76	50.0	1245	3	US-09-173-891-8	Sequence 8, Appl
77	50.0	1252	2	US-08-682-517-9	Sequence 9, Appl
78	50.0	1313	2	US-08-244-537-2	Sequence 2, Appl
79	50.0	1566	2	US-08-687-956A-23	Sequence 23, Appl
80	50.0	1627	1	US-07-665-792E-9	Sequence 9, Appl
81	50.0	2232	4	US-09-091-219-25	Sequence 25, Appl
82	50.0	2247	4	US-08-417-089-6	Sequence 6, Appl
83	50.0	2325	3	US-08-695-651-6	Sequence 6, Appl
84	50.0	2325	4	US-08-930-285-6	Sequence 6, Appl
85	50.0	2325	4	US-08-930-285-6	Sequence 6, Appl
86	50.0	2476	2	US-08-276-967-2	Sequence 2, Appl
87	40.0	4	4	US-08-973-462-28	Sequence 28, Appl
88	40.0	7	1	US-08-261-206A-18	Sequence 18, Appl
89	40.0	7	1	US-09-142-078-11	Sequence 11, Appl
90	40.0	8	2	US-08-769-745-11	Sequence 11, Appl
91	40.0	8	3	US-08-335-733D-38	Sequence 38, Appl
92	40.0	8	3	US-08-335-733D-39	Sequence 39, Appl
93	40.0	8	3	US-08-335-733D-40	Sequence 40, Appl
94	40.0	8	3	US-08-335-733D-41	Sequence 41, Appl
95	40.0	8	3	US-08-335-733D-42	Sequence 42, Appl
96	40.0	9	1	US-08-200-900A-72	Sequence 22, Appl
97	40.0	9	1	US-08-338-634-7	Sequence 7, Appl
98	40.0	9	1	US-08-787-547-77	Sequence 77, Appl
99	40.0	9	3	US-08-335-733D-5	Sequence 5, Appl
100	40.0	9	4	US-09-001-984C-17	Sequence 17, Appl

Db 83 VAPRO 87

RESULT 50
084412
ID 084412 PRELIMINARY; PRT; 124 AA.
AC 084412;
DT 01-NOV-1998 (TREMUREL. 08, Created)
DT 01-NOV-1998 (TREMUREL. 08, Last sequence update)
DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)
DE DNA SUPPRESSOR.
GN DKSA.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UM-3/CX;
RX MEDLINE=99000809; Pubmed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatunov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
DR EMBL: AE001314; AAC68004.1; -
DR InterPro: IPR000962; -
DR Pfam: PF01258; zf_dskA_trar; 1.
DR PRINTS: PR00618; DKSANFINGER.
SQ SEQUENCE 124 AA; 13938 MW; 015FBD5D53B65733 CRC64;

Query Match 50.0%; Score 5; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QEVKK 10
Db 31 QEVKK 35

Search completed: August 15, 2001, 12:42:51
Job time: 536 sec

Wed Aug 15 13:35:26 2001

DB 100 TOEVK 104

RESULT 47

09SVK9 PRELIMINARY: PRT: 114 AA.

AC 09SVK9; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE HYPOTHETICAL 12.9 KDA PROTEIN.

GN F1B3.180.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

RA SEQUENCE FROM N.A.

RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,

RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Queciner F.,

RA Salanoubat M.,

RA Submitted (May-1999) to the EMBL/GenBank/DBJ databases.

RL 12

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (Jun-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL049862; CAB42919.1; -

SK HYPOTHETICAL protein.

QY SEQUENCE 114 AA; 12923 MW; F8156E1465887DBB CRC64;

Query Match 50.0%; Score 5; DB 10; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OEYK 10
DB 43 OEYK 47

RESULT 48

ID 09N3V1 PRELIMINARY: PRT: 121 AA.

AC 09N3V1; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE HYPOTHETICAL PROTEIN Y47D7A.H.

GN Y47D7A.H.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Feloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RA SEQUENCE FROM N.A.

RA STRAIN-BRISTOL N2;

RA MEDLINE=99069613; PubMed=9851916;

RA None;

RT "Genome sequence of the nematode C. elegans: a platform for

RT investigating biology. The C. elegans Sequencing Consortium.";

RT Science 283:2012-2018(1998).

RL 12

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA Waterston R.;

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC024790; AAF60636.1; -

SO SEQUENCE 121 AA; 13441 MW; FF21FD197434C60F CRC64;

Query Match 50.0%; Score 5; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPT 5
DB 46 PVAPT 50

RESULT 49

09VYZ8 PRELIMINARY: PRT: 122 AA.

AC 09VYZ8; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE CG11750 PROTEIN.

GN CG11750.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RA SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bailev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,

RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yen R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,

RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

DR EMBL: AE003485; AAF48034.1; -

DR Flybase: FBgn0030294; CG11750.

SO SEQUENCE 122 AA; 13243 MW; D7AB3CA104BCID9D CRC64;

Query Match 50.0%; Score 5; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAPTQ 6

RESULT 43
 09WK87 PRELIMINARY: PRT: 113 AA.
 ID 09WK87
 AC 09WK87
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE P24 CORE PROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K88, CLADE A;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 RT "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ228278; CAA12887.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 FT NON_TER 1 1
 FT 113 113
 SO SEQUENCE 113 AA; 12856 MW; 60D790BE02A1F9AF CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYK 9
 11111
 DB 100 TOEYK 104

RESULT 44
 09WK86 PRELIMINARY: PRT: 113 AA.
 ID 09WK86
 AC 09WK86
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE P24 CORE PROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K101, CLADE A;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 RT "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ228280; CAA12888.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 FT NON_TER 1 1
 FT 113 113
 SO SEQUENCE 113 AA; 12953 MW; 3883B5A94D5F3227 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYK 9
 11111
 DB 100 TOEYK 104

RESULT 45
 09WK47 PRELIMINARY: PRT: 113 AA.
 ID 09WK47
 AC 09WK47
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE P24 CORE PROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K36, CLADE D;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 RT "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ228320; CAA12927.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 FT NON_TER 1 1
 FT 113 113
 SO SEQUENCE 113 AA; 13047 MW; 8B74BB2619F608A3 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYK 9
 11111
 DB 100 TOEYK 104

RESULT 46
 09WK45 PRELIMINARY: PRT: 113 AA.
 ID 09WK45
 AC 09WK45
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE P24 CORE PROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K100, CLADE D;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 RT "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ228322; CAA12929.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 FT NON_TER 1 1
 FT 113 113
 SO SEQUENCE 113 AA; 13060 MW; 6789B057FC791F27 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYK 9
 11111

Q9WK93
ID Q9WK93 PRELIMINARY: PRT: 113 AA.
AC Q9WK93:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K78, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ228272; CA12881.1; -
DR InterPro: IPR000721; -
DR Pfam: PF00607; gag_p24; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12886 MW; 3CD5A0F417EDEFF1A CRC64;

Query Match: 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
DB 100 TOEVK 104

RESULT 40
Q9WK91
ID Q9WK91 PRELIMINARY: PRT: 113 AA.
AC Q9WK91:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K81, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ228274; CA12883.1; -
DR InterPro: IPR000721; -
DR Pfam: PF00607; gag_p24; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12928 MW; E93F1F9A75D0408A CRC64;

Query Match: 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
DB 100 TOEVK 104

RESULT 41
Q9WK90
ID Q9WK90 PRELIMINARY: PRT: 113 AA.
AC Q9WK90:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K82, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ228275; CA12884.1; -
DR InterPro: IPR000721; -
DR Pfam: PF00607; gag_p24; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12928 MW; 993ED8EA7185148B CRC64;

Query Match: 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
DB 100 TOEVK 104

RESULT 42
Q9WK88
ID Q9WK88 PRELIMINARY: PRT: 113 AA.
AC Q9WK88:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K87, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Biryahwaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ228277; CA12886.1; -
DR InterPro: IPR000721; -
DR Pfam: PF00607; gag_p24; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12890 MW; A12E6EC8AEC53510 CRC64;

Query Match: 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
DB 100 TOEVK 104

AC 09WK1: 09WK98: 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K29, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Bityahaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ228262; CAA12872.1; -
DR InterPro; IPR000721; -
DR Pfam; PF00607; gag_P24; 1.
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12932 MW; 3710BEDF76F0F193 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
|||||
DB 100 TOEVR 104

RESULT 36
09WK98: PRELIMINARY; PRT; 113 AA.
ID 09WK98:
AC 09WK98:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K54, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Bityahaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ228267; CAA12876.1; -
DR InterPro; IPR000721; -
DR Pfam; PF00607; gag_P24; 1.
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12946 MW; 04C146666476C072 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
|||||
DB 100 TOEVR 104

RESULT 37
09WK96

ID 09WK96: PRELIMINARY; PRT; 113 AA.
AC 09WK96:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K73, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Bityahaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ228269; CAA12878.1; -
DR InterPro; IPR000721; -
DR Pfam; PF00607; gag_P24; 1.
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12989 MW; 1A192C3958851E90 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
|||||
DB 100 TOEVR 104

RESULT 38
09WK94: PRELIMINARY; PRT; 113 AA.
ID 09WK94:
AC 09WK94:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P24 CORE PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K75, CLADE A;
RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
RA Duffield M., Bityahaho B., Whitworth J., Oram J.;
RT "Molecular epidemiology of HIV-1 in a rural community in south west
RT Uganda."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ228271; CAA12880.1; -
DR InterPro; IPR000721; -
DR Pfam; PF00607; gag_P24; 1.
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12956 MW; 8A19AE2BC185118F CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
|||||
DB 100 TOEVR 104

RESULT 39

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12, CLADE A;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RT Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AJ228259; CAI2870.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 KM Core protein; Polyprotein.
 FT NON_TER 1
 FT 113
 SQ SEQUENCE 113 AA; 12826 MW; FD2B3B6BE6958BE4 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
 |||||
 DB 100 TOEVR 104

RESULT 32
 O93053
 ID 093053 PRELIMINARY; PRT; 113 AA.
 AC O93053;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 GN GAG POLYPROTEIN [CONTAINS: CORE PROTEIN(S) P24] (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K38, CLADE A;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RT Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AJ228263; CAI2874.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 KM Core protein; Polyprotein.
 FT NON_TER 1
 FT 113
 SQ SEQUENCE 113 AA; 13035 MW; 35EB47CDEB22A620 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
 |||||
 DB 100 TOEVR 104

RESULT 33
 O9WKA3 PRELIMINARY; PRT; 113 AA.
 ID O9WKA3;
 AC O9WKA3;

DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE P24 CORE PROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K11, CLADE A;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RT Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ228258; CAI2869.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 FT NON_TER 1
 FT 113
 SQ SEQUENCE 113 AA; 12919 MW; 87EB5C54D76C063 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
 |||||
 DB 100 TOEVR 104

RESULT 34
 O9WKA2
 ID O9WKA2 PRELIMINARY; PRT; 113 AA.
 AC O9WKA2;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 GN P24 CORE PROTEIN (FRAGMENT).
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K13, CLADE A;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RT Duffield M., Biryahwaho B., Whitworth J., Oram J.;
 "Molecular epidemiology of HIV-1 in a rural community in south west
 Uganda";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ228260; CAI2871.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 FT NON_TER 1
 FT 113
 SQ SEQUENCE 113 AA; 12878 MW; 03972190189E3FD3 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVR 9
 |||||
 DB 100 TOEVR 104

RESULT 35
 O9WKA1 PRELIMINARY; PRT; 113 AA.
 ID O9WKA1

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HCV-BB8;
 RA Soergsallal S., Kanlstanon D.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: U23395; AAA64861.1; -.
 DR InterPro: IPR002519; -.
 DR Pfam: PF01539; HCV_env; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 FT NON_TER 1 1
 SO SEQUENCE 102 AA; 11040 MW; 2C560825E0AD043E CRC64;

Query Match 50.0%; Score 5; DB 14; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
 Db 24 PVAPT 28

RESULT 28
 ID 091E25 PRELIMINARY; PRT; 108 AA.
 AC 091E25;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN GP105 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 2.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11709;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Parreira R., Esteves A., Piedade J., Venenno T., Canas-Ferreira F.;
 RT "Intra-individual genetic variability of immunodeficiency virus type 2
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ246878; CAB95055.1; -.
 DR InterPro: IPR000777; -.
 DR Pfam: PF00516; GP120; 1.
 DR NON_TER 1 1
 FT NON_TER 108 108
 SO SEQUENCE 108 AA; 12547 MW; FC22486D50C03680 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
 Db 72 TOEVK 76

RESULT 29
 ID 09UG25 PRELIMINARY; PRT; 112 AA.
 AC 09UG25;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE HYPOHETICAL. 12.8 KDA PROTEIN.
 GN KRF2P564A122.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL110269; CAB53708.1; -.
 DR InterPro: IPR001496; -.
 DR InterPro: IPR001680; -.
 DR SMART: SM00320; WD40; 1.
 KW Hypothetical protein.
 SO SEQUENCE 112 AA; 12790 MW; 76795A2E6D1112B5 CRC64;

Query Match 50.0%; Score 5; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PTOEV 8
 Db 91 PTOEV 95

RESULT 30
 ID 093051 PRELIMINARY; PRT; 113 AA.
 AC 093051;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN(S) P24] (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KI, CLADE A;
 RA Kaleebu P., Hamilton L., Rutebemberwa A., Lyagoba F., Morgan D.,
 RA Dufield M., Bityawho B., Whitworth J., Oram J.;
 RT "Molecular epidemiology of HIV-1 in a rural community in south west
 RT Uganda."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AJ228255; CAAL2866.1; -.
 DR InterPro: IPR000721; -.
 DR Pfam: PF00607; gag_P24; 1.
 DR Core protein; Polypeptide.
 KW NON_TER 1 1
 FT NON_TER 113 113
 SO SEQUENCE 113 AA; 12844 MW; 161CBBC3BCB10CB CRC64;

Query Match 50.0%; Score 5; DB 14; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
 Db 100 TOEVK 104

RESULT 31
 ID 093052 PRELIMINARY; PRT; 113 AA.
 AC 093052;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN(S) P24] (FRAGMENT).
 GN GAG.

RT elegans.":
 RL Nature 368:32-38(1994).
 RP SEQUENCE FROM N.A.
 RA Du Z., Gattung S.:
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.:
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U01277; AAA82477.1;
 SQ SEQUENCE 82 AA; 9058 MW; E6C6AC722EBB125B6 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPTO 6
 DB 40 VAPTO 44

RESULT 24
 Q9DR28 PRELIMINARY; PRT; 88 AA.
 AC Q9DR28:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DD88472;
 RX MEDLINE=21002580; PubMed=11118076;
 RA Abebe A., Pollakis G., Fontanet A.L., Fisseha B., Tegbaru B.,
 RA Kiphus A., Testaye G., Negassa H., Cornelissen M., Goudsmit J.,
 RA Rinde de Wit T.F.:
 RT "Identification of a genetic sub-cluster of HIV-1 subtype C (C')
 RT widespread in Ethiopia.";
 RL AIDS Res. Hum. Retroviruses 16:1909-1914(2000).
 DR EMBL: AF245564; AAC40677.1;
 FT NON_TER 1
 FT NON_TER 88
 SQ SEQUENCE 88 AA; 10146 MW; 501A63053DDC4FEB CRC64;

Query Match 50.0%; Score 5; DB 14; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
 DB 73 QEVKK 77

RESULT 25
 Q9WJ74 PRELIMINARY; PRT; 91 AA.
 AC Q9WJ74:
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GAG PROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=TW396;
 RA Chang K.S.S., Lin C.-I., Salminen M.O., Liao S.-K., Wu A.M.,
 RA Lin H.-C., Lin R.-Y., Twu S.-C.:
 RT "HIV type 1 env gene diversity detected in Taiwan.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U73091; AAD00206.1;
 DR InterPro: IPR000721;
 DR Pfam: PF00607; gag_p24; 1.
 FT NON_TER 1
 FT NON_TER 91
 SQ SEQUENCE 91 AA; 10492 MW; 21A08BBD402AF874 CRC64;

Query Match 50.0%; Score 5; DB 14; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
 DB 60 TOEVK 64

RESULT 26
 Q68302 PRELIMINARY; PRT; 95 AA.
 AC Q68302:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GENOME POLYPROTEIN (CONTAINS: ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35))
 DE (FRAGMENT).
 GN EL.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_Taxid=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HCY-BB43;
 RA Songsivillai S., Kanistanon D.:
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC "- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: U23396; AAA64862.1;
 DR InterPro: IPR002519;
 DR Pfam: PF01539; HCY_env; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 95
 SQ SEQUENCE 95 AA; 10305 MW; 86270AA69397533A CRC64;

Query Match 50.0%; Score 5; DB 14; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
 DB 23 PVAPT 27

RESULT 27
 Q68301 PRELIMINARY; PRT; 102 AA.
 AC Q68301:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GENOME POLYPROTEIN (CONTAINS: ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35))
 DE (FRAGMENT).
 GN EL.
 OS Hepatitis C virus.

OY 3 APTOE 7
|||||
DB 19 APTOE 23

RESULT 20
09GL38 PRELIMINARY; PRT; 52 AA.

AC 09GL38: 09GL38: PRELIMINARY; PRT; 52 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CALPASTATIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chung H.Y., Davis M.E., Hines H.C.;
RT "PCR-SSCP analysis of the bovine calpastatin gene domain 1 region."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY008267; AAC33869.1; -
FT NON_TER 1 1
FT 52 52
SQ SEQUENCE 52 AA; 5749 MW; CBD5A7449AFDDA89 CRC64;

Query Match 50.0%; Score 5; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYK 9
|||||
DB 4 TOEYK 8

RESULT 21

09RRH1 PRELIMINARY; PRT; 75 AA.

AC 09RRH1: 09RRH1: PRELIMINARY; PRT; 75 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 7.7 KDA PROTEIN.
GN DR2520.

OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-R1;
RA MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Maratova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE002081; AAF12064.1; -
DR TIGR; DR2520; -
KW Hypothetical protein.
SQ SEQUENCE 75 AA; 7704 MW; E8E47B7BBAE33B0E CRC64;

Query Match 50.0%; Score 5; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 VAPTO 6
|||||
DB 24 VAPTO 28

RESULT 22
091692 PRELIMINARY; PRT; 77 AA.

AC 091692: 091692: PRELIMINARY; PRT; 77 AA.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 2.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11709;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=6059;
RA Lettner T., Norrgren H., Marquina S., Aaby P., Melbye M.,
RA Poulsen A.-G., Larsen O., Dias F., Escanilla D., Albert J.,
RA Nauci A. Jr.;
RT "HIV-2 genetic variation and DNA load in asymptomatic carriers and
AIDS cases in Guinea-Bissau".
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF023894; AAC63160.1; -
DR InterPro; IPR000777; -
DR Pfam; PF00516; GP120; 1.
KW Envelope protein.

FT NON_TER 1 1
FT 77 77
SQ SEQUENCE 77 AA; 9063 MW; 9970B030D95EC9EC CRC64;

Query Match 50.0%; Score 5; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYK 10
|||||
DB 59 OEYK 63

RESULT 23

017728 PRELIMINARY; PRT; 82 AA.

AC 017728: 017728: PRELIMINARY; PRT; 82 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE C06E4.2 PROTEIN.
GN C06E4.2.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitidae;
OC Rhabdilitae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton R., Connell M., Copestey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kersey J., Kirsten J., Laister N., Latelle P.,
RA Ligniting L., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spratt J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RX MEDLINE-96135216; PubMed-8551561;
 RA Lochelt M., Flugel R.M.;
 RT "The human foamy virus pol gene is expressed as a Pro-pol polyprotein
 and not as a Gag-pol fusion protein.";
 RL J. Virol. 70:1033-1040(1996).
 RN (9)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97126112; PubMed-8971036;
 RA Boden J., Lochelt M., Winkler I., Flower R.P., Dellus H.,
 RA Flugel R.M.;
 RT "Characterization of the spliced pol transcript of feline foamy virus:
 the splice acceptor site of the pol transcript is located in gag of
 foamy viruses.";
 RT J. Virol. 70:9024-9027(1996).
 RL (10)
 RN SEQUENCE FROM N.A.
 RA Flugel R.M.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U21247; AAB48113.1; -.
 KW Envelope protein.
 SQ SEQUENCE 989 AA; 113890 MW; E0E8338ECE4E0A5 CRC64;

Query Match 60.0%; Score 6; DB 14; Length 989;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 TOEVKK 10
 Db 185 TOEVKK 190

RESULT 17
 ID 025772 PRELIMINARY; PRT; 1230 AA.
 AC 025772;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE HYPOHETICAL 131.8 KDA PROTEIN.
 GN HP1157.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID-210;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-26695 / ATCC 700392;
 RX MEDLINE-97394467; PubMed-9252185;
 RA Tomb J.-F., White O., Kervilave A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khakh H.G., Glick A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Mallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori.";
 RL Nature 388:539-547(1997).
 DR EMBL; AE000621; AAD08205.1; -.
 DR TIGR; HP1157; -.
 DR InterPro; IPR002718; -.
 DR Pfam; PF01856; HP_OMP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1230 AA; 131847 MW; 4BF1506F1E072A10 CRC64;

Query Match 60.0%; Score 6; DB 2; Length 1230;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10
 Db 173 TOEVKK 178

RESULT 18
 ID 091BG3 PRELIMINARY; PRT; 1653 AA.
 AC 091BG3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE PAA.
 GN PAA.
 OS Streptococcus criceti.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID-1335;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-E49;
 RA Tamura H., Kato H.;
 RT "Cell surface antigen I/II - Streptococcus cricetus.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB042239; BAA95000.1; -.
 DR InterPro; IPR001899; -.
 DR InterPro; IPR002965; -.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR PRINTS; PR01217; PRICEXTENSN.
 DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 SQ SEQUENCE 1653 AA; 180862 MW; 93F28E215BF598DE CRC64;

Query Match 60.0%; Score 6; DB 2; Length 1653;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 PVAPTO 6
 Db 955 PVAPTO 960

RESULT 19
 ID 063334 PRELIMINARY; PRT; 23 AA.
 AC 063334;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ALPHA-2-MACROGLOBULIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR;
 RX MEDLINE-85207604; PubMed-2581948;
 RA Northmann W., Heisig M., Kunz D., Heinrich P.C.;
 RT "Molecular cloning of cdna sequences for rat alpha 2-macroglobulin and
 RT measurement of its transcription during experimental inflammation.";
 RL J. Biol. Chem. 260:6200-6205(1985).
 DR EMBL; M84369; AAAA1594.1; -.
 DR InterPro; IPR001599; -.
 DR Pfam; PF00207; A2M; 1.
 DR NON_TER 1
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2526 MW; E2D721FB1B223876 CRC64;

Query Match 50.0%; Score 5; DB 11; Length 23;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 60.0%; Score 6; DB 5; Length 819;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPRO 6
|||||
Db 563 PVAPRO 568

RESULT 14
O98830 PRELIMINARY; PRT; 988 AA.
ID O98830;
AC O98830;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-FEB-1997 (TREMBLrel. 02, Last annotation update)
DE PROVIRAL DNA, HSRV1 DELETION VARIANT.
GN ENV.
OS Human foamy virus.
OC Viruses; Retroid viruses; Retroviridae; Spumavirus.
OX NCBI_TaxID=11641;
RN [1]
RN SEQUENCE FROM N.A.
RA Schmidt M., Herchenröder O., Heeney J.L., Rehwilms A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RA Rehwilms A.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y07723; CA68994.1; -;
DR EMBL; Y07724; CA69000.1; -;
DR EMBL; Y07725; CA69004.1; -;
SQ SEQUENCE 988 AA; 113762 MW; 0E96E53BF7D7C6B CRC64;

Query Match 60.0%; Score 6; DB 14; Length 988;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10
|||||
Db 185 TOEVKK 190

RESULT 15
O87041 PRELIMINARY; PRT; 988 AA.
ID O87041;
AC O87041;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE SFVCPZ, COMPLETE GENOME.
GN ENV.
OS Simian foamy virus.
OC Viruses; Retroid viruses; Retroviridae; Spumavirus.
OX NCBI_TaxID=11642;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN-SFVCPZ;
RX MEDLINE=94240804; Pubmed=8184531;
RA Herchenröder O., Renne R., Loncar D., Cobb E.K., Murthy K.K.,
RA Schneider J., Mergle A., Luciw P.A.;
RT "Isolation, cloning, and sequencing of simian foamy viruses from
RT chimpanzees (SFVCPZ): high homology to human foamy virus (HFV).";
RL Virology 201:187-199(1994).
RN [2]
RN SEQUENCE FROM N.A.
RA STRAIN-SFVCPZ;
RX Luciw P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04327; AAA19979.1; -;

SQ SEQUENCE 988 AA; 113352 MW; 9A88951475BEC62 CRC64;

Query Match 60.0%; Score 6; DB 14; Length 988;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10
|||||
Db 185 TOEVKK 190

RESULT 16
P90288 PRELIMINARY; PRT; 989 AA.
ID P90288;
AC P90288;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ENVELOPE PROTEIN.
OS Human spumaretrovirus (Foamy virus).
OC Viruses; Retroid viruses; Retroviridae; Spumavirus.
OX NCBI_TaxID=11963;
RN [1]
RN SEQUENCE OF 980-989 FROM N.A.
RX MEDLINE=88004420; Pubmed=2820721;
RA Flugel R.M., Rehwilms A., Maurer B., Darai G.;
RT "Nucleotide sequence analysis of the env gene and its flanking regions
RT of the human spumaretrovirus reveals two novel genes.";
RL EMBO J. 6:2077-2084(1987).
RN [2]
RN SEQUENCE FROM N.A.
RA Maurer B., Bannert H., Rehwilms A., Darai G., Flugel R.M.;
RL (In) Bolognesi D.P. (eds.);
RL Human retroviruses, cancer and AIDS, pp.75-88, Alan Liss Inc.,
RL New York (1988).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=91101282; Pubmed=1846194;
RA Murenyi W., Flugel R.M.;
RT "Analysis of splicing patterns of human spumaretrovirus by polymerase
RT chain reaction reveals complex RNA structures.";
RL J. Virol. 65:727-735(1991).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=91335779; Pubmed=1651600;
RA Lochelt M., Zentgraf H., Flugel R.M.;
RT "Construction of an infectious DNA clone of the full-length human
RT spumaretrovirus genome and mutagenesis of the bel 1 gene.";
RL Virology 184:43-54(1991).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=93348264; Pubmed=8394017;
RA Lochelt M., Murenyi W., Flugel R.M.;
RT "Human foamy virus genome possesses an internal, Bel-1-dependent and
RT functional promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7317-7321(1993).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=95000932; Pubmed=7917520;
RA Weissenberger J., Flugel R.M.;
RT "Identification and characterization of the bel 3 protein of human
RT foamy virus.";
RL AIDS Res. Hum. Retroviruses 10:595-600(1994).
RN [7]
RN SEQUENCE FROM N.A.
RX MEDLINE=95380275; Pubmed=7544460;
RA Kogel D., Aboud M., Flugel R.M.;
RT "Mutational analysis of the reverse transcriptase and ribonuclease H
RT domains of the human foamy virus.";
RL Nucleic Acids Res. 23:2621-2625(1995).
RN [8]
RN SEQUENCE FROM N.A.

OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96-62333;
RA Belda F.J., Barlow K.L., Murphy G., Parry J.V., Clewley J.P.;
RT "A dual subtype B/E HIV-1 infection with a novel V3 loop crown motif
among infections acquired in South East Asia and imported into
England";
RL Submitted:(FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
DR EMBL: AJ224197; CAA11887.1; -
DR Interpro: IPR000721; -
DR Pfam: PF00607; gag_p24; 1.
KM Core protein; Polypotein.
FT NON_TER 1 1
SQ SEQUENCE 174 AA; 19667 MW; D6F18B245B0707DF CRC64;

Query Match 60.0%; Score 6; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEYVK 10
|||||
DB 154 TOEYVK 159

RESULT 8
O9KVZ4 PRELIMINARY; PRT; 274 AA.
AC O9KVZ4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE BETA-LACTAMASE PRECURSOR.
GN OXA-23.
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_Taxid=470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RYC 52763/97;
RX MEDLINE=20277880; PubMed=10817708;
RA Bou G., Oliver A., Martinez-Beltran J.;
RT "OXA-24, a novel class D beta-lactamase with carbapenemase activity in
an Acinetobacter baumannii clinical strain";
RL Antimicrob. Agents Chemother. 44:1556-1561(2000).
DR EMBL: AJ239129; CAB92323.1; -
KW Signal.
FT SIGNAL 1 7 POTENTIAL.
SQ SEQUENCE 274 AA; 30810 MW; 5343DC532ABAB4E6 CRC64;

Query Match 60.0%; Score 6; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEYVK 10
|||||
DB 197 TOEYVK 202

RESULT 9
O26617 PRELIMINARY; PRT; 486 AA.
AC O26617;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE SPCF1.

OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_Taxid=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95301110; PubMed=7781910;
RA Zeller R.W., Coffman J.A., Harrington M.G., Britten R.J.,
RT Davidson E.H.;
RT "SPCF1, a sea urchin embryo DNA-binding protein, exists as five
nested variants encoded by a single mRNA";
RL Dev. Biol. 169:713-727(1995).
DR EMBL: U18784; AAA86479.1; -
DR Interpro: IPR000255; -
DR PROSITE: PS00012; PHOSPHOPANTHETINE; UNKNOWN.1.
SQ SEQUENCE 486 AA; 54616 MW; A9AB23F8B26357 CRC64;

Query Match 60.0%; Score 6; DB 5; Length 486;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PTOEYK 9
|||||
DB 40 PTOEYK 45

RESULT 10
O9UNJ0 PRELIMINARY; PRT; 609 AA.
AC O9UNJ0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE POLYCISTIN-2-LIKE PROTEIN.
GN PKD2L2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Veldhuisen B., Spruit L., Dauwerse H.G., Breuning M.H., Peters D.J.M.;
RT "Genes homologous to the autosomal dominant polycystic kidney disease
2 (PKD2) gene";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF118125; AAD46478.1; -
DR Interpro: IPR000636; -
DR Interpro: IPR001682; -
DR Interpro: IPR001696; -
DR Interpro: IPR001668; -
DR Interpro: IPR002111; -
DR Pfam: PF00520; ion_trans; 1.
DR PRINTS: PR00170; NACHANNEL.
DR PRODOM: PD003549; -; 1.
SQ SEQUENCE 609 AA; 71906 MW; D5DCF9829B9A41AB CRC64;

Query Match 60.0%; Score 6; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEYVK 10
|||||
DB 298 TOEYVK 303

RESULT 11
O9NZM6 PRELIMINARY; PRT; 624 AA.
AC O9NZM6;
ID O9NZM6;

Query Match 70.0%; Score 7; DB 14; Length 94;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPTOEV 8
 |||||
 DB 39 VAPTOEV 45

RESULT 4
 Q9PM45 PRELIMINARY; PRT; 227 AA.
 AC Q9PM45;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PUTATIVE TONB TRANSPORT PROTEIN.
 GN TONB2 OR CJI630.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCCTC 11168;
 RA MEDLINE=20150912; PubMed=1068204;
 RA Parhill J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
 RA Jagsall K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 DR EMBL: AL139079; CAB73618.1; -.
 DR InterPro: IPR003538; -.
 DR PRINTS: PR01374; TONBPROTEIN.
 SQ SEQUENCE 227 AA; 26298 MW; 7AEFFB148480DCD CRC64;

Query Match 70.0%; Score 7; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 APPOEVK 9
 |||||
 DB 105 APPOEVK 111

RESULT 5
 O9HYT7 PRELIMINARY; PRT; 102 AA.
 AC O9HYT7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL PROTEIN PA3307.
 GN PA3307.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RA MEDLINE=20437337; PubMed=10984043;
 RA Steyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garner R.L., Coltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laibig K., Lim R.M.,
 RA Smith K.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Ralston J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an

RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004753; AAC06695.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 102 AA; 11114 MW; D92FE4B8B95286B CRC64;

Query Match 60.0%; Score 6; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTO 6
 |||||
 DB 27 PVAPTO 32

RESULT 6
 Q9X9T5 PRELIMINARY; PRT; 116 AA.
 AC Q9X9T5;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE PUTATIVE REGULATORY PROTEIN.
 GN SC011.16.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K., Harris D.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleser H.M., Denaplatte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL MOL. Microbiol. 21:77-96(1996).
 DR EMBL: AF096823; CAB46971.1; -.
 SQ SEQUENCE 116 AA; 12228 MW; 4B6986EB74C7B6CD CRC64;

Query Match 60.0%; Score 6; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10
 |||||
 DB 29 TOEVKK 34

RESULT 7
 O93041 PRELIMINARY; PRT; 174 AA.
 AC O93041;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GAG POLYPROTEIN [CONTAINS: CORE PROTEIN(S) P24] (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.

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969 5 50.0 1566 2 053414 053414 streptococc
970 5 50.0 1566 2 055308 055308 streptococc
971 5 50.0 1569 2 054183 054183 streptococc
972 5 50.0 1576 4 075096 075096 homo sapien
973 5 50.0 1581 4 015065 015065 homo sapien
974 5 50.0 1625 10 008367 008367 zea mays (m
975 5 50.0 1648 4 015058 015058 homo sapien
976 5 50.0 1685 10 043248 043248 zea mays (m
977 5 50.0 1688 5 09V9D0 09V9D0 dtrosophila
978 5 50.0 1698 5 024440 024440 dtrosophila
979 5 50.0 1698 5 03V8R9 03V8R9 dtrosophila
980 5 50.0 1723 2 03JMX8 03JMX8 dtrosophila
981 5 50.0 1785 5 025685 025685 plasmodium
982 5 50.0 1798 5 09VUB6 09VUB6 dtrosophila
983 5 50.0 1819 2 09ZLV0 09ZLV0 helicobacte
984 5 50.0 1819 2 025262 025262 helicobacte
985 5 50.0 1927 2 025262 025262 helicobacte
986 5 50.0 1963 10 09LXT9 09LXT9 arabidopsis
987 5 50.0 2084 3 09HEC9 09HEC9 neurospora
988 5 50.0 2164 13 09IAR9 09IAR9 gallus gall
989 5 50.0 2247 14 039818 039818 equine rhin
990 5 50.0 2272 5 017329 017329 caenorhabdi
991 5 50.0 2325 10 041743 041743 zea mays (m
992 5 50.0 2404 5 03VE34 03VE34 dtrosophila
993 5 50.0 2541 5 019663 019663 caenorhabdi
994 5 50.0 2652 2 09RA21 09RA21 vibrio mari
995 5 50.0 2768 5 09VC00 09VC00 dtrosophila
996 5 50.0 2785 4 075691 075691 homo sapien
997 5 50.0 2796 2 048926 048926 mycobacteri
998 5 50.0 2936 5 09NKR7 09NKR7 leishmania
999 5 50.0 2977 5 09VAP9 09VAP9 dtrosophila
1000 5 50.0 3016 14 092531 092531 hepatitis c

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ALIGNMENTS

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RESULT 1
09RNU3 PRELIMINARY: PRT: 86 AA.
AC 09RNU3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE P60 PROTEIN (FRAGMENT).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP MEDLINE=90256283; PubMed=2111287;
RX Kohler S.; Leimster-Wachter M.; Chakraborty T.; Lottspeich F.;
RA Goebel W.;
RT "The gene coding for protein p60 of Listeria monocytogenes and its use
RT as a specific probe for Listeria monocytogenes."
RL Infect. Immun. 58:1943-1950(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Park S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF179003; AAD55089.1; -.
FT NON-TER 1
FT NON-TER 86
SQ SEQUENCE 86 AA: 9194 MW: 71F649A817D697F6 CRC64;

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Query Match 100.0%; Score 10; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTOEVKK 10

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Db 32 PVAPTOEVKK 41

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RESULT 2
003493 PRELIMINARY: PRT: 478 AA.
AC 003493:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094153; PubMed=1459966;
RA Buber A.; Kuhn M.; Goebel W.; Koehler S.;
RT "Structural and functional properties of the p60 proteins from
RT different Listeria species."
RL J. Bacteriol. 174:8166-8171(1992).
CC -I- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE
CC INVASION OF NONPROFESSIONAL PHAGOCYtic CELLS BY LISTERIA.
DR EMBL: M80351; AAA25280.1; -.
DR InterPro: IPR000064; -.
DR InterPro: IPR002482; -.
DR Pfam: PF00877; NUPC_P60; 1.
DR Pfam: PF01476; LysM; 2.
DR SMART: SM00257; LysM; 1.
KW SIGNAL.
FT CHAIN 1 27 BY SIMILARITY.
FT CHAIN 28 478 PROTEIN P60.
SQ SEQUENCE 478 AA: 49997 MW: D46D050507402344 CRC64;

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Query Match 100.0%; Score 10; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTOEVKK 10

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Db 148 PVAPTOEVKK 157

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RESULT 3
067673 PRELIMINARY: PRT: 94 AA.
AC 067673:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HEXON PROTEIN (FRAGMENT).
OS porcine adenovirus sp.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=47901;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Pring-Akerblom P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X95630; CAA64884.1; -.
DR HSP: P03277; IDHX.
DR InterPro: IPR000736; -.
DR Pfam: PF01065; Adeno_hexon; 1.
KW Hexon protein.
FT NON-TER 1
FT NON-TER 94
SQ SEQUENCE 94 AA: 10807 MW: 2646FBB97DDCC9FD CRC64;

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823	5	50.0	670	6	Q9X762	Q9X762 cercoptihc	896	5	50.0	970	4	Q9Y6X9	Q9Y6X9 homo sapien
824	5	50.0	671	5	Q07431	Q07431 bombyx mori	897	5	50.0	970	4	Q9UGX3	Q9UGX3 homo sapien
825	5	50.0	681	4	Q07543	Q07543 homo sapien	898	5	50.0	977	13	Q91925	Q91925 xenopus lae
826	5	50.0	684	4	Q9Y338	Q9Y338 homo sapien	899	5	50.0	982	3	Q74773	Q74773 schizosach
827	5	50.0	687	11	Q83024	Q83024 mus musculu	900	5	50.0	988	5	Q16851	Q16851 pluteia xy
828	5	50.0	688	5	Q9VXB7	Q9VXB7 drosophila	901	5	50.0	995	14	P90248	P90248 human immun
829	5	50.0	689	11	Q88934	Q88934 mus musculu	902	5	50.0	998	14	Q9UYC6	Q9UYC6 pyrococcus
830	5	50.0	698	5	Q01719	Q01719 strongyloce	903	5	50.0	1000	2	Q9WYK5	Q9WYK5 thermotoga
831	5	50.0	691	2	Q9PMJ3	Q9PMJ3 campylobact	904	5	50.0	1002	5	Q9VTC4	Q9VTC4 drosophila
832	5	50.0	691	13	Q57658	Q57658 gallus gall	905	5	50.0	1004	4	Q9UHN7	Q9UHN7 homo sapien
833	5	50.0	700	5	Q96839	Q96839 drosophila	906	5	50.0	1008	13	Q9DER7	Q9DER7 gallus gall
834	5	50.0	700	5	Q9V887	Q9V887 drosophila	907	5	50.0	1013	4	Q43897	Q43897 homo sapien
835	5	50.0	700	5	Q9UAS6	Q9UAS6 drosophila	908	5	50.0	1013	4	Q9NQ54	Q9NQ54 homo sapien
836	5	50.0	703	5	Q9V850	Q9V850 drosophila	909	5	50.0	1021	4	Q93033	Q93033 homo sapien
837	5	50.0	704	5	Q9VA70	Q9VA70 drosophila	910	5	50.0	1022	5	Q61907	Q61907 caenorhabdi
838	5	50.0	714	2	Q85056	Q85056 moraxella c	911	5	50.0	1022	13	Q57460	Q57460 brachydanio
839	5	50.0	718	5	Q96721	Q96721 encephalito	912	5	50.0	1025	10	Q9LME3	Q9LME3 arabisdopsis
840	5	50.0	728	5	Q9NNK3	Q9NNK3 leishmania	913	5	50.0	1030	4	Q14974	Q14974 homo sapien
841	5	50.0	732	5	Q9YOC4	Q9YOC4 leishmania	914	5	50.0	1052	5	Q9W554	Q9W554 drosophila
842	5	50.0	735	13	Q57381	Q57381 xenopus lae	915	5	50.0	1057	5	Q9W294	Q9W294 drosophila
843	5	50.0	739	5	P91060	P91060 caenorhabdi	916	5	50.0	1066	4	Q9UGX4	Q9UGX4 homo sapien
844	5	50.0	739	5	Q9N8U6	Q9N8U6 trypanosoma	917	5	50.0	1070	5	Q22796	Q22796 arabisdops
845	5	50.0	746	5	Q18350	Q18350 caenorhabdi	918	5	50.0	1071	10	Q49727	Q49727 arabisdops
846	5	50.0	748	3	Q9P3D8	Q9P3D8 neurospora	919	5	50.0	1073	10	Q9SRV6	Q9SRV6 arabisdops
847	5	50.0	750	2	P96256	P96256 mycobacteri	920	5	50.0	1073	10	Q82606	Q82606 arabisdops
848	5	50.0	763	2	Q9ZBL8	Q9ZBL8 mycobacteri	921	5	50.0	1092	2	Q50236	Q50236 zymomonas m
849	5	50.0	775	2	Q912D2	Q912D2 pseudomonas	922	5	50.0	1096	10	Q9LRE5	Q9LRE5 arabisdops
850	5	50.0	782	4	Q9UT94	Q9UT94 homo sapien	923	5	50.0	1113	2	Q9R6S8	Q9R6S8 bacillus ba
851	5	50.0	786	6	Q9X5X1	Q9X5X1 bos taurus	924	5	50.0	1115	4	Q9ULLO	Q9ULLO homo sapien
852	5	50.0	791	5	Q96454	Q96454 drosophila	925	5	50.0	1127	1	Q58221	Q58221 pyrococcus
853	5	50.0	791	5	Q9V765	Q9V765 drosophila	926	5	50.0	1132	2	Q9PAB1	Q9PAB1 xyella fas
854	5	50.0	792	5	Q18174	Q18174 caenorhabdi	927	5	50.0	1181	5	Q9U3A2	Q9U3A2 caenorhabdi
855	5	50.0	792	5	Q9UNG1	Q9UNG1 ephydriasta f	928	5	50.0	1186	5	Q9U3A3	Q9U3A3 caenorhabdi
856	5	50.0	795	5	Q62006	Q62006 branchiost	929	5	50.0	1199	6	Q28139	Q28139 bos taurus
857	5	50.0	797	4	Q95267	Q95267 homo sapien	930	5	50.0	1212	2	Q9L1C8	Q9L1C8 streptomyce
858	5	50.0	797	4	Q9UNN9	Q9UNN9 homo sapien	931	5	50.0	1217	5	P91457	P91457 caenorhabdi
859	5	50.0	803	4	Q9N2L5	Q9N2L5 homo sapien	932	5	50.0	1228	3	Q12754	Q12754 saccharomyc
860	5	50.0	803	4	Q9HBY3	Q9HBY3 homo sapien	933	5	50.0	1251	13	Q91365	Q91365 coturnix co
861	5	50.0	815	4	Q9P200	Q9P200 homo sapien	934	5	50.0	1262	5	Q9N911	Q9N911 leishmania
862	5	50.0	815	10	Q9SHN8	Q9SHN8 arabisdops	935	5	50.0	1268	11	Q63623	Q63623 rattus norv
863	5	50.0	816	4	Q9UFT2	Q9UFT2 homo sapien	936	5	50.0	1274	10	P93125	P93125 dunaliella
864	5	50.0	816	5	Q9VKJ9	Q9VKJ9 drosophila	937	5	50.0	1274	10	Q9M680	Q9M680 dunaliella
865	5	50.0	817	3	Q07229	Q07229 saccharomyc	938	5	50.0	1276	10	Q81059	Q81059 arabisdops
866	5	50.0	822	1	Q27154	Q27154 methanobact	939	5	50.0	1298	11	Q9OYF1	Q9OYF1 rattus norv
867	5	50.0	831	4	Q9UMS6	Q9UMS6 homo sapien	940	5	50.0	1338	5	Q9GQO8	Q9GQO8 gliardia lam
868	5	50.0	831	11	Q9EPZ2	Q9EPZ2 mus musculu	941	5	50.0	1341	4	Q9UFP8	Q9UFP8 homo sapien
869	5	50.0	833	5	Q9S594	Q9S594 mycoplasma	942	5	50.0	1357	5	Q9W4M4	Q9W4M4 drosophila
870	5	50.0	835	5	Q9V714	Q9V714 drosophila	943	5	50.0	1401	5	Q9VAY5	Q9VAY5 drosophila
871	5	50.0	846	5	Q9V210	Q9V210 drosophila	944	5	50.0	1415	5	Q61442	Q61442 caenorhabdi
872	5	50.0	847	14	Q41537	Q41537 human immun	945	5	50.0	1420	5	Q9Y0Y8	Q9Y0Y8 drosophila
873	5	50.0	848	14	Q9QAL9	Q9QAL9 white spot	946	5	50.0	1423	5	Q9W1A0	Q9W1A0 drosophila
874	5	50.0	849	4	Q9NVE4	Q9NVE4 homo sapien	947	5	50.0	1425	14	P90072	P90072 human immun
875	5	50.0	859	14	Q9YUZ4	Q9YUZ4 human immun	948	5	50.0	1427	14	Q9WF74	Q9WF74 human immun
876	5	50.0	866	4	Q9H466	Q9H466 homo sapien	949	5	50.0	1427	14	Q9WF71	Q9WF71 human immun
877	5	50.0	870	5	Q9GRT4	Q9GRT4 leishmania	950	5	50.0	1427	14	Q9WFE8	Q9WFE8 human immun
878	5	50.0	871	2	Q9PIZ1	Q9PIZ1 campylobact	951	5	50.0	1427	14	Q9WFE5	Q9WFE5 human immun
879	5	50.0	882	10	Q9LME2	Q9LME2 arabisdops	952	5	50.0	1429	14	Q9QBE0	Q9QBE0 human immun
880	5	50.0	882	2	Q917T2	Q917T2 drosophila	953	5	50.0	1430	14	Q89290	Q89290 human immun
881	5	50.0	887	5	Q9U712	Q9U712 neisseria m	954	5	50.0	1433	14	P90071	P90071 human immun
882	5	50.0	887	2	Q9J0U8	Q9J0U8 neisseria m	955	5	50.0	1433	14	Q9QMM2	Q9QMM2 human immun
883	5	50.0	889	5	Q9V8R8	Q9V8R8 drosophila	956	5	50.0	1433	14	Q9QML4	Q9QML4 human immun
884	5	50.0	899	3	Q06132	Q06132 saccharomyc	957	5	50.0	1433	14	Q91BE9	Q91BE9 human immun
885	5	50.0	904	5	Q9VEX7	Q9VEX7 drosophila	958	5	50.0	1433	14	Q9DHS5	Q9DHS5 human immun
886	5	50.0	908	5	Q9VDQ0	Q9VDQ0 drosophila	959	5	50.0	1435	14	Q41791	Q41791 human immun
887	5	50.0	912	2	Q9ZLY5	Q9ZLY5 helicobacte	960	5	50.0	1435	14	Q9WLJ3	Q9WLJ3 human immun
888	5	50.0	912	5	Q9NHCI	Q9NHCI drosophila	961	5	50.0	1440	5	Q27395	Q27395 caenorhabdi
889	5	50.0	912	5	Q9NH99	Q9NH99 drosophila	962	5	50.0	1440	14	Q91CT9	Q91CT9 chimpanzee
890	5	50.0	916	5	Q9NHC2	Q9NHC2 drosophila	963	5	50.0	1449	5	Q10922	Q10922 caenorhabdi
891	5	50.0	916	5	Q9NHC0	Q9NHC0 drosophila	964	5	50.0	1449	14	Q91080	Q91080 human immun
892	5	50.0	919	5	Q9Z7K3	Q9Z7K3 chlamydia p	965	5	50.0	1452	14	Q92888	Q92888 human immun
893	5	50.0	928	14	Q91MX9	Q91MX9 cercopitlhi	966	5	50.0	1457	5	Q9VT35	Q9VT35 drosophila
894	5	50.0	969	2	Q9RZ15	Q9RZ15 delnocooc	967	5	50.0	1490	5	Q9U485	Q9U485 drosophila
895	5	50.0	969	4	Q9Y214	Q9Y214 homo sapien	968	5	50.0	1534	6	Q28298	Q28298 canis famli

677	5	50.0	492	14	089962	089962 human immun	750	5	50.0	528	10	09SRE2	09SRE2 arabisdopsi
678	5	50.0	492	14	09WF75	09WF75 human immun	751	5	50.0	530	2	09I008	09I008 pseudomonas
679	5	50.0	492	14	09WF72	09WF72 human immun	752	5	50.0	535	14	09QMK6	09QMK6 chltia viru
680	5	50.0	492	14	09WF69	09WF69 human immun	753	5	50.0	535	14	09IV39	09IV39 human calic
681	5	50.0	492	14	09WF66	09WF66 human immun	754	5	50.0	537	2	09Z8U8	09Z8U8 chlamydia p
682	5	50.0	492	14	09QRM9	09QRM9 human immun	755	5	50.0	537	2	09JRV7	09JRV7 chlamydia p
683	5	50.0	492	14	09EAL3	09EAL3 human immun	756	5	50.0	539	10	080914	080914 arabisdopsi
684	5	50.0	493	10	024326	024326 phaseolus v	757	5	50.0	539	11	060664	060664 mus musculu
685	5	50.0	493	10	09FMR2	09FMR2 arabisdopsi	758	5	50.0	540	4	060230	060230 homo sapien
686	5	50.0	493	10	09FMR2	09FMR2 arabisdopsi	759	5	50.0	542	5	023446	023446 caenorhabdl
687	5	50.0	493	14	09QMH9	09QMH9 human immun	760	5	50.0	543	10	022188	022188 arabisdopsi
688	5	50.0	493	14	09IV95	09IV95 human immun	761	5	50.0	544	11	060764	060764 mus musculu
689	5	50.0	494	14	09I256	09I256 human immun	762	5	50.0	547	13	091349	091349 xenopus lae
690	5	50.0	494	14	09O257	09O257 human immun	763	5	50.0	548	2	09ZEY1	09ZEY1 listeria mo
691	5	50.0	494	14	09O259	09O259 human immun	764	5	50.0	548	2	09EXF6	09EXF6 listeria mo
692	5	50.0	494	14	09OSU0	09OSU0 human immun	765	5	50.0	549	5	024441	024441 drosophila
693	5	50.0	494	14	09OC00	09OC00 human immun	766	5	50.0	552	5	09VT52	09VT52 drosophila
694	5	50.0	494	14	09QBY4	09QBY4 human immun	767	5	50.0	553	2	09RSN4	09RSN4 delnoccocus
695	5	50.0	494	14	09I1W4	09I1W4 human immun	768	5	50.0	557	2	067869	067869 aquifex aeo
696	5	50.0	495	14	09OP03	09OP03 human immun	769	5	50.0	557	2	09K926	09K926 bacillus ha
697	5	50.0	495	14	09OB22	09OB22 human immun	770	5	50.0	558	2	P73902	P73902 synechocyst
698	5	50.0	495	14	09IWS3	09IWS3 human immun	771	5	50.0	562	1	09HRL9	09HRL9 halobacteri
699	5	50.0	495	14	076126	076126 human immun	772	5	50.0	567	2	033932	033932 listeria mo
700	5	50.0	496	5	017537	017537 caenorhabdl	773	5	50.0	572	5	026042	026042 penaeus jap
701	5	50.0	496	14	09WSG0	09WSG0 human immun	774	5	50.0	573	3	008179	008179 saccharomyc
702	5	50.0	496	14	09WS51	09WS51 human immun	775	5	50.0	574	2	019963	019963 caenorhabdl
703	5	50.0	496	14	09WLR9	09WLR9 human immun	776	5	50.0	574	2	P74297	P74297 synechocyst
704	5	50.0	496	14	09OST1	09OST1 human immun	777	5	50.0	578	5	09TYL0	09TYL0 caenorhabdl
705	5	50.0	496	14	09DKED	09DKED human immun	778	5	50.0	580	10	09ZVU7	09ZVU7 arabisdopsi
706	5	50.0	497	14	041792	041792 human immun	779	5	50.0	583	5	019777	019777 caenorhabdl
707	5	50.0	497	14	089926	089926 human immun	780	5	50.0	584	4	09UNR7	09UNR7 homo sapien
708	5	50.0	497	14	09WLR2	09WLR2 human immun	781	5	50.0	596	10	09LSW2	09LSW2 arabisdopsi
709	5	50.0	497	14	09WLR1	09WLR1 human immun	782	5	50.0	604	2	000509	000509 streptococ
710	5	50.0	497	14	09ID96	09ID96 human immun	783	5	50.0	606	2	053561	053561 streptococ
711	5	50.0	498	14	P88150	P88150 human immun	784	5	50.0	609	13	013027	013027 xenopus lae
712	5	50.0	498	14	077372	077372 human immun	785	5	50.0	609	14	082670	082670 influenza c
713	5	50.0	498	14	079665	079665 human immun	786	5	50.0	609	14	082670	082670 influenza c
714	5	50.0	498	14	09WLR6	09WLR6 human immun	787	5	50.0	609	14	082671	082671 influenza c
715	5	50.0	498	14	P90239	P90239 human immun	788	5	50.0	609	14	082672	082672 influenza c
716	5	50.0	498	14	09OMM1	09OMM1 human immun	789	5	50.0	609	14	082673	082673 influenza c
717	5	50.0	498	14	09OML3	09OML3 human immun	790	5	50.0	609	14	082674	082674 influenza c
718	5	50.0	498	14	09OML3	09OML3 human immun	791	5	50.0	609	14	082675	082675 influenza c
719	5	50.0	498	14	09OML3	09OML3 human immun	792	5	50.0	620	5	09Y0D4	09Y0D4 penaeus mon
720	5	50.0	498	14	09OML3	09OML3 human immun	793	5	50.0	624	4	09P2U4	09P2U4 homo sapien
721	5	50.0	498	14	09OML3	09OML3 human immun	794	5	50.0	626	4	09P2U3	09P2U3 homo sapien
722	5	50.0	498	14	09OML3	09OML3 human immun	795	5	50.0	627	4	09H172	09H172 homo sapien
723	5	50.0	499	14	072860	072860 human immun	796	5	50.0	633	2	059526	059526 mycoplasma
724	5	50.0	499	14	074834	074834 human immun	797	5	50.0	637	3	008484	008484 saccharomyc
725	5	50.0	499	14	P89692	P89692 human immun	798	5	50.0	641	5	001667	001667 drosophila
726	5	50.0	499	14	09Q712	09Q712 human immun	799	5	50.0	641	5	09VU01	09VU01 drosophila
727	5	50.0	499	14	09IW66	09IW66 human immun	800	5	50.0	641	14	09I072	09I072 influenza c
728	5	50.0	500	14	P89971	P89971 human immun	801	5	50.0	645	5	09NEF7	09NEF7 penaeus van
729	5	50.0	500	14	074806	074806 human immun	802	5	50.0	645	14	09I073	09I073 influenza c
730	5	50.0	500	14	09YX54	09YX54 human immun	803	5	50.0	645	14	09I069	09I069 influenza c
731	5	50.0	500	14	09WQ10	09WQ10 human immun	804	5	50.0	646	2	007625	007625 bacillus su
732	5	50.0	502	14	09OML3	09OML3 human immun	805	5	50.0	646	14	067417	067417 influenza c
733	5	50.0	502	14	09OML3	09OML3 human immun	806	5	50.0	647	14	067386	067386 influenza c
734	5	50.0	502	14	09ICM8	09ICM8 chimpanzee	807	5	50.0	648	14	09I066	09I066 influenza c
735	5	50.0	503	14	09ICM8	09ICM8 chimpanzee	808	5	50.0	649	14	09I066	09I066 influenza c
736	5	50.0	503	14	09LD28	09LD28 arabisdopsi	809	5	50.0	649	14	067416	067416 influenza v
737	5	50.0	505	2	025089	025089 human immun	810	5	50.0	649	14	067418	067418 influenza c
738	5	50.0	505	4	09UNR8	09UNR8 homo sapien	811	5	50.0	649	14	067419	067419 influenza c
739	5	50.0	507	4	013064	013064 homo sapien	812	5	50.0	649	14	09I071	09I071 influenza c
740	5	50.0	507	14	09Q079	09Q079 chimpanzee	813	5	50.0	649	14	09I070	09I070 influenza c
741	5	50.0	508	6	09QMC8	09QMC8 felis silve	814	5	50.0	650	14	09I067	09I067 influenza c
742	5	50.0	509	6	09QMC7	09QMC7 bison bison	815	5	50.0	651	5	019659	019659 caenorhabdl
743	5	50.0	512	14	09I079	09I079 human immun	816	5	50.0	662	5	062139	062139 caenorhabdl
744	5	50.0	516	10	09SVB0	09SVB0 arabisdopsi	817	5	50.0	667	10	09LJES	09LJES arabisdopsi
745	5	50.0	517	14	071261	071261 human immun	818	5	50.0	668	5	09VWM7	09VWM7 drosophila
746	5	50.0	517	14	073329	073329 human immun	819	5	50.0	669	5	09VNT0	09VNT0 drosophila
747	5	50.0	519	5	09NEU8	09NEU8 caenorhabdl	820	5	50.0	670	4	075714	075714 homo sapien
748	5	50.0	520	11	035731	035731 mus musculu	821	5	50.0	670	4	09UPF5	09UPF5 homo sapien
749	5	50.0	526	4	09P280	09P280 homo sapien	822	5	50.0	670	4	09UNK7	09UNK7 homo sapien

531	5	50.0	353	14	Q9ENC6	Q9enc6 human immun	604	5	50.0	452	5	Q27696	Q27696 musca domes
532	5	50.0	353	14	Q9ENC4	Q9enc4 human immun	605	5	50.0	456	11	Q9JTB8	Q9jtb8 mus musculus
533	5	50.0	355	14	Q67685	Q67685 aquifex aeo	606	5	50.0	457	2	Q9ZHC0	Q9zhc0 streptococc
534	5	50.0	359	8	Q37749	Q37749 cephalospor	607	5	50.0	459	14	Q9JTB3	Q9jtb3 human papil
535	5	50.0	360	4	Q9UDM6	Q9udm6 homo sapien	608	5	50.0	460	5	Q9XTQ9	Q9xtq9 caenorhabd1
536	5	50.0	362	2	Q9KRG9	Q9krg9 yersinia en	609	5	50.0	461	5	Q45051	Q45051 caenorhabd1
537	5	50.0	362	5	Q9NEZ1	Q9nez1 caenorhabd1	610	5	50.0	462	5	Q9W143	Q9w143 drosophila
538	5	50.0	362	10	Q9NEZ1	Q9nez1 caenorhabd1	611	5	50.0	464	2	P74828	P74828 sphingomona
539	5	50.0	363	10	Q9M6B4	Q9m6b4 vitis vinif	612	5	50.0	465	14	Q90729	Q90729 human papil
540	5	50.0	366	14	Q86313	Q86313 reovirus sp	613	5	50.0	467	4	Q9NXX1	Q9nxx1 homo sapien
541	5	50.0	366	14	Q86314	Q86314 reovirus sp	614	5	50.0	467	14	Q40461	Q40461 human immun
542	5	50.0	366	14	Q86315	Q86315 reovirus sp	615	5	50.0	468	14	Q9ENB2	Q9enb2 human immun
543	5	50.0	366	14	Q86316	Q86316 reovirus sp	616	5	50.0	469	2	Q9ZL71	Q9ztl71 helicobacte
544	5	50.0	366	14	Q86317	Q86317 reovirus sp	617	5	50.0	469	14	Q9IXN9	Q9ixn9 human immun
545	5	50.0	366	14	Q86318	Q86318 reovirus sp	618	5	50.0	469	14	Q9END0	Q9end0 human immun
546	5	50.0	366	14	Q86319	Q86319 reovirus sp	619	5	50.0	469	14	Q9ENC2	Q9enc2 human immun
547	5	50.0	366	14	Q86320	Q86320 reovirus sp	620	5	50.0	469	14	Q9ENB0	Q9enb0 human immun
548	5	50.0	366	14	Q86323	Q86323 reovirus sp	621	5	50.0	469	14	Q9ENB0	Q9enb0 human immun
549	5	50.0	366	14	Q86307	Q86307 reovirus sp	622	5	50.0	470	5	Q19087	Q19087 caenorhabd1
550	5	50.0	366	14	Q86308	Q86308 reovirus sp	623	5	50.0	470	14	Q9ENB4	Q9enb4 human immun
551	5	50.0	366	14	Q86309	Q86309 reovirus sp	624	5	50.0	472	14	Q9ENB4	Q9enb4 human immun
552	5	50.0	366	14	Q86310	Q86310 reovirus sp	625	5	50.0	472	14	Q9ENB4	Q9enb4 human immun
553	5	50.0	366	14	Q86311	Q86311 reovirus sp	626	5	50.0	473	2	Q9ENB9	Q9enb9 human immun
554	5	50.0	366	14	Q86312	Q86312 reovirus sp	627	5	50.0	473	14	Q9ENB0	Q9enb0 human immun
555	5	50.0	366	14	Q9ENM1	Q9enm1 reovirus (t	628	5	50.0	473	14	Q9ENB8	Q9enb8 human immun
556	5	50.0	367	14	Q87097	Q87097 chimpanzee	629	5	50.0	473	14	Q9ENB6	Q9enb6 human immun
557	5	50.0	368	2	Q9F010	Q9f010 pseudomonas	630	5	50.0	473	14	Q9ENB7	Q9enb7 human immun
558	5	50.0	369	5	Q9N405	Q9n405 caenorhabd1	631	5	50.0	473	14	Q9ENB4	Q9enb4 human immun
559	5	50.0	378	2	Q55307	Q55307 streptococc	632	5	50.0	474	14	Q9ENB0	Q9enb0 human immun
560	5	50.0	382	4	Q9H878	Q9h878 homo sapien	633	5	50.0	476	5	Q03996	Q03996 plasmodium
561	5	50.0	385	6	Q9GL14	Q9gl14 micropotamo	634	5	50.0	476	14	Q9ENB2	Q9enb2 human immun
562	5	50.0	385	10	Q9ZP00	Q9zp00 brassica ju	635	5	50.0	477	2	Q9RXT6	Q9rxt6 delnoccocc
563	5	50.0	385	14	Q80627	Q80627 human immun	636	5	50.0	478	5	Q25684	Q25684 plasmodium
564	5	50.0	386	5	P91632	P91632 drosophila	637	5	50.0	481	2	Q9L4Q8	Q9l4q8 clostiridium
565	5	50.0	387	4	Q9H8P7	Q9h8p7 homo sapien	638	5	50.0	481	14	Q77697	Q77697 human immun
566	5	50.0	389	2	Q9K7L3	Q9k7l3 bacillus ha	639	5	50.0	481	14	Q9JVL9	Q9jvl9 human immun
567	5	50.0	392	4	Q9NPL5	Q9npl5 homo sapien	640	5	50.0	482	5	Q9XY38	Q9xy38 acanthamoeb
568	5	50.0	393	14	Q41549	Q41549 human immun	641	5	50.0	482	5	Q03998	Q03998 plasmodium
569	5	50.0	394	5	Q9VMU4	Q9vmu4 drosophila	642	5	50.0	484	5	Q9U9P0	Q9u9p0 hydra atten
570	5	50.0	395	2	Q9KE01	Q9ke01 bacillus ha	643	5	50.0	484	14	Q77699	Q77699 human immun
571	5	50.0	398	4	Q9UGL3	Q9ugl3 homo sapien	644	5	50.0	484	14	Q77700	Q77700 human immun
572	5	50.0	400	11	Q9EQU2	Q9equ2 apodemus ag	645	5	50.0	484	14	Q80622	Q80622 human immun
573	5	50.0	407	5	Q9VBM4	Q9vbm4 drosophila	646	5	50.0	486	4	Q9UCX4	Q9ucx4 homo sapien
574	5	50.0	408	2	Q9FD10	Q9fd10 salmonella	647	5	50.0	486	14	Q77804	Q77804 human immun
575	5	50.0	408	4	Q9UGL4	Q9ugl4 homo sapien	648	5	50.0	486	14	Q78566	Q78566 human immun
576	5	50.0	409	2	Q9LKA3	Q9lka3 shigella dy	649	5	50.0	486	14	Q79451	Q79451 human immun
577	5	50.0	410	2	Q05446	Q05446 mycobacteri	650	5	50.0	486	14	Q80628	Q80628 human immun
578	5	50.0	411	14	Q81814	Q81814 hepatitis c	651	5	50.0	486	14	Q80629	Q80629 human immun
579	5	50.0	414	14	Q81329	Q81329 hepatitis c	652	5	50.0	486	14	Q80634	Q80634 human immun
580	5	50.0	414	14	P89958	P89958 hepatitis c	653	5	50.0	487	14	Q80621	Q80621 human immun
581	5	50.0	414	14	P89959	P89959 hepatitis c	654	5	50.0	488	14	Q79362	Q79362 human immun
582	5	50.0	415	14	Q81554	Q81554 hepatitis c	655	5	50.0	489	14	Q79350	Q79350 human immun
583	5	50.0	416	2	Q31444	Q31444 bacillus su	656	5	50.0	489	14	Q79354	Q79354 human immun
584	5	50.0	418	2	Q9K9F3	Q9k9f3 bacillus ha	657	5	50.0	489	14	Q79360	Q79360 human immun
585	5	50.0	418	4	Q75066	Q75066 homo sapien	658	5	50.0	489	14	Q80306	Q80306 human immun
586	5	50.0	418	4	Q9NUA8	Q9nuu8 homo sapien	659	5	50.0	489	14	Q80307	Q80307 human immun
587	5	50.0	421	4	Q9UNN6	Q9unn6 homo sapien	660	5	50.0	489	14	Q80631	Q80631 human immun
588	5	50.0	421	4	Q9UDH9	Q9udh9 homo sapien	661	5	50.0	489	14	Q80305	Q80305 human immun
589	5	50.0	422	2	Q9Y617	Q9y617 homo sapien	662	5	50.0	490	14	Q9RNV1	Q9rnmv1 bacillus an
590	5	50.0	422	2	P96208	P96208 mycobacteri	663	5	50.0	490	14	Q80623	Q80623 human immun
591	5	50.0	423	2	Q49939	Q49939 mycobacteri	664	5	50.0	490	14	P90073	P90073 human immun
592	5	50.0	434	14	Q89933	Q89933 human immun	665	5	50.0	490	14	P90255	P90255 human immun
593	5	50.0	435	5	Q93322	Q93322 caenorhabd1	666	5	50.0	490	14	Q9MC83	Q9mc83 human immun
594	5	50.0	436	14	Q91V79	Q91v79 human immun	667	5	50.0	491	2	Q9F518	Q9f518 alteromonas
595	5	50.0	438	5	Q9NG13	Q9ng13 brachlosto	668	5	50.0	491	14	Q80181	Q80181 human immun
596	5	50.0	439	5	Q9V9N5	Q9v9n5 drosophila	669	5	50.0	491	14	Q9WLH4	Q9wlh4 human immun
597	5	50.0	440	2	Q25464	Q25464 helicobacte	670	5	50.0	491	14	Q9OEP9	Q9oep9 human immun
598	5	50.0	443	1	Q58579	Q58579 pyrococcus	671	5	50.0	491	14	Q9QBZ6	Q9qbz6 human immun
599	5	50.0	444	5	Q26861	Q26861 tryppanosoma	672	5	50.0	492	2	Q9ZND0	Q9znd0 clostiridium
600	5	50.0	445	2	Q45794	Q45794 bacteroides	673	5	50.0	492	14	Q79351	Q79351 human immun
601	5	50.0	445	2	Q9K199	Q9k199 bacteroides	674	5	50.0	492	14	Q74452	Q74452 human immun
602	5	50.0	446	5	Q9N3V2	Q9n3v2 caenorhabd1	675	5	50.0	492	14	Q89291	Q89291 human immun
603	5	50.0	447	2	Q86673	Q86673 streptomyce	676	5	50.0	492	14	Q89958	Q89958 human immun

385	5	50.0	230	14	0910T5	0910T5 human immun	458	5	50.0	255	14	010731	010731 human immun
386	5	50.0	231	14	0910M3	0910M3 human immun	459	5	50.0	255	14	093746	093746 human immun
387	5	50.0	231	14	0910U5	0910U5 human immun	460	5	50.0	255	14	093742	093742 human immun
388	5	50.0	232	14	0910P8	0910P8 human immun	461	5	50.0	255	14	0936X0	0936X0 human immun
389	5	50.0	232	14	0910U9	0910U9 human immun	462	5	50.0	255	14	0936U2	0936U2 human immun
390	5	50.0	232	14	0910U8	0910U8 human immun	463	5	50.0	256	4	09N0R3	09N0R3 homo sapien
391	5	50.0	232	14	0910T4	0910T4 human immun	464	5	50.0	256	14	093709	093709 human immun
392	5	50.0	233	14	0910V0	0910V0 human immun	465	5	50.0	256	14	0936U7	0936U7 human immun
393	5	50.0	233	14	0910V4	0910V4 human immun	466	5	50.0	256	14	0936T6	0936T6 human immun
394	5	50.0	233	14	0910U7	0910U7 human immun	467	5	50.0	257	14	0937A5	0937A5 human immun
395	5	50.0	233	14	0910P8	0910P8 human immun	468	5	50.0	257	14	0936W3	0936W3 human immun
396	5	50.0	234	14	0910P0	0910P0 human immun	469	5	50.0	257	14	0936P0	0936P0 human immun
397	5	50.0	234	14	0910V9	0910V9 human immun	470	5	50.0	258	2	09K410	09K410 streptomyce
398	5	50.0	234	14	0910V6	0910V6 human immun	471	5	50.0	258	14	0936R3	0936R3 human immun
399	5	50.0	235	14	093728	093728 human immun	472	5	50.0	258	14	0936P4	0936P4 human immun
400	5	50.0	235	14	0936O5	0936O5 human immun	473	5	50.0	259	1	09HWK32	09HWK32 thermoplasm
401	5	50.0	236	14	093758	093758 human immun	474	5	50.0	259	14	010736	010736 human immun
402	5	50.0	237	10	09F039	09F039 oryza sativ	475	5	50.0	260	5	0176Z5	0176Z5 caenorhabd1
403	5	50.0	237	14	093725	093725 human immun	476	5	50.0	261	14	0936R5	0936R5 human immun
404	5	50.0	237	14	0910V5	0910V5 human immun	477	5	50.0	261	14	0936P5	0936P5 human immun
405	5	50.0	238	14	093785	093785 human immun	478	5	50.0	261	14	0936M6	0936M6 human immun
406	5	50.0	238	14	093757	093757 human immun	479	5	50.0	262	14	093736	093736 human immun
407	5	50.0	241	11	092135	092135 rattus norv	480	5	50.0	263	2	P94481	P94481 bacillus su
408	5	50.0	241	14	0936T8	0936T8 human immun	481	5	50.0	263	10	09FEL5	09FEL5 arabisdopsis
409	5	50.0	243	14	0936M7	0936M7 human immun	482	5	50.0	264	14	010730	010730 human immun
410	5	50.0	244	14	093724	093724 human immun	483	5	50.0	265	14	010729	010729 homo sapien
411	5	50.0	245	14	093774	093774 human immun	484	5	50.0	266	4	015795	015795 homo sapien
412	5	50.0	245	14	093723	093723 human immun	485	5	50.0	266	5	025732	025732 plasmodium
413	5	50.0	245	14	093717	093717 human immun	486	5	50.0	268	14	010735	010735 human immun
414	5	50.0	245	14	093716	093716 human immun	487	5	50.0	271	5	021382	021382 caenorhabd1
415	5	50.0	245	14	093704	093704 human immun	488	5	50.0	273	2	005936	005936 pseudomonas
416	5	50.0	246	2	09RGC4	09RGC4 mycoplasma	489	5	50.0	275	4	09N0R1	09N0R1 homo sapien
417	5	50.0	246	14	093721	093721 human immun	490	5	50.0	276	2	P73137	P73137 synecocyst
418	5	50.0	246	14	093718	093718 human immun	491	5	50.0	276	5	094215	094215 caenorhabd1
419	5	50.0	246	14	093715	093715 human immun	492	5	50.0	278	2	068435	068435 leptospira
420	5	50.0	246	14	093714	093714 human immun	493	5	50.0	278	2	068437	068437 leptospira
421	5	50.0	247	14	093773	093773 human immun	494	5	50.0	282	5	090221	090221 caenorhabd1
422	5	50.0	247	14	093768	093768 human immun	495	5	50.0	287	1	0937J3	0937J3 pyrococcus
423	5	50.0	247	14	0936M9	0936M9 human immun	496	5	50.0	288	2	0937X2	0937X2 neisseria m
424	5	50.0	248	14	093719	093719 human immun	497	5	50.0	289	2	067230	067230 aquifex aeo
425	5	50.0	249	10	065058	065058 picea maria	498	5	50.0	289	2	09KYN4	09KYN4 streptomyce
426	5	50.0	249	14	093708	093708 human immun	499	5	50.0	291	2	006449	006449 serratia ma
427	5	50.0	249	14	0936V5	0936V5 human immun	500	5	50.0	291	2	007464	007464 salmonella
428	5	50.0	250	11	09WV64	09WV64 rattus norv	501	5	50.0	293	2	09PDL4	09PDL4 xylella fas
429	5	50.0	250	14	093770	093770 human immun	502	5	50.0	293	4	014836	014836 homo sapien
430	5	50.0	250	14	093763	093763 human immun	503	5	50.0	293	10	049020	049020 gossypium h
431	5	50.0	251	14	093762	093762 human immun	504	5	50.0	296	10	022812	022812 arabisdopsis
432	5	50.0	252	10	0936L8	0936L8 arabisdopsis	505	5	50.0	297	5	09VD14	09VD14 drosophila
433	5	50.0	252	14	093794	093794 human immun	506	5	50.0	298	5	09V090	09V090 drosophila
434	5	50.0	252	14	093775	093775 human immun	507	5	50.0	305	14	0934M8	0934M8 human immun
435	5	50.0	252	14	093767	093767 human immun	508	5	50.0	305	2	09K9M1	09K9M1 bacillus ha
436	5	50.0	252	14	093760	093760 human immun	509	5	50.0	306	10	09SDN3	09SDN3 prunus dulc
437	5	50.0	252	14	093755	093755 human immun	510	5	50.0	307	2	055410	055410 synecocyst
438	5	50.0	252	14	093749	093749 human immun	511	5	50.0	308	2	09R0Q2	09R0Q2 delnecoccus
439	5	50.0	252	14	093748	093748 human immun	512	5	50.0	312	14	09WIT5	09WIT5 human immun
440	5	50.0	252	14	093702	093702 human immun	513	5	50.0	312	14	09WIT2	09WIT2 human immun
441	5	50.0	252	14	093700	093700 human immun	514	5	50.0	315	5	018121	018121 caenorhabd1
442	5	50.0	253	1	059562	059562 pyrococcus	515	5	50.0	327	2	09PAP3	09PAP3 xylella fas
443	5	50.0	253	1	09V177	09V177 pyrococcus	516	5	50.0	327	10	09ID07	09ID07 oryza sativ
444	5	50.0	253	14	093729	093729 human immun	517	5	50.0	327	11	09QW06	09QW06 mus musculu
445	5	50.0	253	14	093727	093727 human immun	518	5	50.0	329	5	09Y205	09Y205 ephydatia f
446	5	50.0	253	14	093726	093726 human immun	519	5	50.0	329	5	09VY11	09VY11 drosophila
447	5	50.0	253	14	093711	093711 human immun	520	5	50.0	330	14	072628	072628 human immun
448	5	50.0	253	14	093701	093701 human immun	521	5	50.0	335	2	09RSG0	09RSG0 delnecoccus
449	5	50.0	254	5	021223	021223 caenorhabd1	522	5	50.0	335	5	09UD3	09UD3 caenorhabd1
450	5	50.0	254	14	093795	093795 human immun	523	5	50.0	337	2	053089	053089 iactobacill
451	5	50.0	254	14	093789	093789 human immun	524	5	50.0	339	14	091E68	091E68 human immun
452	5	50.0	254	14	093739	093739 human immun	525	5	50.0	342	2	0925F8	0925F8 mycobacteri
453	5	50.0	254	14	093732	093732 human immun	526	5	50.0	343	2	09KRG7	09KRG7 vibrio chol
454	5	50.0	254	14	093707	093707 human immun	527	5	50.0	343	8	092238	092238 trichophyto
455	5	50.0	254	14	0936Z2	0936Z2 human immun	528	5	50.0	344	14	0937A5	0937A5 human immun
456	5	50.0	254	14	0936U6	0936U6 human immun	529	5	50.0	347	5	09VRJ9	09VRJ9 drosophila
457	5	50.0	254	14	0936N7	0936N7 human immun	530	5	50.0	351	10	023142	023142 arabisdopsis

239	5	50.0	207	14	Q9DUW8	Q9duw8 human immun	312	5	50.0	219	14	Q9IUK0	Q9Iuk0 human immun
240	5	50.0	207	14	Q9DUW6	Q9duw6 human immun	313	5	50.0	220	14	Q9IV08	Q9Ivq8 human immun
241	5	50.0	207	14	Q9DUW5	Q9duw5 human immun	314	5	50.0	220	14	Q9IVP3	Q9Ivq3 human immun
242	5	50.0	207	14	Q9DUW3	Q9duw3 human immun	315	5	50.0	220	14	Q9IUV5	Q9Iuv5 human immun
243	5	50.0	207	14	Q9DUW1	Q9duw1 human immun	316	5	50.0	220	14	Q9IUV4	Q9Iuv4 human immun
244	5	50.0	207	14	Q9DUV9	Q9duv9 human immun	317	5	50.0	220	14	Q9IUR3	Q9Iur3 human immun
245	5	50.0	207	14	Q9DUV8	Q9duv8 human immun	318	5	50.0	220	14	Q9IDR8	Q9Idr8 human immun
246	5	50.0	207	14	Q9DUV6	Q9duv6 human immun	319	5	50.0	220	14	Q9IDP4	Q9Idp4 human immun
247	5	50.0	207	14	Q9DUV5	Q9duv5 human immun	320	5	50.0	221	2	P70813	P70813 borrelia af
248	5	50.0	207	14	Q9DUV4	Q9duv4 human immun	321	5	50.0	221	14	Q9Q2K7	Q9q2k7 human immun
249	5	50.0	207	14	Q9DUV1	Q9duv1 human immun	322	5	50.0	221	14	Q9IUX5	Q9Iux3 human immun
250	5	50.0	207	14	Q9DUV9	Q9duv9 human immun	323	5	50.0	221	14	Q9IUW0	Q9Iuw0 human immun
251	5	50.0	208	2	Q9RB27	Q9rb27 pseudomonas	324	5	50.0	221	14	Q9IU06	Q9Iuw6 human immun
252	5	50.0	208	14	Q37393	Q37393 human immun	325	5	50.0	222	14	Q9J7A4	Q9j7a4 human immun
253	5	50.0	208	14	Q9J394	Q9j394 human immun	326	5	50.0	222	14	Q9J6Z1	Q9j6z1 human immun
254	5	50.0	208	14	Q9J6Z4	Q9j6z4 human immun	327	5	50.0	222	14	Q9IVN0	Q9Ivn0 human immun
255	5	50.0	208	14	Q9IUP8	Q9Iup8 human immun	328	5	50.0	222	14	Q9IVJ2	Q9Ivj2 human immun
256	5	50.0	208	14	Q9IUL5	Q9Iul5 human immun	329	5	50.0	222	14	Q9IVJ2	Q9Ivj2 human immun
257	5	50.0	208	14	Q9IUL6	Q9Iul6 human immun	330	5	50.0	222	14	Q9IUV3	Q9Iuv3 human immun
258	5	50.0	209	14	Q9J7A6	Q9j7a6 human immun	331	5	50.0	222	14	Q9IDQ8	Q9Idq8 human immun
259	5	50.0	209	14	Q9IUS7	Q9Ius7 human immun	332	5	50.0	222	14	Q9IDP0	Q9Idp0 human immun
260	5	50.0	209	14	Q9IUS7	Q9Ius7 human immun	333	5	50.0	223	14	Q9J730	Q9j730 human immun
261	5	50.0	209	14	Q9IUQ6	Q9Iuq6 human immun	334	5	50.0	223	14	Q9IVQ9	Q9Ivq9 human immun
262	5	50.0	209	14	Q9IUL7	Q9Iul7 human immun	335	5	50.0	223	14	Q9IUV2	Q9Iuv2 human immun
263	5	50.0	209	14	Q9IUL7	Q9Iul7 human immun	336	5	50.0	223	14	Q9IUU0	Q9Iuw0 human immun
264	5	50.0	210	14	Q9J776	Q9j776 human immun	337	5	50.0	223	14	Q9IUT7	Q9Iut7 human immun
265	5	50.0	210	14	Q9J6T4	Q9j6t4 human immun	338	5	50.0	223	14	Q9J792	Q9j792 human immun
266	5	50.0	210	14	Q9IUX8	Q9Iux8 human immun	339	5	50.0	224	14	Q9IVN9	Q9Ivn9 human immun
267	5	50.0	210	14	Q9IUX1	Q9Iux1 human immun	340	5	50.0	224	14	Q9IVL4	Q9Ivl4 human immun
268	5	50.0	210	14	Q9IUR4	Q9Iur4 human immun	341	5	50.0	224	14	Q9IVJ9	Q9Ivj9 human immun
269	5	50.0	210	14	Q9DUW9	Q9duw9 human immun	342	5	50.0	224	14	Q9IVJ8	Q9Ivj8 human immun
270	5	50.0	211	5	Q9XU58	Q9xu58 caenorhabdit	343	5	50.0	224	14	Q9IUV8	Q9Iuv8 human immun
271	5	50.0	211	14	Q56887	Q56887 human immun	344	5	50.0	224	14	Q9IUV3	Q9Iuv3 human immun
272	5	50.0	211	14	Q56888	Q56888 human immun	345	5	50.0	224	14	Q9IUV9	Q9Iuv9 human immun
273	5	50.0	211	14	Q56889	Q56889 human immun	346	5	50.0	224	14	Q9IUV2	Q9Iuv2 human immun
274	5	50.0	211	14	Q56890	Q56890 human immun	347	5	50.0	224	14	Q9IDN9	Q9Idn9 human immun
275	5	50.0	211	14	Q56891	Q56891 human immun	348	5	50.0	225	14	Q9J6Z9	Q9j6z9 human immun
276	5	50.0	211	14	Q56892	Q56892 human immun	349	5	50.0	225	14	Q9J6R4	Q9j6r4 human immun
277	5	50.0	211	14	Q93157	Q93157 human immun	350	5	50.0	225	14	Q9IVR2	Q9Ivr2 human immun
278	5	50.0	211	14	Q9IUV3	Q9Iuv3 human immun	351	5	50.0	225	14	Q9IUX9	Q9Iux9 human immun
279	5	50.0	211	14	Q9IUV4	Q9Iuv4 human immun	352	5	50.0	225	14	Q9IUX4	Q9Iux4 human immun
280	5	50.0	211	14	Q9IUR0	Q9Iur0 human immun	353	5	50.0	225	14	Q9IUV7	Q9Iuv7 human immun
281	5	50.0	211	14	Q9IUN5	Q9Iun5 human immun	354	5	50.0	225	14	Q9IDQ5	Q9Idq5 human immun
282	5	50.0	212	14	Q9IUV01	Q9Iuv01 human immun	355	5	50.0	226	14	Q9IWM5	Q9Iwm5 human immun
283	5	50.0	213	14	Q9WMM0	Q9wmm0 human immun	356	5	50.0	226	14	Q9IWL5	Q9Iwl5 human immun
284	5	50.0	214	14	Q9J7B0	Q9j7b0 human immun	357	5	50.0	226	14	Q9IVK7	Q9Ivk7 human immun
285	5	50.0	214	14	Q9J7A9	Q9j7a9 human immun	358	5	50.0	226	14	Q9IVK2	Q9Ivk2 human immun
286	5	50.0	214	14	Q9J7A1	Q9j7a1 human immun	359	5	50.0	226	14	Q9IVK1	Q9Ivk1 human immun
287	5	50.0	214	14	Q9J777	Q9j777 human immun	360	5	50.0	226	14	Q9IUV5	Q9Iuv5 human immun
288	5	50.0	214	14	Q9IVR3	Q9Ivr3 human immun	361	5	50.0	226	14	Q9IDP7	Q9Idp7 human immun
289	5	50.0	215	14	Q9J7B2	Q9j7b2 human immun	362	5	50.0	226	14	Q9IDP5	Q9Idp5 human immun
290	5	50.0	215	14	Q9IUS0	Q9Ius0 human immun	363	5	50.0	226	14	Q9IDP1	Q9Idp1 human immun
291	5	50.0	216	14	Q9J759	Q9j759 human immun	364	5	50.0	227	2	Q31975	Q31975 bacillus su
292	5	50.0	216	14	Q9IUK1	Q9Iuk1 human immun	365	5	50.0	227	9	Q37974	Q37974 bacteriophage
293	5	50.0	217	14	Q9IUV9	Q9Iuv9 human immun	366	5	50.0	227	9	Q38576	Q38576 unidentified
294	5	50.0	217	14	Q9IUV0	Q9Iuv0 human immun	367	5	50.0	227	10	Q38R64	Q38r64 zea mays (m
295	5	50.0	217	14	Q9IUV2	Q9Iuv2 human immun	368	5	50.0	227	14	Q9IUV5	Q9Iuv5 human immun
296	5	50.0	217	14	Q9IUN8	Q9Iun8 human immun	369	5	50.0	227	14	Q9IUV8	Q9Iuv8 human immun
297	5	50.0	217	14	Q9IUN3	Q9Iun3 human immun	370	5	50.0	227	14	Q9IUV6	Q9Iuv6 human immun
298	5	50.0	218	14	Q9J778	Q9j778 human immun	371	5	50.0	227	14	Q9IDQ3	Q9Idq3 human immun
299	5	50.0	218	14	Q9J754	Q9j754 human immun	372	5	50.0	228	14	Q9QNX0	Q9qnx0 human immun
300	5	50.0	218	14	Q9IUV1	Q9Iuv1 human immun	373	5	50.0	228	14	Q9IVR4	Q9Ivr4 human immun
301	5	50.0	218	14	Q9IUX2	Q9Iux2 human immun	374	5	50.0	228	14	Q9IUV2	Q9Iuv2 human immun
302	5	50.0	218	14	Q9IDR5	Q9Idr5 human immun	375	5	50.0	228	14	Q9IVK6	Q9Ivk6 human immun
303	5	50.0	219	4	Q9I656	Q9i656 homo sapien	376	5	50.0	228	14	Q9IUV1	Q9Iuv1 human immun
304	5	50.0	219	14	Q9J6V9	Q9j6v9 human immun	377	5	50.0	228	14	Q9IUV0	Q9Iuv0 human immun
305	5	50.0	219	14	Q9IVN7	Q9Ivn7 human immun	378	5	50.0	228	14	Q9IUV3	Q9Iuv3 human immun
306	5	50.0	219	14	Q9IVN3	Q9Ivn3 human immun	379	5	50.0	229	14	Q9J713	Q9j713 human immun
307	5	50.0	219	14	Q9IUV2	Q9Iuv2 human immun	380	5	50.0	229	14	Q9IUV2	Q9Iuv2 human immun
308	5	50.0	219	14	Q9IUX0	Q9Iux0 human immun	381	5	50.0	229	14	Q9IUV9	Q9Iuv9 human immun
309	5	50.0	219	14	Q9IUV8	Q9Iuv8 human immun	382	5	50.0	230	14	Q9IVN5	Q9Ivn5 human immun
310	5	50.0	219	14	Q9IUV5	Q9Iuv5 human immun	383	5	50.0	230	14	Q9IVJ5	Q9Ivj5 human immun
311	5	50.0	219	14	Q9IUV4	Q9Iuv4 human immun	384	5	50.0	230	14	Q9IUV1	Q9Iuv1 human immun

93	5	50.0	156	6	Q9N146	Q9n146 macaca mula	166	5	50.0	203	14	Q91UP7	Q91up7 human immun
94	5	50.0	157	5	Q9GYJ6	Q9gyj6 caenorhabdi	167	5	50.0	203	14	Q91UK9	Q91uk9 human immun
95	5	50.0	161	2	Q9FBC1	Q9fbc1 streptococc	168	5	50.0	204	14	Q9Q2J1	Q9q2j1 human immun
96	5	50.0	161	10	Q9SSS3	Q9sss3 arabidopsis	169	5	50.0	204	14	Q9J7A8	Q9j7a8 human immun
97	5	50.0	161	14	Q9J771	Q9j771 human immun	170	5	50.0	204	14	Q9J797	Q9j797 human immun
98	5	50.0	161	14	Q9J6U4	Q9j6u4 human immun	171	5	50.0	204	14	Q9J782	Q9j782 human immun
99	5	50.0	162	14	Q9J6U0	Q9j6u0 human immun	172	5	50.0	204	14	Q9J741	Q9j741 human immun
100	5	50.0	163	5	Q9N3V0	Q9n3v0 caenorhabdi	173	5	50.0	204	14	Q9J6Q4	Q9j6q4 human immun
101	5	50.0	165	14	Q9J788	Q9j788 human immun	174	5	50.0	204	14	Q9J6Q3	Q9j6q3 human immun
102	5	50.0	165	14	Q9J752	Q9j752 human immun	175	5	50.0	204	14	Q9JUM7	Q9jum7 human immun
103	5	50.0	166	4	Q9NFTU0	Q9nftu0 homo saplen	176	5	50.0	204	14	Q9JUL4	Q9jul4 human immun
104	5	50.0	166	14	Q9J7A7	Q9j7a7 human immun	177	5	50.0	205	14	Q9J6P1	Q9j6p1 human immun
105	5	50.0	166	14	Q9J6V7	Q9j6v7 human immun	178	5	50.0	205	14	Q9JUP5	Q9jup5 human immun
106	5	50.0	167	14	Q9J6U3	Q9j6u3 human immun	179	5	50.0	205	14	Q9JUP0	Q9jup0 human immun
107	5	50.0	171	5	Q9N927	Q9n927 trypanosoma	180	5	50.0	205	14	Q9JUN6	Q9jun6 human immun
108	5	50.0	172	14	Q9J784	Q9j784 human immun	181	5	50.0	205	14	Q9JUN0	Q9jun0 human immun
109	5	50.0	172	14	Q9J6S9	Q9j6s9 human immun	182	5	50.0	205	14	Q9JUM2	Q9jum2 human immun
110	5	50.0	173	14	Q9J781	Q9j781 human immun	183	5	50.0	205	14	Q9JUM0	Q9jum0 human immun
111	5	50.0	175	14	Q9J6Z3	Q9j6z3 human immun	184	5	50.0	206	14	Q9J772	Q9j772 human immun
112	5	50.0	175	14	Q9J6W9	Q9j6w9 human immun	185	5	50.0	206	14	Q9J6W1	Q9j6w1 human immun
113	5	50.0	177	14	Q9J791	Q9j791 human immun	186	5	50.0	206	14	Q9J6V6	Q9j6v6 human immun
114	5	50.0	178	14	Q9J751	Q9j751 human immun	187	5	50.0	206	14	Q9JUK3	Q9juk3 human immun
115	5	50.0	178	14	Q9J750	Q9j750 human immun	188	5	50.0	207	14	Q9JMW6	Q9jmw6 human immun
116	5	50.0	179	14	Q9J747	Q9j747 human immun	189	5	50.0	207	14	Q9JMW4	Q9jmw4 human immun
117	5	50.0	179	10	Q9ZQD4	Q9zqd4 arabidopsis	190	5	50.0	207	14	Q9JMW3	Q9jmw3 human immun
118	5	50.0	179	14	Q9J786	Q9j786 human immun	191	5	50.0	207	14	Q9JMW2	Q9jmw2 human immun
119	5	50.0	179	14	Q9J6V2	Q9j6v2 human immun	192	5	50.0	207	14	Q9JMW1	Q9jmw1 human immun
120	5	50.0	180	14	Q9J737	Q9j737 human immun	193	5	50.0	207	14	Q9JMW9	Q9jmw9 human immun
121	5	50.0	181	14	Q9J7A3	Q9j7a3 human immun	194	5	50.0	207	14	Q9JMW8	Q9jmw8 human immun
122	5	50.0	181	14	Q9J793	Q9j793 human immun	195	5	50.0	207	14	Q9QNX4	Q9qnx4 human immun
123	5	50.0	181	14	Q9J780	Q9j780 human immun	196	5	50.0	207	14	Q9Q2L6	Q9q2l6 human immun
124	5	50.0	183	14	Q9J706	Q9j706 human immun	197	5	50.0	207	14	Q9Q2L5	Q9q2l5 human immun
125	5	50.0	184	14	Q9J6T7	Q9j6t7 human immun	198	5	50.0	207	14	Q9Q2K8	Q9q2k8 human immun
126	5	50.0	185	10	Q9MAI5	Q9mai5 arabidopsis	199	5	50.0	207	14	Q9Q2K5	Q9q2k5 human immun
127	5	50.0	186	14	Q9WKB9	Q9wkb9 human immun	200	5	50.0	207	14	Q9Q2K3	Q9q2k3 human immun
128	5	50.0	186	14	Q9J6Z5	Q9j6z5 human immun	201	5	50.0	207	14	Q9Q2K2	Q9q2k2 human immun
129	5	50.0	187	5	Q9N344	Q9n344 caenorhabdi	202	5	50.0	207	14	Q9Q2K0	Q9q2k0 human immun
130	5	50.0	187	14	Q9JUP3	Q9jup3 human immun	203	5	50.0	207	14	Q9Q2J9	Q9q2j9 human immun
131	5	50.0	190	1	Q9VIG6	Q9vig6 pyrococcus	204	5	50.0	207	14	Q9Q2J8	Q9q2j8 human immun
132	5	50.0	190	14	Q9J308	Q9j308 human immun	205	5	50.0	207	14	Q9Q2J7	Q9q2j7 human immun
133	5	50.0	190	14	Q9J6N5	Q9j6n5 human immun	206	5	50.0	207	14	Q9Q2J6	Q9q2j6 human immun
134	5	50.0	192	14	Q9J390	Q9j390 hepeatitis c	207	5	50.0	207	14	Q9Q2J5	Q9q2j5 human immun
135	5	50.0	192	14	Q9J733	Q9j733 human immun	208	5	50.0	207	14	Q9Q2J4	Q9q2j4 human immun
136	5	50.0	192	14	Q9J6N9	Q9j6n9 human immun	209	5	50.0	207	14	Q9Q2J3	Q9q2j3 human immun
137	5	50.0	193	14	Q9J7B3	Q9j7b3 human immun	210	5	50.0	207	14	Q9Q2J2	Q9q2j2 human immun
138	5	50.0	195	14	Q9J769	Q9j769 human immun	211	5	50.0	207	14	Q9Q2J1	Q9q2j1 human immun
139	5	50.0	195	14	Q9J731	Q9j731 human immun	212	5	50.0	207	14	Q9Q2I6	Q9q2i6 human immun
140	5	50.0	195	14	Q9J6U1	Q9j6u1 human immun	213	5	50.0	207	14	Q9Q2I5	Q9q2i5 human immun
141	5	50.0	195	14	Q9JUQ4	Q9juq4 human immun	214	5	50.0	207	14	Q9Q2I3	Q9q2i3 human immun
142	5	50.0	196	14	Q9J796	Q9j796 human immun	215	5	50.0	207	14	Q9Q2I2	Q9q2i2 human immun
143	5	50.0	197	14	Q9JUN4	Q9jun4 human immun	216	5	50.0	207	14	Q9JUS6	Q9jus6 human immun
144	5	50.0	198	14	Q9J787	Q9j787 human immun	217	5	50.0	207	14	Q9JUN2	Q9jun2 human immun
145	5	50.0	198	14	Q9JUL8	Q9jul8 human immun	218	5	50.0	207	14	Q9JUN1	Q9jun1 human immun
146	5	50.0	198	14	Q9JUL3	Q9jul3 human immun	219	5	50.0	207	14	Q9JVO9	Q9jvo9 human immun
147	5	50.0	199	14	Q9JUL2	Q9jul2 human immun	220	5	50.0	207	14	Q9JVO8	Q9jvo8 human immun
148	5	50.0	199	14	Q9J6Z7	Q9j6z7 human immun	221	5	50.0	207	14	Q9JVO5	Q9jvo5 human immun
149	5	50.0	199	14	Q9JUP4	Q9jup4 human immun	222	5	50.0	207	14	Q9JVO3	Q9jvo3 human immun
150	5	50.0	199	14	Q9JUM8	Q9jum8 human immun	223	5	50.0	207	14	Q9JVO1	Q9jvo1 human immun
151	5	50.0	200	14	Q9J6Q2	Q9j6q2 human immun	224	5	50.0	207	14	Q9JVO0	Q9jvo0 human immun
152	5	50.0	200	14	Q9JUP2	Q9jup2 human immun	225	5	50.0	207	14	Q9JUZ9	Q9juz9 human immun
153	5	50.0	201	14	Q9J744	Q9j744 human immun	226	5	50.0	207	14	Q9JUZ5	Q9juz5 human immun
154	5	50.0	201	14	Q9JIV7	Q9jiv7 human immun	227	5	50.0	207	14	Q9JUZ4	Q9juz4 human immun
155	5	50.0	201	14	Q9JUS1	Q9jus1 human immun	228	5	50.0	207	14	Q9JUZ1	Q9juz1 human immun
156	5	50.0	201	14	Q9JUL1	Q9jul1 human immun	229	5	50.0	207	14	Q9JUZ0	Q9juz0 human immun
157	5	50.0	202	14	Q9J7A2	Q9j7a2 human immun	230	5	50.0	207	14	Q9JUY9	Q9juy9 human immun
158	5	50.0	202	14	Q9JUT1	Q9jut1 human immun	231	5	50.0	207	14	Q9JUY3	Q9juy3 human immun
159	5	50.0	202	14	Q9JUMP	Q9jum6 human immun	232	5	50.0	207	14	Q9JUY2	Q9juy2 human immun
160	5	50.0	202	14	Q9JUM4	Q9jum4 human immun	233	5	50.0	207	14	Q9JUY1	Q9juy1 human immun
161	5	50.0	202	14	Q9JUL9	Q9jul9 human immun	234	5	50.0	207	14	Q9JUY0	Q9juy0 human immun
162	5	50.0	202	14	Q9JUL0	Q9jul0 human immun	235	5	50.0	207	14	Q9JUX9	Q9jux9 human immun
163	5	50.0	203	14	Q9J6T3	Q9j6t3 human immun	236	5	50.0	207	14	Q9JUX7	Q9jux7 human immun
164	5	50.0	203	14	Q9JUT5	Q9jut5 human immun	237	5	50.0	207	14	Q9JUX4	Q9jux4 human immun
165	5	50.0	203	14	Q9JUU0	Q9juu0 human immun	238	5	50.0	207	14	Q9JUX3	Q9jux3 human immun

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:42:49 ; Search time 58.01 Seconds
(without alignments)
22.807 Million cell updates/sec

Title: US-09-372-036-31
Perfect score: 10
Sequence: 1 PVAPEQEVKK 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_16: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_unclassified: *
13: sp_vertebrate: *
14: sp_virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	86	2	09RNU3	Q9RNU3 listeria mo
2	100.0	478	2	003493	Q03493 listeria mo
3	70.0	94	14	067673	Q67673 porcine ade
4	70.0	227	2	09PM45	Q9PM45 campylobact
5	60.0	102	2	09HYT7	Q9HYT7 pseudomonas
6	60.0	116	2	09XPT5	Q9XPT5 streptomyce
7	60.0	174	14	093041	Q93041 human immun
8	60.0	274	2	09KVZ4	Q9KVZ4 acinetobact
9	60.0	486	5	026617	Q26617 strongyloce
10	60.0	609	4	09UNU0	Q9UNU0 homo sapien
11	60.0	624	4	09NZM6	Q9NZM6 homo sapien
12	60.0	748	10	022907	Q22907 arabidopsis
13	60.0	819	5	09VY48	Q9VY48 drosophila
14	60.0	988	14	098830	Q98830 human foamy
15	60.0	988	14	087041	Q87041 simian foam
16	60.0	988	14	P90288	P90288 human spuma
17	60.0	1230	2	025772	Q25772 helicobacte
18	60.0	1653	2	09LBC3	Q9LBC3 streptococc
19	50.0	23	11	063334	Q63334 rattus norv

20	50.0	52	6	09GL38	Q9GL38 bos taurus
21	50.0	75	2	09RRH1	Q9RRH1 deinococcus
22	50.0	77	14	091692	Q91692 human immun
23	50.0	82	5	017728	Q17728 caenorhabdi
24	50.0	88	14	09DR28	Q9DR28 human immun
25	50.0	91	14	09WJT4	Q9WJT4 human immun
26	50.0	95	14	068302	Q68302 hepatitis c
27	50.0	102	14	068301	Q68301 hepatitis c
28	50.0	108	14	09IE25	Q9IE25 human immun
29	50.0	112	4	09UG25	Q9UG25 homo sapien
30	50.0	113	14	093051	Q93051 human immun
31	50.0	113	14	093052	Q93052 human immun
32	50.0	113	14	093053	Q93053 human immun
33	50.0	113	14	09WKA3	Q9WKA3 human immun
34	50.0	113	14	09WKA2	Q9WKA2 human immun
35	50.0	113	14	09WKA1	Q9WKA1 human immun
36	50.0	113	14	09WKA8	Q9WKA8 human immun
37	50.0	113	14	09WKA9	Q9WKA9 human immun
38	50.0	113	14	09WKA9	Q9WKA9 human immun
39	50.0	113	14	09WKA9	Q9WKA9 human immun
40	50.0	113	14	09WKA9	Q9WKA9 human immun
41	50.0	113	14	09WKA9	Q9WKA9 human immun
42	50.0	113	14	09WKA9	Q9WKA9 human immun
43	50.0	113	14	09WKA9	Q9WKA9 human immun
44	50.0	113	14	09WKA9	Q9WKA9 human immun
45	50.0	113	14	09WKA9	Q9WKA9 human immun
46	50.0	113	14	09WKA9	Q9WKA9 human immun
47	50.0	114	10	09SVK9	Q9SVK9 arabidopsis
48	50.0	121	5	09R3V1	Q9R3V1 caenorhabdi
49	50.0	122	5	09VY28	Q9VY28 drosophila
50	50.0	124	2	084412	Q84412 chlamydia t
51	50.0	124	2	09Z818	Q9Z818 chlamydia p
52	50.0	124	5	094045	Q94045 caenorhabdi
53	50.0	127	2	09X6R1	Q9X6R1 yersinia pe
54	50.0	130	14	0560B5	Q560B5 human immun
55	50.0	130	14	09Q145	Q9Q145 human immun
56	50.0	130	14	09Q142	Q9Q142 human immun
57	50.0	130	14	09Q141	Q9Q141 human immun
58	50.0	130	14	09Q140	Q9Q140 human immun
59	50.0	130	14	09Q135	Q9Q135 human immun
60	50.0	130	14	09Q135	Q9Q135 human immun
61	50.0	130	14	09Q135	Q9Q135 human immun
62	50.0	130	14	09Q135	Q9Q135 human immun
63	50.0	130	14	09Q135	Q9Q135 human immun
64	50.0	130	14	09Q135	Q9Q135 human immun
65	50.0	130	14	09Q135	Q9Q135 human immun
66	50.0	130	14	09Q135	Q9Q135 human immun
67	50.0	131	14	09Q135	Q9Q135 human immun
68	50.0	131	14	09Q135	Q9Q135 human immun
69	50.0	131	14	09Q135	Q9Q135 human immun
70	50.0	131	14	09Q135	Q9Q135 human immun
71	50.0	131	14	09Q135	Q9Q135 human immun
72	50.0	131	14	09Q135	Q9Q135 human immun
73	50.0	131	14	09Q135	Q9Q135 human immun
74	50.0	131	14	09Q135	Q9Q135 human immun
75	50.0	131	14	09Q135	Q9Q135 human immun
76	50.0	132	2	09K2C0	Q9K2C0 human immun
77	50.0	132	14	09Q123	Q9Q123 human immun
78	50.0	133	2	087645	Q87645 methylococc
79	50.0	133	3	09UTJ5	Q9UTJ5 schizosacch
80	50.0	133	14	09Q105	Q9Q105 human immun
81	50.0	133	14	09Q105	Q9Q105 human immun
82	50.0	134	2	09P1Y9	Q9P1Y9 chlamydia m
83	50.0	137	5	09W3U4	Q9W3U4 caenorhabdi
84	50.0	140	5	09R3B1	Q9R3B1 caenorhabdi
85	50.0	141	1	09VAL8	Q9VAL8 aeropyrum p
86	50.0	141	3	005690	Q05690 saccharomyc
87	50.0	142	14	09J6S4	Q9J6S4 human immun
88	50.0	147	2	09WYK3	Q9WYK3 thermotoga
89	50.0	147	5	076560	Q76560 caenorhabdi
90	50.0	148	10	09FPI3	Q9FPI3 arabidopsis
91	50.0	149	14	068732	Q68732 hepatitis c
92	50.0	152	14	09J756	Q9J756 human immun

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Wed Aug 15 13:35:24 2001

us-09-372-036-31.011.rpr

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Search completed: August 15, 2001, 12:34:46
Job time: 111 sec

A:Residues: 1-211 <WILD>
A:Cross-references: EMBL:283226; PIDN:CAB05723.1; GSPDB:GN00023; CESP:F43D2.3
A:Experimental source: clone F43D2
C:Genetics:
A:Gene: CESP:F43D2.3
A:Map position: 5
A:Introns: 44/3; 126/3; 166/3

Query Match 50.0%; Score 5; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
DB 146 PVAPT 150

RESULT 47
S10212
late 33k protein - human adenovirus 41
N:Alternate names: 33k phosphoprotein
C:Species: Mastadenovirus h41 (human adenovirus 41)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
C:Accession: S10212; S04851
R:Slamende, S.B.; Plenzak, N.J.; Velarde Jr., J.; Plenzak, D.; Luftig, R.B.
Nucleic Acids Res. 18, 3069, 1990
A:Title: Nucleotide sequence of the region coding for 100k and 33k proteins of human ent
A:Reference number: S10206; MID:90272433
A:Accession: S10212
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-217 <SLE>
A:Cross-references: EMBL:X52532
R:Plenzak, N.; Velarde Jr., J.; Plenzak, D.; Luftig, R.B.
Nucleic Acids Res. 17, 5398, 1989
A:Title: Nucleotide sequence of human enteric adenovirus type 41 hexon-associated protei
A:Reference number: S04851; MID:89345113
A:Accession: S04851
A:Molecule type: DNA
A:Residues: 203-217 <PIE>
A:Cross-references: EMBL:X15137; NID:958481; PIDN:CAA33236.1; PID:9832970
C:Genetics:
A:Introns: 120/1
A:Superfamily: adenovirus late 33k protein
C:Keywords: late protein; phosphoprotein

Query Match 50.0%; Score 5; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
DB 118 PVAPT 122

RESULT 48
T37859
probable transcription factor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37859
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21750
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <DEV>
A:Cross-references: EMBL:Z69795; PIDN:CAA93690.1; GSPDB:GN00066; SPDB:SPAC1768.07
A:Experimental source: strain 972n-; cosmid c1768
C:Genetics:

A:Gene: SPDB:SPAC1768.07
A:Map position: 1

Query Match 50.0%; Score 5; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVK 10
DB 191 QEVK 195

RESULT 49
C86847
transcription regulator Tena [imported] - Lactococcus lactis subsp. lactis (strain IL
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86847
R:Polotin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: C86847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <STO>
A:Cross-references: GB:AE005176; NID:912724803; PIDN:AAK05877.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: tena
C:Superfamily: transcription activator tena

Query Match 50.0%; Score 5; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
DB 104 PVAPT 108

RESULT 50
H86860
protein serine/threonine phosphatase [imported] - Lactococcus lactis subsp. lactis (s
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C:Accession: H86860
R:Polotin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: H86860
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <STO>
A:Cross-references: GB:AE005176; NID:912724922; PIDN:AAK05986.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: pppL
C:Superfamily: conserved hypothetical protein ylo0; conserved hypothetical protein y1

Query Match 50.0%; Score 5; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PROEV 8
DB 216 PROEV 220

ribosomal protein L29 - Mycoplasma genitalium
 C:Species: Mycoplasma genitalium
 C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999
 C:Accession: F64217
 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
 , C.A.; Venter, J.C.
 Science 270, 397-403, 1995
 A:Title: The minimal gene complement of Mycoplasma genitalium.
 A:Reference number: A64200; MUID:96026346
 A:Accession: F64217
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-200 <TIGR>
 A:Cross-references: GB:U39695; GB:L43967; NID:g1045833; PID:g1045843; TIGR:MG159
 A:Experimental source: strain G-37
 A:Genetics:
 A:Genetic code: SGC3

Query Match 50.0%; Score 5; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OEVRK 10
 |||||
 DB 170 QEVKK 174

RESULT 43
 IMPSB
 Immunity protein - phage SP-beta
 C:Species: phage SP-beta
 A:Note: host Bacillus subtilis
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Oct-1997
 C:Accession: A24499
 R:McLaughlin, J.R.; Wong, H.C.; Ting, Y.E.; Van Arsdell, J.N.; Chang, S.
 J. Bacteriol. 167, 952-959, 1986
 A:Title: Control of lysogeny and immunity of Bacillus subtilis temperate bacteriophage S
 A:Reference number: A24499; MUID:86304188
 A:Accession: A24499
 A:Molecule type: DNA
 A:Residues: 1-201 <MCL>
 A:Cross-references: GB:M13821
 C:Genetics:
 A:Gene: d
 C:Superfamily: phage SP-beta immunity protein
 C:Keywords: Immunity protein

Query Match 50.0%; Score 5; DB 1; Length 201;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQEV 8
 |||||
 DB 156 PQEV 160

RESULT 44
 A71326
 Probable V-type ATPase, subunit D (atpD-1) - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C:Accession: A71326
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MDC
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71326; MUID:98332770
 A:Accession: A71326
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-206 <COI>
 A:Cross-references: GB:AE001220; GB:AE000520; NID:g33322705; PIDN:AC65414.1; PID:g3332
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0428
 C:Superfamily: H+-transporting ATPase chain D

Query Match 50.0%; Score 5; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OEVRK 10
 |||||
 DB 80 QEVKK 84

RESULT 45
 S04827
 gene 40A protein - phage phi-80
 N:Contains: gene 40A protein; gene 40B protein
 C:Species: phage phi-80
 C:Date: 19-May-1994 #sequence_revision 24-May-1996 #text_change 04-Mar-2000
 C:Accession: S04827; S04826
 R:Ogawa, T.; Ogawa, H.; Tomizawa, J.I.
 J. Mol. Biol. 202, 537-550, 1988
 A:Title: Organization of the early region of bacteriophage phi-80. Genes and proteins
 A:Reference number: S01776; MUID:89011978
 A:Accession: S04827
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-209 <OGA>
 A:Cross-references: EMBL:X13065; NID:g14800; PIDN:CAA31470.1; PID:g14803
 A:Genetics: G40A
 A:Accession: S04826
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 115-209 <OG2>
 A:Cross-references: EMBL:X13065; NID:g14800; PIDN:CAA31469.1; PID:g14802
 A:Genetics: G40B
 A:Note: the authors show Met-115 as alternative initiator
 C:Genetics: <G40A>
 A:Gene: 40A
 C:Genetics: <G40B>
 A:Gene: 40B
 C:Superfamily: phage phi-80 gene 40A protein
 C:Keywords: alternative initiators
 F:1-209/Product: gene 40A protein #status predicted <MAT1>
 F:115-209/Product: gene 40B protein #status predicted <MAT2>

Query Match 50.0%; Score 5; DB 2; Length 209;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEVK 9
 |||||
 DB 59 TOEVK 63

RESULT 46
 T22122
 hypothetical protein F43D2.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T22122
 R:Mortimore, B.
 submitted to the EMBL Data Library, December 1996
 A:Reference number: T22122
 A:Accession: T22122
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Gene: F12M16.6
A:Map position: 1

Query Match 50.0%; Score 5; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
|||||
DB 12 PVAPT 16

RESULT 38
JC4806
core protein G - phage phi-K
C:Species: phage phi-K
C>Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 20-Jun-2000
C:Accession: JC4806; B04253; A04253
R:Kodaira, K.; Okai, M.; Kakikawa, M.; Kimoto, H.; Taketo, A.
J. Biochem. 119, 1062-1069, 1996
A:Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant ph
A:Reference number: JC4804; MUID:96424987
A:Accession: JC4806
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-187 <KOD>
R:Sim: J.; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628, 1979
A:Title: dnaG (primase)-dependent origins of DNA replication. Nucleotide sequences of th
A:Reference number: A92247; MUID:80049950
A:Accession: B04253
A:Molecule type: DNA
A:Residues: 165-187 <SIM>
C:Comment: This protein is one of the structural components of the bacteriophage capsid.
C:Genetics:
A:Gene: G
C:Superfamily: phage phi-X174 gene G protein
C:Keywords: capsid protein

Query Match 50.0%; Score 5; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
|||||
DB 26 PVAPT 30

RESULT 39
H75162
anthranilate synthase component II (trpG) PAB2046 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: H75162
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: H75162
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <RAW>
A:Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49383.1; PID:9545785
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2046
C:Superfamily: glutamine amidotransferase; trpG homology
F:2-186/Domain: trpG homology <TRG>

Query Match 50.0%; Score 5; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
|||||
DB 35 QEVKK 39

RESULT 40
A41050
repressor protein c - phage Mu
C:Species: phage Mu
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 14-Jul-1994
C:Accession: A41050; A41049
R:Genkens, V.; Vogel, J.L.; Grimaud, R.; Desmet, L.; Higgins, N.P.; Toussaint, A.
J. Bacteriol. 173, 6578-6585, 1991
A:Title: Frameshift mutations in the bacteriophage Mu repressor gene can confer a tra
A:Reference number: A41050; MUID:92011434
A:Accession: A41050
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-196 <GEU>
R:Vogel, J.L.; Li, Z.J.; Howe, M.M.; Toussaint, A.; Higgins, N.P.
J. Bacteriol. 173, 6568-6577, 1991
A:Title: Temperature-sensitive mutations in the bacteriophage Mu c repressor locate a
A:Reference number: A41049; MUID:92011433
A:Accession: A41049
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-196 <VOG>

Query Match 50.0%; Score 5; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
|||||
DB 190 QEVKK 194

RESULT 41
F86832
hypothetical protein yrbB [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: F86832
R:Boioclin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. In press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86525
A:Accession: F86832
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <STO>
A:Cross-references: GB:AE005176; NID:912724674; PIDN:AAK05760.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yrbB

Query Match 50.0%; Score 5; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPRQ 6
|||||
DB 96 VAPRQ 100

RESULT 42
F64217

A:Reference number: A86625
A:Accession: D86699
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <STO>
A:Cross-References: GB:AE005176; NID:g12723488; PIDN:AAK04694.1; GSPDB:GN00146
A:Experimental source: strain IIL403
C:Genetics:
A:Gene: yfII

Query Match 50.0%; Score 5; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
|||||
DB 94 QEVKK 98

RESULT 34

hypothetical protein Atg37200 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: G84789
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;
Eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84789
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <STO>
A:Cross-References: GB:AE002093; NID:g4371281; PIDN:AAD18139.1; GSPDB:GN00139
C:Genetics:
A:Gene: Atg37200
A:Map position: 2

Query Match 50.0%; Score 5; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
|||||
DB 15 PVAPT 19

RESULT 35

elongation factor P [imported] - Chlamydomonas reinhardtii (strain J138)
C:Species: Chlamydomonas reinhardtii (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: H86513
R:Shital, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydomonas reinhardtii J138.
A:Reference number: A86491; MUID:20330349
A:Accession: H86513
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <STO>
A:Cross-References: GB:BA000008; NID:g8978557; PIDN:BA038394.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: efp_1
C:Superfamily: translation elongation factor EF-P

Query Match 50.0%; Score 5; DB 2; Length 185;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
|||||
DB 57 TOEVK 61

RESULT 36

translation elongation factor P CP0584 [imported] - Chlamydomonas reinhardtii (strain J138)
C:Species: Chlamydomonas reinhardtii (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: G72110; E81560
R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydomonas reinhardtii and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: G72110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <ARN>
A:Cross-References: GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD18337.1; PID:g437
A:Experimental source: strain CWD029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydomonas trachomatis Mopn and Chlamydomonas reinhardtii AR39
A:Reference number: A81500; MUID:20150255
A:Accession: E81560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <REA>
A:Cross-References: GB:AE002217; GB:AE002161; NID:g7189493; PIDN:AAF38402.1; PID:g718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: efp_1; CP0584
C:Superfamily: translation elongation factor EF-P

Query Match 50.0%; Score 5; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVK 9
|||||
DB 57 TOEVK 61

RESULT 37

protein P12M16.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96572
R:Theodoridis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D96572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <STO>
A:Cross-References: GB:AE005173; NID:g7769876; PIDN:AAF9554.1; GSPDB:GN00141
C:Genetics:

Db 39 OEYKK 43

RESULT 24

T50083

probable cytidine deaminase [imported] - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000

C:Accession: T50083

R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, November 1999

A:Reference number: 225035

A:Accession: T50083

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Cross-references: EMBL:AL132984; PIDN:CAH61215.1; GSPDB:GN00066; SPDB:SPAC1556.04C

A:Experimental source: strain 972h(-); cosmid c1556

C:Genetics:

A:Gene: SPDB:SPAC1556.04C

A:Map position: 1

A:Introns: 47/1; 67/3; 95/2; 121/3

C:Superfamily: cytidine deaminase

Query Match

Best Local Similarity 50.0%; Score 5; DB 2; Length 133;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYKK 10
Db 11 OEYKK 15

RESULT 25

AB1676

conserved hypothetical protein TC0687 [imported] - *Chlamydia muridarum* (strain N199)

C:Species: *Chlamydia muridarum*, *Chlamydia trachomatis* MOPn

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000

C:Accession: AB1676

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of *Chlamydia trachomatis* MOPn and *Chlamydia pneumoniae* AR39.

A:Reference number: AB1500; MUID:20150255

A:Accession: AB1676

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-134 <TER>

A:Cross-references: GB:AE002337; GB:AE002160; NID:g7190714; PIDN:AAF39504.1; PID:g719071

A:Experimental source: strain N199 (MOPn)

C:Genetics:

A:Gene: TC0687

C:Superfamily: *Escherichia coli* dosage-dependent dnaK suppressor protein dksA

Query Match

Best Local Similarity 50.0%; Score 5; DB 2; Length 134;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYKK 10
Db 41 OEYKK 45

RESULT 26

E72580

hypothetical protein APE1924 - *Aeropyrum pernix* (strain K1)

C:Species: *Aeropyrum pernix*

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: E72580

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hukawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aero*

A:Reference number: A72450; MUID:99310339

A:Accession: E72580

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-141 <KAW>

A:Cross-references: DBJ:AP000062; NID:g5105244; PIDN:BAH80930.1; PID:d1044716; PID:g

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1924

Query Match

Best Local Similarity 50.0%; Score 5; DB 2; Length 141;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPTO 6
Db 66 VAPTO 70

RESULT 27

G72384

conserved hypothetical protein - *Thermotoga maritima* (strain MSB8)

C:Species: *Thermotoga maritima*

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: G72384

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316

A:Accession: G72384

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-147 <ARN>

A:Cross-references: GB:AE001717; GB:AE000512; NID:g4980871; PIDN:AAJ35456.1; PID:g498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0369

Query Match

Best Local Similarity 50.0%; Score 5; DB 2; Length 147;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYKK 10
Db 127 OEYKK 131

RESULT 28

T33327

hypothetical protein C40D2.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T33327

R:Madson, C.; Wamsley, P.; O'Brien, D.

submitted to the EMBL Data Library, July 1998

A:Description: The sequence of *Caenorhabditis elegans* cosmid C40D2.

A:Reference number: Z21323

A:Accession: T33327

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-147 <MAD>

A:Cross-references: EMBL:AF077530; PIDN:AAJ26267.1; GSPDB:GN00020; CESP:C40D2.4

A:Experimental source: strain Bristol NZ; clone C40D2

C:Genetics:

A:Gene: CESP:C40D2.4

A:Map position: 2

A71518
probable dnaK suppressor - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jun-2000
C:Accession: A71518
R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, S.
Science 282, 754-759, 1998
A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809
A:Accession: A71518
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <ARN>
A:Cross-references: GB:AE001314; GB:AE001273; NID:g3328833; PIDN:AAC68004.1; PID:g3328833
C:Genetics:
A:Gene: dksA
C:Superfamily: Escherichia coli dosage-dependent dnaK suppressor protein dksA

Query Match 50.0%; Score 5; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QEVKK 10
|||||
Db 31 QEVKK 35

RESULT 20
G72066
dnaK suppressor - Chlamydia pneumoniae (strain CML029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jun-2000
C:Accession: G72066
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: G72066
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <ARN>
A:Cross-references: GB:AE001638; GB:AE001363; NID:g4376819; PIDN:AAD18674.1; PID:g437682
A:Experimental source: strain CML029
C:Genetics:
A:Gene: dksA
C:Superfamily: Escherichia coli dosage-dependent dnaK suppressor protein dksA

Query Match 50.0%; Score 5; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QEVKK 10
|||||
Db 31 QEVKK 35

RESULT 21
T24876
hypothetical protein T13F2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T24876
R:Swindburne, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24876
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-124 <WTL>
A:Cross-references: EMBL:Z81122; PIDN:CAB03353.1; GSPDB:GN00022; CESP:T13F2.2

A:Experimental source: clone T13F2
C:Genetics:
A:Gene: CESP:T13F2.2
A:Map position: 4
A:Introns: 27/3; 61/3; 91/3
C:Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match 50.0%; Score 5; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QEVKK 10
|||||
Db 39 QEVKK 43

RESULT 22
D86684
prophage p11 protein 41, tail component [imported] - Lactococcus lactis subsp. lactis
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: D86684
R:Boletín, A.; Winkler, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A>Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: D86684
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-131 <STO>
A:Cross-references: GB:AE005176; NID:g12723355; PIDN:AAK04574.1; GSPDB:GN00146
A:Experimental source: strain IL4403
C:Genetics:
A:Gene: p1141

Query Match 50.0%; Score 5; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PTOEV 8
|||||
Db 3 PTOEV 7

RESULT 23
B81600
conserved hypothetical protein CP0218 [imported] - Chlamydia pneumoniae (strain A
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C:Accession: B81600
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MOPn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255
A:Accession: B81600
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <REA>
A:Cross-references: GB:AE002183; GB:AE002161; NID:g7189146; PIDN:AAF38087.1; PID:g718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0218
C:Superfamily: Escherichia coli dosage-dependent dnaK suppressor protein dksA

Query Match 50.0%; Score 5; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QEVKK 10

A:Reference number: A93891; MUID:82060334
 A:Accession: A93891
 A:Molecule type: mRNA
 A:Residues: 1-103 <HEI>
 R:Chen, K.C.S.; Kindt, T.J.; Krause, R.M.
 J. Biol. Chem. 250, 3289-3296, 1975
 A:Title: Primary structure of the L chain from a rabbit homogeneous antibody to streptococcal antigen A92176; MUID:75133568
 A:Accession: A92176
 A:Molecule type: protein
 A:Residues: 1-57, D, 59-103 <CHE>
 A:Note: This chain was obtained from antibody to the specific carbohydrate of group C streptococcus. An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 16 C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
 C:Keywords: heterotrimer
 F:19-87/Domain: Immunoglobulin homology <IMM>

Query Match 50.0%; Score 5; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
 |||||
 DB 2 PVAPT 6

RESULT 15
 F53275
 Ig kappa-1 chain C region b95 allotype - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: F53275
 R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
 Immunogenetics 34, 201-207, 1991
 A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
 A:Reference number: A53275; MUID:91372868
 A:Accession: F53275
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-104 <AYA>
 A:Note: sequence inconsistent with nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBI:P:56170)
 C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:19-87/Domain: Immunoglobulin homology <IMM>

Query Match 50.0%; Score 5; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
 |||||
 DB 2 PVAPT 6

RESULT 16
 T14788
 hypothetical protein DKFZP564A122.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14788
 R:Dueterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, August 1999
 A:Reference number: Z18178
 A:Accession: T14788
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-112 <DUE>
 A:Cross-references: EMBL:AL110269
 A:Experimental source: fetal brain; clone DKFZP564A122

C:Genetics:
 A:Note: DKFZP564A122.1

Query Match 50.0%; Score 5; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PROEV 8
 |||||
 DB 91 PROEV 95

RESULT 17
 T08411
 hypothetical protein F18B3.180 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
 C:Accession: T08411
 R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16409
 A:Accession: T08411
 A:Molecule type: DNA
 A:Residues: 1-114 <QUE>
 A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.180
 A:Experimental source: cultivar Columbia; BAC clone F18B3
 C:Genetics:
 A:Gene: ATSP:F18B3.180
 A:Map position: 3
 C:Superfamily: Arabidopsis hypothetical protein F18B3.180

Query Match 50.0%; Score 5; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
 |||||
 DB 43 QEVKK 47

RESULT 18
 B86557
 Dnak suppressor [imported] - Chlamydia pneumoniae (strain J138)
 C:Species: Chlamydia pneumoniae; Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: B86557
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shida, T.;
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349
 A:Accession: B86557
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-124 <STO>
 A:Cross-references: GB:BA000008; NID:98978905; PIDN:BA98740.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: dksA
 C:Superfamily: Escherichia coli dosage-dependent dnk suppressor protein dksA

Query Match 50.0%; Score 5; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
 |||||
 DB 31 QEVKK 35

RESULT 19

Query Match 60.0%; Score 6; DB 2; Length 1133;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYKK 10
|||||
DB 1099 TOEYKK 1104

RESULT 10

E64664
Outer membrane protein - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: E64664

R:Tomb, J.F.; White, O.; Kariavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatkhat, H.G.; Glodex, A.; McNamee

son, J.D.; Kelley, J.M.; Cotton, M.D.; Welden, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467

A:Accession: E64664

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1230 <TOM>

A:Cross-references: GB:AE000621; GB:AE000511; NID:g2314301; PIDN:AAD08205.1; PID:g231431

Query Match 60.0%; Score 6; DB 2; Length 1230;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEYKK 10
|||||
DB 173 TOEYKK 178

RESULT 11

E75264

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: E75264

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: E75264

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-75 <WHI>

A:Cross-references: GB:AE002081; GB:AE000513; NID:g6460337; PIDN:AAF12064.1; PID:g646034

A:Experimental source: strain R1

A:Genetics:

A:Gene: DR2520

A:Map position: 1

Query Match 50.0%; Score 5; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPRO 6
|||||
DB 24 VAPRO 28

RESULT 12

T29802

hypothetical protein C06E4.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29802

R:Du, Z.; Gattung, S.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C06E4.

A:Reference number: 220688

A:Accession: T29802

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-82 <DUZ>

A:Cross-references: EMBL:U41277; PIDN:AAA82477.1; CESP:C06E4.2

C:Genetics:

A:Gene: CESP:C06E4.2

A:introns: 31/1

Query Match 50.0%; Score 5; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPRO 6
|||||
DB 40 VAPRO 44

RESULT 13

B56581

major basic nuclear protein, variant HCC2 - dinoflagellate (Cryptocodinium cohnii) (

N:Alternate names: protein alpha chain p14

C:Species: Cryptocodinium cohnii

C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000

C:Accession: B56581; S14640; S14644

R:Salas-Rovira, M.; Gerard, M.L.; Caput, D.; Jacques, F.; Soyer-Gobillard, M.O.; Verne

Chromosoma 100, 510-518, 1991

A:Title: Molecular cloning and immunolocalization of two variants of the major basic

A:Reference number: A56581; MUID:92111321

A:Accession: B56581

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-102 <SAL>

A:Cross-references: EMBL:X58444; NID:g17962; PIDN:CAA41350.1; PID:g17963

A:Note: sequence extracted from NCBI backbone (NCBIN:77122, NCBI:77123)

C:Keywords: DNA binding; nucleus

Query Match 50.0%; Score 5; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OEYKK 10
|||||
DB 43 OEYKK 47

RESULT 14

KARB

Ig kappa-b4 chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Jan-1981 #sequence_revision 15-Oct-1982 #text_change 16-Aug-1996

C:Accession: A93971; A93891; A92176; A02122

R:Emorine, L.; Dreher, K.; Kindt, T.J.; Max, E.E.

Proc. Natl. Acad. Sci. U.S.A. 80, 5709-5713, 1983

A:Title: Rabbit immunoglobulin kappa genes: structure of a germline b4 allotype J-C 1

A:Reference number: A93971; MUID:83300036

A:Accession: A93971

A:Molecule type: DNA

A:Note: the sequence was determined from the germline gene

R:Heidmann, O.; Aufray, C.; Cazenave, P.A.; Rougeon, F.

Proc. Natl. Acad. Sci. U.S.A. 78, 5802-5806, 1981

A:Title: Nucleotide sequence of constant and 3' untranslated regions of a kappa immun

|||||
Db 29 TQEVKK 34

RESULT 5
H85574
hypothetical protein 20891 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: H85574
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: H85574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-456 <STO>
A:Cross-references: GB:AE005174; NID:g12513654; PIDN:AG55060.1; GSPDB:GN00145; UWGP:Z08
A:Experimental source: strain O157:H7, substrain EDL933
A:Gene: 20891

Query Match
Best Local Similarity 100.0%; Score 6; DB 2; Length 456;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAPTQE 7
|||||
Db 378 VAPTQE 383

RESULT 6
S42719
actin-binding protein ABP1 - Saccharomyces exiguus
C:Species: Saccharomyces exiguus
C:Date: 07-Sep-1994 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S42719
R:Langue, U.; Stehner, S.; Grolj, F.; Wagner, G.; Philippson, P.
Biochem. Biophys. Acta 1217, 214-218, 1994
A:Title: Cloning and sequencing of a gene coding for an actin binding protein of Sacchar
A:Reference number: S42719; MUID:94154001
A:Accession: S42719
A:Molecule type: DNA
A:Residues: 1-617 <LAN>
A:Cross-references: EMBL:X73977; NID:g433513; PIDN:CAA52156.1; PID:g433514
C:Superfamily: actin-binding protein ABP1; SH3 homology
C:Keywords: actin binding; cytoskeleton
F:564-613/Domain: SH3 homology <SH3>

Query Match
Best Local Similarity 100.0%; Score 6; DB 2; Length 617;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQEVKK 10
|||||
Db 412 TQEVKK 417

RESULT 7
H84913
Probable ATP-dependent RNA helicase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84913
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Kofiec, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487
A:Accession: H84913
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-748 <STO>
A:Cross-references: GB:AE002093; NID:g2275211; PIDN:AB63833.1; GSPDB:GN00139
C:Gene: At2g47330
A:Map position: 2

Query Match
Best Local Similarity 100.0%; Score 6; DB 2; Length 748;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPTRQ 6
|||||
Db 725 PVAPTRQ 730

RESULT 8
VCLJSP
env polyprotein - human foamy virus
N:Alternate names: coat polyprotein
C:Species: human foamy virus
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: C29685
R:Fliegel, R.M.; Reithwilm, A.; Maurer, B.; Darai, G.
EMBO J. 6, 2077-2084, 1987
A:Title: Nucleotide sequence analysis of the env gene and its flanking regions of the
A:Reference number: A91074; MUID:88004420
A:Accession: C29685
A:Molecule type: genomic RNA
A:Residues: 1-985 <FLU>
A:Cross-references: GB:X05591; GB:Y00070; NID:g61759; PIDN:CAA29086.1; PID:g61762
A:Gene: env
A:Superfamily: foamy virus env polyprotein
C:Keywords: coat protein; polyprotein; transmembrane protein
F:64-87/Domain: transmembrane #status predicted <TN1>
F:579-595/Domain: transmembrane #status predicted <TN2>
F:936-972/Domain: transmembrane #status predicted <TN3>

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 985;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQEVKK 10
|||||
Db 181 TQEVKK 186

RESULT 9
T30302
P-type ATPase - Tetrahymena thermophila
C:Species: Tetrahymena thermophila
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 07-Dec-1999
C:Accession: T30302
R:Wang, S.; Takeyasu, K.
submitted to the EMBL Data Library, November 1995
A:Description: The starvation-induced P-type ATPase in Tetrahymena thermophila.
A:Reference number: Z20815
A:Accession: T30302
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1133 <MAN>
A:Cross-references: EMBL:U41063; NID:g1545827; PID:g1545828; PIDN:AB08071.1
C:Gene: SGC5
A:Note: TPAP

979 4 40.0 163 2 B72225 conserved hypothe
980 4 40.0 164 2 H71850 flavodoxin - helic
981 4 40.0 164 2 A64655 flavodoxin - helic
982 4 40.0 164 2 G02777 durr pyrophosphata
983 4 40.0 164 2 A26490 histone H1, macron
984 4 40.0 164 2 S21830 apolipoprotein A-I
985 4 40.0 164 2 S15641 pillin (variant NGF
986 4 40.0 164 2 T38684 mitochondrial inne
987 4 40.0 164 2 B70922 hypotheical prote
988 4 40.0 164 2 S4459 ZK353.3 protein -
989 4 40.0 164 2 S18038 homeotic protein S
990 4 40.0 164 2 H70431 hypotheical prote
991 4 40.0 165 1 A35702 destrin - chicken
992 4 40.0 165 2 A27195 histone H1 - Tetra
993 4 40.0 165 2 S75414 probable ribosomal
994 4 40.0 165 2 S61230 cytochrome-c biosy
995 4 40.0 165 2 T39187 probable arylalkyl
996 4 40.0 165 2 T47011 hypotheical prote
997 4 40.0 166 1 S12632 cofillin - human
998 4 40.0 166 1 A29240 cofillin - pig
999 4 40.0 166 1 S12584 cofillin - mouse
1000 4 40.0 166 2 B70369 cytochrome c552 -

ALIGNMENTS

RESULT 1
A41487
protein p60 precursor - Listeria monocytogenes
N:Alternate names: invasion-associated protein
C:Species: Listeria monocytogenes
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1996
C:Accession: A41487; B41487
R:Kochler, S.; Leimaster-Waechter, M.; Chakraborty, T.; Lottspeich, F.; Goebel, W.
Infect. Immun. 58, 1943-1950, 1990
A:Title: The gene coding for protein p60 of Listeria monocytogenes and its use as a spec
A:Reference number: A41487; MUID:90256283
A:Accession: A41487
A:Molecule type: DNA
A:Residues: 1484 <KOE>
A:Cross-references: GB:X52268
A:Accession: B41487
A:Molecule type: protein
A:Residues: 28-49 <KO2>
C:Genetics:
A:Gene: lpp
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-484/Product: protein 60 #status predicted <MAT>

Query Match 100.0%; Score 10; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
Db 148 PVAPTOEVKK 157

RESULT 2
D81259
probable long transport protein Cj1630 [imported] - Campylobacter jejuni (strain NCRC 11
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: D81259
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kealey, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyllet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h
A:Reference number: A81250; MUID:20150912
A:Accession: D81259
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-227 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:96968971; PIDN:CAB72618.1; PID:9696
A:Experimental source: serotype O2, strain NCRC 11168
C:Genetics:
A:Gene: tonB2; Cj1630

Query Match 70.0%; Score 7; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 APTOEVK 9
Db 105 APTOEVK 111

RESULT 3
F83231
hypotheical protein PA3307 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83231
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: F83231
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <SNO>
A:Cross-references: GB:AE004753; GB:AE004091; NID:99949433; PIDN:ANG06695.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3307

Query Match 60.0%; Score 6; DB 2; Length 102;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTO 6
Db 27 PVAPTO 32

RESULT 4
T37186
probable regulatory protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T37186
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T37186
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-116 <SEE>
A:Cross-references: EMBL:AL096823; PIDN:CAB46971.1; GSPDB:GN000070; SCOEDB:SCQ11.16
C:Genetics:
A:Gene: SCOEDB:SCQ11.16
C:Superfamily: Streptomyces ambifaciens replication activator protein pra

Query Match 60.0%; Score 6; DB 2; Length 116;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TOEVKK 10

833	4	40.0	142	2	E71079	hypothetical prote	906	4	40.0	153	2	S59125	histone H2B [valid
834	4	40.0	142	2	T51479	hypothetical prote	907	4	40.0	153	2	T07624	heat shock protein
835	4	40.0	143	2	G84471	En/Spm-like transp	908	4	40.0	153	2	B47748	trans-regulatory s
836	4	40.0	143	2	T03321	hypothetical prote	909	4	40.0	153	2	S29277	hypothetical prote
837	4	40.0	143	2	T08789	hypothetical prote	910	4	40.0	153	2	E71229	probable purine ph
838	4	40.0	144	1	A61632	granulocyte-macrop	911	4	40.0	153	2	A75197	purine phosphoribo
839	4	40.0	144	1	SMXD12	hexon-associated p	912	4	40.0	153	2	JC5854	polyketide synthas
840	4	40.0	144	2	JH0469	granulocyte-macrop	913	4	40.0	154	2	S12629	heat shock cognate
841	4	40.0	144	2	PH1563	Ig heavy chain v r	914	4	40.0	154	2	T07625	heat shock protein
842	4	40.0	144	2	E41287	Ig heavy chain pre	915	4	40.0	154	2	T07629	small heat shock p
843	4	40.0	144	2	A36335	ribosomal protein	916	4	40.0	154	2	B69105	hypothetical prote
844	4	40.0	144	2	E75128	glycine cleavage s	917	4	40.0	154	2	A72029	hypothetical prote
845	4	40.0	144	2	S66570	biotin carboxyl c	918	4	40.0	154	2	H86594	conserved hypoteth
846	4	40.0	144	2	B70404	transcription regu	919	4	40.0	154	2	A85551	CT556 hypothetical
847	4	40.0	144	2	H70971	hypothetical prote	920	4	40.0	154	2	T17580	hypothetical prote
848	4	40.0	144	2	C75376	hypothetical prote	921	4	40.0	154	2	C82207	hypothetical prote
849	4	40.0	144	2	UC2102	lectin-related pro	922	4	40.0	154	2	PC4031	hypothetical 154 p
850	4	40.0	144	2	T46334	hypothetical prote	923	4	40.0	154	2	S55017	hypothetical prote
851	4	40.0	144	2	B75284	Mutr/ndix family	924	4	40.0	154	2	F72741	hypothetical prote
852	4	40.0	145	2	A83843	peptidyl-prolyl ci	925	4	40.0	155	1	SNR82	pathogenesis-relat
853	4	40.0	145	2	H69082	ribosomal protein	926	4	40.0	155	1	S59956	DNA-directed RNA p
854	4	40.0	145	2	F69214	heat shock protein	927	4	40.0	155	2	S21659	ribonuclease H (EC
855	4	40.0	145	2	S04042	embryonic abundant	928	4	40.0	155	2	T06449	probable heat shoc
856	4	40.0	145	2	C70328	conserved hypoteth	929	4	40.0	155	2	T11670	pathogenesis relat
857	4	40.0	145	2	S63134	probable membrane	930	4	40.0	155	2	E64105	acetyl-CoA carboxy
858	4	40.0	146	2	S60700	gag protein - huma	931	4	40.0	155	2	H75302	conserved hypoteth
859	4	40.0	146	2	S60697	gag protein - huma	932	4	40.0	155	2	A82884	conserved hypoteth
860	4	40.0	146	2	S60699	gag protein - huma	933	4	40.0	156	1	SNR81	pathogenesis-relat
861	4	40.0	146	2	S60708	gag protein - huma	934	4	40.0	156	1	C64390	probable transcrip
862	4	40.0	146	2	G75544	hypothetical prote	935	4	40.0	156	2	S71566	heat shock protein
863	4	40.0	146	2	T49867	hypothetical prote	936	4	40.0	156	2	D81343	probable integral
864	4	40.0	146	2	B71430	hypothetical prote	937	4	40.0	157	2	D70541	hypothetical prote
865	4	40.0	147	2	PH1561	Ig heavy chain v r	938	4	40.0	157	2	S04939	heat shock 22k pro
866	4	40.0	147	2	A58345	myoglobin - tremet	939	4	40.0	157	2	S31634	hypothetical prote
867	4	40.0	147	2	C47056	ctr regulatory pro	940	4	40.0	157	2	F71406	hypothetical prote
868	4	40.0	147	2	T49624	hypothetical prote	941	4	40.0	158	2	S16247	heat shock protein
869	4	40.0	147	2	D32804	chorismate mutase	942	4	40.0	158	2	S20518	hypothetical prote
870	4	40.0	147	2	S70833	methylated-DNA--pr	943	4	40.0	158	2	S20517	hypothetical prote
871	4	40.0	147	2	A42366	flagellar basal bo	944	4	40.0	158	2	B75141	hypothetical prote
872	4	40.0	147	2	T02273	hypothetical prote	945	4	40.0	158	2	D75069	hypothetical prote
873	4	40.0	147	2	T26223	hypothetical prote	946	4	40.0	159	2	S72544	heat shock protein
874	4	40.0	147	2	B70436	hypothetical prote	947	4	40.0	159	2	C72210	conserved hypoteth
875	4	40.0	148	2	S29257	Ig heavy chain v r	948	4	40.0	159	2	C64547	hypothetical prote
876	4	40.0	148	2	G83613	probable acetylra	949	4	40.0	159	2	T48837	hypothetical prote
877	4	40.0	148	2	A70077	conserved hypoteth	950	4	40.0	159	2	D70133	conserved hypoteth
878	4	40.0	148	2	T75205	molybdopterin bios	951	4	40.0	159	2	T17768	hypothetical prote
879	4	40.0	148	2	T05143	hypothetical prote	952	4	40.0	159	2	T46954	peptidylprolyl iso
880	4	40.0	148	2	T21488	hypothetical prote	953	4	40.0	160	2	S78308	plastoquinol--plas
881	4	40.0	148	2	A86878	non-heme iron-bind	954	4	40.0	160	2	T05740	heat shock protein
882	4	40.0	149	2	D71929	ribosomal protein	955	4	40.0	160	2	H69015	ribosomal protein
883	4	40.0	149	2	E69653	transcription regu	956	4	40.0	160	2	D75461	hypothetical prote
884	4	40.0	149	2	F71240	molybdopterin bios	957	4	40.0	160	2	F84350	hypothetical prote
885	4	40.0	149	2	S49527	zona pellucida bin	958	4	40.0	160	2	E81211	hypothetical prote
886	4	40.0	150	1	MORTA2	myosin alkali ligh	959	4	40.0	161	2	S44757	ribosomal protein
887	4	40.0	150	1	MORBL2	myosin alkali ligh	960	4	40.0	161	2	S00646	heat shock protein
888	4	40.0	150	1	T25581	hypothetical prote	961	4	40.0	161	2	S43260	helix-loop-helix p
889	4	40.0	150	2	B64584	hypothetical prote	962	4	40.0	161	2	D82042	transcription elon
890	4	40.0	150	2	S20874	ribosomal protein	963	4	40.0	161	2	C36810	hypothetical prote
891	4	40.0	150	2	B23253	heat shock protein	964	4	40.0	161	2	C36810	hypothetical prote
892	4	40.0	150	2	G72660	myosin A2 catalyti	965	4	40.0	161	2	H82782	hypothetical prote
893	4	40.0	150	2	G84173	hypothetical prote	966	4	40.0	161	2	E69328	3-isopropylmalate
894	4	40.0	151	1	HHWT17	archaeal histone A	967	4	40.0	162	2	T23912	hypothetical prote
895	4	40.0	151	2	S21600	heat shock protein	968	4	40.0	162	2	B72371	hypothetical prote
896	4	40.0	151	2	T05739	heat shock protein	969	4	40.0	163	1	G96671	hypothetical prote
897	4	40.0	151	2	T42298	probable heat shoc	970	4	40.0	163	1	YC8C3H	acetoacetate synth
898	4	40.0	151	2	F82427	hypothetical prote	971	4	40.0	163	2	S15940	acetoacetate synth
899	4	40.0	152	2	S08350	superoxide dismuta	972	4	40.0	163	2	B64131	acetoacetate synth
900	4	40.0	152	2	B71119	probable aspartate	973	4	40.0	163	2	B85490	hypothetical prote
901	4	40.0	152	2	C72227	conserved hypoteth	974	4	40.0	163	2	F83059	acetoacetate synth
902	4	40.0	152	2	T49126	hypothetical prote	975	4	40.0	163	2	H81066	acetoacetate synth
903	4	40.0	153	1	MYTWM	myoglobin - map tu	976	4	40.0	163	2	S71567	small heat-shock p
904	4	40.0	153	1	MYTNG	myoglobin - green	977	4	40.0	163	2	A72762	probable bacteriof
905	4	40.0	153	1	WRBP15	early protein gpl7	978	4	40.0	163	2	D71062	hypothetical prote
												B96842	hypothetical prote

687	4	40.0	124	1	TIBMB	trypsin inhibitor	760	4	40.0	132	2	S31596	Ig heavy chain V r
688	4	40.0	124	1	M1HUML	Ig heavy chain V-I	761	4	40.0	132	2	S46394	Ig heavy chain V r
689	4	40.0	124	1	M1HUSI	Ig heavy chain V-I	762	4	40.0	132	2	S49160	hypothetical prote
690	4	40.0	124	1	S19665	Ig heavy chain V r	763	4	40.0	132	2	B70312	hypothetical prote
691	4	40.0	124	2	F72403	glycine cleavage s	764	4	40.0	132	2	S30969	gene 24 protein -
692	4	40.0	124	2	B70472	flagellar protein	765	4	40.0	132	2	T139773	hypothetical prote
693	4	40.0	124	2	G75116	hypothetical prote	766	4	40.0	133	1	SKADP1	hexon-associated p
694	4	40.0	124	2	E82196	RetB1 protein VC14	767	4	40.0	133	2	S73769	adenine phosphorib
695	4	40.0	124	2	T36292	hypothetical prote	768	4	40.0	133	2	C33548	Ig heavy chain V-I
696	4	40.0	125	1	S1PSPT	steroid Delta-1som	769	4	40.0	133	2	T31427	profilin - common
697	4	40.0	125	1	HVHUMO	Ig heavy chain V-I	770	4	40.0	133	2	A60758	17k antigen - nema
698	4	40.0	125	1	PH1410	Ig heavy chain V r	771	4	40.0	134	2	S54628	cysteine proteinas
699	4	40.0	125	2	PH0957	Ig heavy chain V r	772	4	40.0	134	2	JC4882	cystatin - maize
700	4	40.0	125	2	A64502	hypothetical prote	773	4	40.0	134	2	PH1422	Ig heavy chain V r
701	4	40.0	125	2	S78697	probable export pr	774	4	40.0	134	2	T22275	hypothetical prote
702	4	40.0	125	2	H86722	hypothetical prote	775	4	40.0	134	2	F72802	gp24 protein - Myc
703	4	40.0	125	2	T38537	probable single-st	776	4	40.0	134	2	F75416	hypothetical prote
704	4	40.0	126	2	PH1417	Ig heavy chain V r	777	4	40.0	135	2	JC4007	cystatin II - maiz
705	4	40.0	126	2	PH1418	Ig heavy chain V r	778	4	40.0	135	2	S27239	cysteine proteinas
706	4	40.0	126	2	PH1424	Ig heavy chain V r	779	4	40.0	135	2	PH0953	Ig heavy chain V r
707	4	40.0	126	2	PH1412	Ig heavy chain V r	780	4	40.0	135	2	B32274	Ig heavy chain pre
708	4	40.0	126	2	B33548	Ig heavy chain V-I	781	4	40.0	135	2	S49530	anti-Sm antibody V
709	4	40.0	126	2	A56657	PEMW2/MESA protei	782	4	40.0	135	2	T09876	denhydrin - upland
710	4	40.0	126	2	G83571	conserved hypochet	783	4	40.0	135	2	C64453	translatin initia
711	4	40.0	126	2	H75433	hypothetical prote	784	4	40.0	135	2	A70317	hypothetical prote
712	4	40.0	127	1	C64140	probable glycy l ra	785	4	40.0	135	2	T40119	hypothetical prote
713	4	40.0	127	2	PH1414	Ig heavy chain V r	786	4	40.0	135	2	D36891	transfer complex p
714	4	40.0	127	2	PH1415	Ig heavy chain V r	787	4	40.0	135	2	G72714	hypothetical prote
715	4	40.0	127	2	PH1421	Ig heavy chain V r	788	4	40.0	136	2	PH1559	Ig heavy chain V r
716	4	40.0	127	2	PH1411	Ig heavy chain V r	789	4	40.0	136	2	A49047	Ig heavy chain V r
717	4	40.0	127	2	PH1420	Ig heavy chain V r	790	4	40.0	136	2	S31600	Ig heavy chain V r
718	4	40.0	127	2	PH0955	Ig heavy chain V r	791	4	40.0	136	2	PH0960	Ig heavy chain V r
719	4	40.0	127	2	S34014	Ig heavy chain V r	792	4	40.0	136	2	S46102	hypothetical prote
720	4	40.0	127	2	E82197	RetB2 protein VC14	793	4	40.0	136	2	T13388	hypothetical prote
721	4	40.0	128	2	T69024	MHC sex-limited pr	794	4	40.0	136	2	B81388	hypothetical prote
722	4	40.0	128	2	S16685	Ig heavy chain V r	795	4	40.0	136	2	E70182	hypothetical prote
723	4	40.0	128	2	PH0952	Ig heavy chain V r	796	4	40.0	137	2	PH1562	Ig heavy chain V r
724	4	40.0	128	2	S76468	hypothetical prote	797	4	40.0	137	2	T22043	hypothetical prote
725	4	40.0	128	2	T22276	hypothetical prote	798	4	40.0	137	2	H70472	conserved hypochet
726	4	40.0	128	2	D75575	5-carboxymethyl-2-	799	4	40.0	137	2	S74770	hypothetical prote
727	4	40.0	128	2	S76955	hypothetical prote	800	4	40.0	138	2	A05005	ribulose-bisphosph
728	4	40.0	128	2	D72481	hypothetical prote	801	4	40.0	138	2	FN0538	Ig heavy chain V r
729	4	40.0	128	2	H70435	hypothetical prote	802	4	40.0	138	2	PH1564	Ig heavy chain V r
730	4	40.0	128	2	T115911	hypothetical prote	803	4	40.0	138	2	PH1565	Ig heavy chain V r
731	4	40.0	128	2	S75366	hypothetical prote	804	4	40.0	138	2	S24078	envelope protein -
732	4	40.0	128	2	T32789	hypothetical prote	805	4	40.0	138	2	D83833	hypothetical prote
733	4	40.0	129	2	A33548	Ig heavy chain V-I	806	4	40.0	138	2	B45244	transcription regu
734	4	40.0	129	2	S36260	Ig heavy chain V r	807	4	40.0	138	2	T04560	hypothetical prote
735	4	40.0	129	2	S46393	Ig heavy chain V r	808	4	40.0	138	2	B83366	hypothetical prote
736	4	40.0	129	2	B71350	probable ribosomal	809	4	40.0	138	2	G85806	hypothetical prote
737	4	40.0	129	2	S53806	ribosomal protein	810	4	40.0	139	2	T29558	hypothetical prote
738	4	40.0	129	2	S37713	hypothetical prote	811	4	40.0	139	2	T47152	hypothetical prote
739	4	40.0	129	2	F83764	ectoine synthase	812	4	40.0	139	2	PH1558	Ig heavy chain V r
740	4	40.0	130	1	F64376	hypothetical prote	813	4	40.0	139	2	C70114	ribosomal protein
741	4	40.0	130	1	C69883	ribonucleoprotein	814	4	40.0	139	2	T34633	hypothetical prote
742	4	40.0	130	1	PC6025	cysteine proteinas	815	4	40.0	139	2	G69497	iron-dependent rep
743	4	40.0	130	2	S08079	Ig kappa chain pre	816	4	40.0	139	2	T23471	hypothetical prote
744	4	40.0	130	2	F25733	T-cell receptor al	817	4	40.0	140	2	H69526	methylmalonyl-CoA
745	4	40.0	130	2	G70813	probable lipqS proc	818	4	40.0	140	2	H64664	conserved hypochet
746	4	40.0	130	2	S77271	hypothetical prote	819	4	40.0	140	2	B69323	hypothetical prote
747	4	40.0	130	2	D70966	probable phage pro	820	4	40.0	141	2	C69269	hypothetical prote
748	4	40.0	130	2	F64348	hypothetical prote	821	4	40.0	141	2	A46256	dUTP pyrophosphata
749	4	40.0	130	2	D84363	hypothetical prote	822	4	40.0	141	2	S31685	Ig heavy chain V r
750	4	40.0	130	2	T51879	hypothetical prote	823	4	40.0	141	2	G71099	hypothetical prote
751	4	40.0	131	1	CCTW5T	cytochrome c552 [v	824	4	40.0	141	2	S34629	hypothetical prote
752	4	40.0	131	2	PH1425	Ig heavy chain V r	825	4	40.0	141	2	H84059	hypothetical prote
753	4	40.0	131	2	S21924	Ig heavy chain V r	826	4	40.0	141	2	T48839	hypothetical prote
754	4	40.0	131	2	T35341	hypothetical prote	827	4	40.0	141	2	T15990	hypothetical prote
755	4	40.0	131	2	G75208	hypothetical prote	828	4	40.0	142	1	S42722	interleukin-3 prec
756	4	40.0	131	2	G86802	conserved hypochet	829	4	40.0	142	2	E70356	hypothetical prote
757	4	40.0	132	1	E70434	Ig heavy chain V r	830	4	40.0	142	2	A32483	Ig heavy chain V r
758	4	40.0	132	2	PH1427	Ig heavy chain V r	831	4	40.0	142	2	D69510	oxaloacetate decar
759	4	40.0	132	2	PH0954	Ig heavy chain V r	832	4	40.0	142	2		

541	4	40.0	107	2	S40290	protein-tyrosine-p
542	4	40.0	107	2	S76718	hypothetical prote
543	4	40.0	107	2	T45621	hypothetical prote
544	4	40.0	107	2	E83182	hypothetical prote
545	4	40.0	107	2	E83040	DNA-binding protei
546	4	40.0	107	2	G81080	hypothetical prote
547	4	40.0	108	2	PH1664	Ig heavy chain v r
548	4	40.0	108	2	C49056	T-cell receptor al
549	4	40.0	108	2	T51146	ring-box protein 1
550	4	40.0	108	2	A86675	hypothetical prote
551	4	40.0	108	2	S61627	hypothetical prote
552	4	40.0	108	2	D72662	hypothetical prote
553	4	40.0	108	2	A72516	hypothetical prote
554	4	40.0	108	2	T26681	hypothetical prote
555	4	40.0	108	2	A72704	hypothetical prote
556	4	40.0	109	2	S16437	ribulose-bisphosph
557	4	40.0	109	2	PH1672	Ig heavy chain v r
558	4	40.0	109	2	PH1668	Ig heavy chain v r
559	4	40.0	109	2	PH1671	Ig heavy chain v r
560	4	40.0	109	2	D71279	hypothetical prote
561	4	40.0	109	2	F84010	hypothetical prote
562	4	40.0	109	2	T51864	probable heat-shoc
563	4	40.0	110	1	A37414	parvalbumin - mou
564	4	40.0	110	2	PH1669	Ig heavy chain v r
565	4	40.0	110	2	PH1670	Ig heavy chain v r
566	4	40.0	110	2	G70305	ribosomal protein
567	4	40.0	110	2	S50100	ribosomal protein
568	4	40.0	110	2	A55263	transcripton-asso
569	4	40.0	110	2	JV0102	hypothetical 12.8k
570	4	40.0	110	2	T30125	hypothetical prote
571	4	40.0	110	2	D70610	probable pg protei
572	4	40.0	110	2	T27823	hypothetical prote
573	4	40.0	110	2	T46071	hypothetical prote
574	4	40.0	110	2	T48382	hypothetical prote
575	4	40.0	111	2	S21925	Ig heavy chain v r
576	4	40.0	111	2	S17200	protein kinase (EC
577	4	40.0	111	2	D72646	hypothetical prote
578	4	40.0	112	2	S77344	carbon dioxide con
579	4	40.0	112	2	A71515	hypothetical prote
580	4	40.0	112	2	A64976	galactitol utiliza
581	4	40.0	112	2	C83938	hypothetical prote
582	4	40.0	112	2	C86415	hypothetical prote
583	4	40.0	113	1	RKWT55	ribulose-bisphosph
584	4	40.0	113	1	R6D0P1	acidic ribosomal p
585	4	40.0	113	2	PH1428	Ig heavy chain v r
586	4	40.0	113	2	PH1663	Ig heavy chain v r
587	4	40.0	113	2	PC1281	NS5 protein - hepa
588	4	40.0	113	2	S11640	hypothetical prote
589	4	40.0	113	2	A56581	major basic nuclea
590	4	40.0	113	2	A83429	hypothetical prote
591	4	40.0	113	2	D83220	hypothetical prote
592	4	40.0	113	2	A83697	hypothetical prote
593	4	40.0	113	2	T08623	probable sensor ki
594	4	40.0	113	2	S66805	hypothetical prote
595	4	40.0	113	2	T49533	hypothetical prote
596	4	40.0	113	2	PC2331	hobo-like transpos
597	4	40.0	114	2	S07898	endothelin 3 - tab
598	4	40.0	114	2	PH1667	Ig heavy chain v r
599	4	40.0	115	1	JN0318	guanylin precursor
600	4	40.0	115	2	PH1560	Ig heavy chain v r
601	4	40.0	115	2	PH1557	Ig heavy chain v r
602	4	40.0	115	2	G72568	hypothetical prote
603	4	40.0	115	2	E70702	hypothetical prote
604	4	40.0	115	2	E86809	hypothetical prote
605	4	40.0	115	2	D84501	hypothetical prote
606	4	40.0	115	2	E84512	probable MYB fami1
607	4	40.0	115	2	PC2330	hobo-like transpos
608	4	40.0	115	2	B49094	methylmalonyl-CoA
609	4	40.0	116	1	B46279	guanylin precursor
610	4	40.0	116	2	S31698	Ig heavy chain pre
611	4	40.0	116	2	PH0959	Ig heavy chain v r
612	4	40.0	116	2	S36261	Ig heavy chain v r
613	4	40.0	116	2	S31667	Ig heavy chain v r
614	4	40.0	116	2	PN0618	ribosomal protein
615	4	40.0	116	2	JC5188	sporulation-specif
616	4	40.0	116	2	PC4228	N-acetylglucosamin
617	4	40.0	116	2	T33195	hypothetical prote
618	4	40.0	116	2	H72489	hypothetical prote
619	4	40.0	117	1	G1H0EU	Ig heavy chain V-I
620	4	40.0	117	1	HVH0UG	Ig heavy chain pre
621	4	40.0	117	1	HVH0UG	Ig heavy chain pre
622	4	40.0	117	2	T02872	probable lipid tra
623	4	40.0	117	2	S19669	Ig heavy chain v r
624	4	40.0	117	2	S19670	Ig heavy chain v r
625	4	40.0	117	2	A28846	Ig heavy chain pre
626	4	40.0	117	2	PT0371	Ig gamma chain pre
627	4	40.0	117	2	S21668	Ig kappa chain v r
628	4	40.0	117	2	S31680	Ig kappa chain v r
629	4	40.0	117	2	S18551	Ig heavy chain v r
630	4	40.0	117	2	S18552	Ig heavy chain v r
631	4	40.0	117	2	S18553	Ig heavy chain v r
632	4	40.0	117	2	B82614	hypothetical prote
633	4	40.0	118	2	H86640	ribonuclease P (EC
634	4	40.0	118	2	PH1666	Ig heavy chain v r
635	4	40.0	118	2	S36265	Ig heavy chain v r
636	4	40.0	118	2	S12440	Ig lambda chain (M
637	4	40.0	118	2	S12441	Ig lambda chain (K
638	4	40.0	118	2	S12442	Ig lambda chain (K
639	4	40.0	118	2	T35747	hypothetical prote
640	4	40.0	118	2	T07905	low-carbon dioxide
641	4	40.0	119	2	S08077	Ig kappa chain pre
642	4	40.0	119	2	PH0295	Ig heavy chain V-D
643	4	40.0	119	2	PH0961	Ig heavy chain v r
644	4	40.0	119	2	S44106	Ig heavy chain V-D
645	4	40.0	119	2	S58445	Lipoprotein D - Sa
646	4	40.0	119	2	T00151	hypothetical prote
647	4	40.0	119	2	E83674	hypothetical prote
648	4	40.0	119	2	G86843	hypothetical prote
649	4	40.0	119	2	D64002	Ig kappa chain v r
650	4	40.0	120	2	S21667	Ig kappa chain v r
651	4	40.0	120	2	S21666	Ig kappa chain v r
652	4	40.0	120	2	PH0962	Ig heavy chain v r
653	4	40.0	120	2	T29774	hypothetical prote
654	4	40.0	120	2	D71039	hypothetical prote
655	4	40.0	120	2	C85849	unknown protein en
656	4	40.0	120	2	A72539	hypothetical prote
657	4	40.0	121	2	E70313	histidine triad-11
658	4	40.0	121	2	A28678	T-cell receptor ga
659	4	40.0	121	2	S20783	Ig heavy chain v r
660	4	40.0	121	2	A49590	Ig heavy chain v r
661	4	40.0	121	2	D75089	hypothetical prote
662	4	40.0	121	2	T32888	hypothetical prote
663	4	40.0	121	2	S74021	hypothetical prote
664	4	40.0	121	2	S75660	hypothetical prote
665	4	40.0	122	2	PC4279	anti-SS-A/Ro 60k p
666	4	40.0	122	2	PC4280	anti-SS-A/Ro 60k p
667	4	40.0	122	2	PH1426	Ig heavy chain v r
668	4	40.0	122	2	PH0958	Ig heavy chain v r
669	4	40.0	122	2	S36271	Ig heavy chain v r
670	4	40.0	122	2	C49590	Ig heavy chain v r
671	4	40.0	122	2	B49590	Ig heavy chain v r
672	4	40.0	122	2	T22096	Ig heavy chain v r
673	4	40.0	123	1	RKSPS	hypothetical prote
674	4	40.0	123	2	D33548	ribulose-bisphosph
675	4	40.0	123	2	PH1413	Ig heavy chain V-1
676	4	40.0	123	2	PH1423	Ig heavy chain v r
677	4	40.0	123	2	S38492	Ig heavy chain - h
678	4	40.0	123	2	C36006	Ig heavy chain v r
679	4	40.0	123	2	S44108	Ig heavy chain V-D
680	4	40.0	123	2	E64418	conserved hypotet
681	4	40.0	123	2	G71143	hypothetical prote
682	4	40.0	123	2	H75059	hypothetical prote
683	4	40.0	123	2	B75546	hypothetical prote
684	4	40.0	123	2	C71423	hypothetical prote
685	4	40.0	123	2	A05125	hypothetical prote
686	4	40.0	123	2	T20279	hypothetical prote

395	4	40.0	81	2	T29888	hypothetical prote
396	4	40.0	82	2	S37173	ribosomal protein
397	4	40.0	82	2	G82366	tata protein WC008
398	4	40.0	82	2	T29889	hypothetical prote
399	4	40.0	82	2	T29893	hypothetical prote
400	4	40.0	82	2	T29891	hypothetical prote
401	4	40.0	82	2	T33088	hypothetical prote
402	4	40.0	83	2	C47188	MHC class II histo
403	4	40.0	83	2	T08338	gas-vesicle operon
404	4	40.0	83	2	J01124	gas-vesicle operon
405	4	40.0	84	2	A53012	serum response fac
406	4	40.0	84	2	S61465	p83/100 protein -
407	4	40.0	84	2	S61466	p83/100 protein -
408	4	40.0	84	2	T47420	hypothetical prote
409	4	40.0	84	2	E82709	hypothetical prote
410	4	40.0	86	2	F85748	unknown protein en
411	4	40.0	86	2	A70005	conserved hypotet
412	4	40.0	87	2	T27141	hypothetical prote
413	4	40.0	87	2	S27040	VAT-1 protein - Pa
414	4	40.0	88	1	O6BP77	gene 6.7 protein -
415	4	40.0	88	2	S60815	M protein precursor
416	4	40.0	88	2	A57399	BM12 protein - Ba
417	4	40.0	88	2	A83659	hypothetical prote
418	4	40.0	89	2	B69352	acylphosphatase (a
419	4	40.0	90	2	S78047	DNA-directed RNA p
420	4	40.0	90	2	B71983	hypothetical prote
421	4	40.0	91	2	B96574	hypothetical prote
422	4	40.0	92	2	C82174	ribosomal protein
423	4	40.0	92	2	F84620	similar to late em
424	4	40.0	92	2	T34744	hypothetical prote
425	4	40.0	92	2	T51187	small zinc finger-
426	4	40.0	92	2	JU0239	nuclear matrix pro
427	4	40.0	93	2	B85537	unknown [imported]
428	4	40.0	93	2	T45593	small zinc finger-
429	4	40.0	94	2	S49470	hypothetical prote
430	4	40.0	94	2	B84539	hypothetical prote
431	4	40.0	94	2	G36943	chemoreceptor prot
432	4	40.0	94	2	S43903	hypothetical prote
433	4	40.0	95	2	S68231	PHG22 protein prec
434	4	40.0	95	2	B32830	homeotic protein H
435	4	40.0	95	2	A56644	inverted repeat co
436	4	40.0	95	2	H81119	conserved hypotet
437	4	40.0	95	2	G81901	hypothetical prote
438	4	40.0	95	2	C69905	hypothetical prote
439	4	40.0	96	2	S10069	regulatory protein
440	4	40.0	97	1	USPSBM	small acid-soluble
441	4	40.0	97	2	PH0870	Ig heavy chain V r
442	4	40.0	97	2	I51262	aggreccan chondroit
443	4	40.0	97	2	A69061	hypothetical prote
444	4	40.0	98	2	PH1429	Ig heavy chain V r
445	4	40.0	98	2	PH1274	Ig heavy chain V r
446	4	40.0	98	2	PH0877	Ig heavy chain V r
447	4	40.0	98	2	A30523	Ig heavy chain V r
448	4	40.0	98	2	PH0871	Ig heavy chain V r
449	4	40.0	98	2	S24680	Ig heavy chain V r
450	4	40.0	98	2	S46463	Ig heavy chain VI
451	4	40.0	98	2	S26910	Ig heavy chain V r
452	4	40.0	98	2	S26914	Ig heavy chain V r
453	4	40.0	98	2	S26918	Ig heavy chain V r
454	4	40.0	98	2	S26938	Ig heavy chain V r
455	4	40.0	98	2	S26909	Ig heavy chain V r
456	4	40.0	98	2	S26919	Ig heavy chain V r
457	4	40.0	98	2	S26913	Ig heavy chain V r
458	4	40.0	98	2	S26912	Ig heavy chain V r
459	4	40.0	98	2	S26911	Ig heavy chain V r
460	4	40.0	98	2	S26920	Ig heavy chain V r
461	4	40.0	98	2	S26921	Ig heavy chain V r
462	4	40.0	98	2	S26915	Ig heavy chain V r
463	4	40.0	98	2	S26907	Ig heavy chain V r
464	4	40.0	98	2	S22592	hypothetical prote
465	4	40.0	98	2	T24286	hypothetical prote
466	4	40.0	99	1	R6MKL2	ribosomal protein
467	4	40.0	99	1	Q00YBW	hypothetical prote
468	4	40.0	99	2	H69000	translation initia
469	4	40.0	100	2	T08763	hypothetical prote
470	4	40.0	100	2	B49598	hypothetical prote
471	4	40.0	100	2	S77878	hypothetical prote
472	4	40.0	101	2	S12424	Ig heavy chain V r
473	4	40.0	101	2	S12428	Ig heavy chain V r
474	4	40.0	101	2	S12431	Ig heavy chain V r
475	4	40.0	101	2	H65009	hypothetical prote
476	4	40.0	101	2	B72079	hypothetical prote
477	4	40.0	101	2	F86544	hypothetical prote
478	4	40.0	101	2	S76550	hypothetical prote
479	4	40.0	102	1	W7WLEP	E7 protein - Europ
480	4	40.0	102	2	PH1232	Ig heavy chain V r
481	4	40.0	102	2	PH1234	Ig heavy chain V r
482	4	40.0	102	2	PH1235	Ig heavy chain V r
483	4	40.0	102	2	PH1237	Ig heavy chain V r
484	4	40.0	102	2	PH1238	Ig heavy chain V r
485	4	40.0	102	2	PH1239	Ig heavy chain V r
486	4	40.0	102	2	PH1240	Ig heavy chain V r
487	4	40.0	102	2	PH1243	Ig heavy chain V r
488	4	40.0	102	2	PH1248	Ig heavy chain V r
489	4	40.0	102	2	PH1262	Ig heavy chain V r
490	4	40.0	102	2	PH1264	Ig heavy chain V r
491	4	40.0	102	2	PH1268	Ig heavy chain V r
492	4	40.0	102	2	PH1276	Ig heavy chain V r
493	4	40.0	102	2	PH1280	Ig heavy chain V r
494	4	40.0	102	2	PH1241	Ig heavy chain V r
495	4	40.0	102	2	PH1244	Ig heavy chain V r
496	4	40.0	102	2	PH1247	Ig heavy chain V r
497	4	40.0	102	2	PH1249	Ig heavy chain V r
498	4	40.0	102	2	PH1252	Ig heavy chain V r
499	4	40.0	102	2	PH1254	Ig heavy chain V r
500	4	40.0	102	2	PH1258	Ig heavy chain V r
501	4	40.0	102	2	PH1259	Ig heavy chain V r
502	4	40.0	102	2	PH1260	Ig heavy chain V r
503	4	40.0	102	2	PH1263	Ig heavy chain V r
504	4	40.0	102	2	PH1265	Ig heavy chain V r
505	4	40.0	102	2	PH1266	Ig heavy chain V r
506	4	40.0	102	2	PH1267	Ig heavy chain V r
507	4	40.0	102	2	PH1275	Ig heavy chain V r
508	4	40.0	102	2	PH1278	Ig heavy chain V r
509	4	40.0	102	2	PH1279	Ig heavy chain V r
510	4	40.0	102	2	PH1281	Ig heavy chain V r
511	4	40.0	102	2	PH1282	Ig heavy chain V r
512	4	40.0	102	2	PH1271	Ig heavy chain V r
513	4	40.0	102	2	PH1272	Ig heavy chain V r
514	4	40.0	102	2	PH1273	Ig heavy chain V r
515	4	40.0	102	2	H69841	conserved hypotet
516	4	40.0	102	2	S28361	hypothetical prote
517	4	40.0	102	2	T39407	hypothetical prote
518	4	40.0	103	2	B26167	Ig lambda chain C
519	4	40.0	103	2	B60608	myosin heavy chain
520	4	40.0	103	2	B65238	parvalbumin - mous
521	4	40.0	103	2	I51248	ACBP/DBI - duck
522	4	40.0	103	2	G75513	conserved hypotet
523	4	40.0	104	1	GMBO	gastriin precursor
524	4	40.0	104	2	PH1665	Ig heavy chain V r
525	4	40.0	104	2	S69899	Ig heavy chain V r
526	4	40.0	104	2	J00863	hypothetical 11.6K
527	4	40.0	104	2	A83871	probable inner mem
528	4	40.0	104	2	B81787	Ig lambda chain C
529	4	40.0	105	1	L2HU	spdp protein - Str
530	4	40.0	105	2	T36213	Ig lambda chain C
531	4	40.0	105	2	T49655	hypothetical prote
532	4	40.0	105	2	S27493	nodc protein - Bra
533	4	40.0	105	2	S44838	KO2D10.3 protein -
534	4	40.0	105	2	D82734	outer membrane pro
535	4	40.0	106	1	CCDV3S	cytochrome c3 - De
536	4	40.0	106	1	K4RBBS	Ig kappa-2 chain C
537	4	40.0	106	2	S20774	Ig heavy chain V r
538	4	40.0	106	2	G20907	Ig kappa-B4 chain
539	4	40.0	106	2	G72632	hypothetical prote
540	4	40.0	106	2	S64649	RBL2 protein - yea

249	5	50.0	1098	2	S38100	hypothetical prote
250	5	50.0	1113	2	H84105	hypothetical prote
251	5	50.0	1123	2	S36846	myosin-binding pro
252	5	50.0	1127	1	E71156	endopeptidase Ia h
253	5	50.0	1132	2	B82538	ribonuclease E XF2
254	5	50.0	1138	2	S24614	myosin-binding pro
255	5	50.0	1150	1	A55289	kinasin-like prote
256	5	50.0	1196	2	T23832	protein-tyrosine k
257	5	50.0	1199	2	S20969	Na+/Ca2+, K+-exchan
258	5	50.0	1210	2	I39410	AF-4 protein, spli
259	5	50.0	1213	2	A58198	serine/proline-ric
260	5	50.0	1217	2	T25894	hypothetical prote
261	5	50.0	1228	2	S59681	probable membrane
262	5	50.0	1233	2	S56271	hypothetical prote
263	5	50.0	1245	2	T18211	delta endotoxin -
264	5	50.0	1251	2	A56677	neuronal cell cycl
265	5	50.0	1252	2	S02004	I-phosphatidylinos
266	5	50.0	1265	2	A34163	C-terminal domain-
267	5	50.0	1268	2	T31420	transferrin-like p
268	5	50.0	1274	2	T10729	probable calmoduli
269	5	50.0	1276	2	T02711	chromosomal protei
270	5	50.0	1290	2	A55094	acetyl-CoA carboxy
271	5	50.0	1306	2	S42659	nuclear pore membr
272	5	50.0	1337	2	A53824	hypothetical prote
273	5	50.0	1341	2	T17285	zyg-9 protein - Ca
274	5	50.0	1415	2	T21244	lin-15B protein -
275	5	50.0	1440	2	T27942	alpha-2-macroglobu
276	5	50.0	1472	2	A26122	salivary agglutini
277	5	50.0	1473	2	A35186	ribosome receptor,
278	5	50.0	1534	2	A56734	cell surface anti
279	5	50.0	1566	2	A43607	hypothetical prote
280	5	50.0	1582	2	T15308	acetyl-CoA carboxy
281	5	50.0	1625	2	T02921	adhesin p1 precurs
282	5	50.0	1627	1	IYMAP	adhesin p1, group
283	5	50.0	1635	2	A41480	acetyl-CoA carboxy
284	5	50.0	1685	2	T02750	coracle gene prote
285	5	50.0	1698	2	T13800	major merizoite su
286	5	50.0	1785	2	A45546	cag island protein
287	5	50.0	1819	2	A71928	vitellogenin I pre
288	5	50.0	1912	2	T29088	cag pathogenicity
289	5	50.0	1927	2	G64585	myosin heavy chain
290	5	50.0	1928	2	S46773	callose synthase C
291	5	50.0	1963	2	T49914	gag, pol and env p
292	5	50.0	2272	2	T18572	acetyl-CoA carboxy
293	5	50.0	2325	2	T02235	hypothetical prote
294	5	50.0	2376	2	T34022	hypothetical prote
295	5	50.0	2541	2	T29340	vacuolar protein s
296	5	50.0	2796	2	UC4743	hemocytin - silkw
297	5	50.0	3131	2	T39553	connectin/ctlin -
298	5	50.0	3131	2	S39842	ALR protein - huma
299	5	50.0	3133	2	S52093	protein UNC-89 - C
300	5	50.0	4162	2	T42633	163K exoantigen -
301	5	50.0	4957	2	T03455	conanotkin T - con
302	5	50.0	5262	2	T03454	calcium-activated
303	5	50.0	6642	2	T29757	seed protein ws-6
304	5	50.0	6642	2	A33099	potassium channel
305	5	50.0	12	1	A35225	flavodoxin isoform
306	5	50.0	22	2	C39800	30K serine protein
307	5	50.0	23	2	E61491	H+-transporting AT
308	5	50.0	23	2	P50446	R-phycocerythrin ga
309	5	50.0	27	2	S55234	primase - Escheric
310	5	50.0	30	2	B60291	hypothetical prote
311	5	50.0	32	2	S21245	muonate cycloisom
312	5	50.0	33	2	S21245	hypothetical myeli
313	5	50.0	36	2	T25565	trifoliotxin precu
314	5	50.0	38	2	T15728	K4 protein - vacci
315	5	50.0	38	2	T31479	GuM8-2a protein -
316	5	50.0	41	2	B54357	histone H1 II-1 (c
317	5	50.0	41	4	I68622	
318	5	50.0	42	4	A47116	
319	5	50.0	44	1	MMVZK4	
320	5	50.0	44	2	S56313	
321	5	50.0	47	2	E47395	
322	4	40.0				hypothetical prote
323	4	40.0				hypothetical prote
324	4	40.0				myosin-binding pro
325	4	40.0				endopeptidase Ia h
326	4	40.0				ribonuclease E XF2
327	4	40.0				myosin-binding pro
328	4	40.0				kinasin-like prote
329	4	40.0				protein-tyrosine k
330	4	40.0				Na+/Ca2+, K+-exchan
331	4	40.0				AF-4 protein, spli
332	4	40.0				serine/proline-ric
333	4	40.0				hypothetical prote
334	4	40.0				probable membrane
335	4	40.0				hypothetical prote
336	4	40.0				delta endotoxin -
337	4	40.0				neuronal cell cycl
338	4	40.0				I-phosphatidylinos
339	4	40.0				C-terminal domain-
340	4	40.0				transferrin-like p
341	4	40.0				probable calmoduli
342	4	40.0				chromosomal protei
343	4	40.0				acetyl-CoA carboxy
344	4	40.0				nuclear pore membr
345	4	40.0				hypothetical prote
346	4	40.0				zyg-9 protein - Ca
347	4	40.0				lin-15B protein -
348	4	40.0				alpha-2-macroglobu
349	4	40.0				salivary agglutini
350	4	40.0				ribosome receptor,
351	4	40.0				cell surface anti
352	4	40.0				hypothetical prote
353	4	40.0				acetyl-CoA carboxy
354	4	40.0				adhesin p1 precurs
355	4	40.0				adhesin p1, group
356	4	40.0				acetyl-CoA carboxy
357	4	40.0				coracle gene prote
358	4	40.0				major merizoite su
359	4	40.0				cag island protein
360	4	40.0				vitellogenin I pre
361	4	40.0				cag pathogenicity
362	4	40.0				myosin heavy chain
363	4	40.0				callose synthase C
364	4	40.0				gag, pol and env p
365	4	40.0				acetyl-CoA carboxy
366	4	40.0				hypothetical prote
367	4	40.0				hypothetical prote
368	4	40.0				vacuolar protein s
369	4	40.0				hemocytin - silkw
370	4	40.0				connectin/ctlin -
371	4	40.0				ALR protein - huma
372	4	40.0				protein UNC-89 - C
373	4	40.0				163K exoantigen -
374	4	40.0				conanotkin T - con
375	4	40.0				calcium-activated
376	4	40.0				seed protein ws-6
377	4	40.0				potassium channel
378	4	40.0				flavodoxin isoform
379	4	40.0				30K serine protein
380	4	40.0				H+-transporting AT
381	4	40.0				R-phycocerythrin ga
382	4	40.0				primase - Escheric
383	4	40.0				hypothetical prote
384	4	40.0				muonate cycloisom
385	4	40.0				hypothetical myeli
386	4	40.0				trifoliotxin precu
387	4	40.0				K4 protein - vacci
388	4	40.0				GuM8-2a protein -
389	4	40.0				histone H1 II-1 (c
390	4	40.0				
391	4	40.0				
392	4	40.0				
393	4	40.0				
394	4	40.0				
48	2	40.0			T12940	hypothetical prote
49	2	40.0			S39857	ribosomal protein
49	2	40.0			B56448	cofilin-like prote
49	2	40.0			B86888	50S ribosomal prot
50	2	40.0			B60718	phospholipase A2 h
50	2	40.0			F84075	hypothetical prote
52	2	40.0			A38942	chemoreceptor prot
52	2	40.0			A69330	ISORP2-like protei
52	2	40.0			T00141	hypothetical prote
53	2	40.0			S66602	aldehyde oxidase (
53	2	40.0			F47395	histone H1 II-1 (c
53	2	40.0			B47395	histone H1 II-1 (c
53	2	40.0			C47395	histone H1 II-1 (c
53	2	40.0			G47395	histone H1 II-2 (c
53	2	40.0			A72614	hypothetical prote
54	2	40.0			B36943	chemoreceptor prot
55	2	40.0			T03337	gene e30 protein -
56	2	40.0			I56605	I7 alpha-hydroxyia
56	2	40.0			B64368	hypothetical prote
58	2	40.0			I79344	interferon alpha O
59	2	40.0			J70289	phosphoprotein PP3
59	2	40.0			B70306	conserved hypotnet
61	2	40.0			T43672	hypothetical prote
62	1	40.0			CCBO17	ubiquinol--cytochr
62	2	40.0			T44918	hypothetical prote
62	2	40.0			T26847	hypothetical prote
62	2	40.0			H82849	hypothetical prote
64	2	40.0			H82849	hypothetical prote
65	2	40.0			G69542	hypothetical prote
65	2	40.0			S35024	hypothetical prote
66	2	40.0			S65971	yyed protein - Bac
66	2	40.0			PN0644	hypothetical prote
67	2	40.0			I47395	histone H1 I-1 (cl
67	2	40.0			A64321	archaeal histone -
67	2	40.0			A64457	archaeal histone -
67	2	40.0			D64416	archaeal histone -
68	2	40.0			D64513	trpC protein - Bac
68	2	40.0			JH0100	small acid-soluble
68	2	40.0			C83767	lysine kallikrein
69	2	40.0			S28195	synaptoagmin II p
69	2	40.0			PC7068	conserved hypotnet
69	2	40.0			H69383	50S ribosomal prot
70	2	40.0			A47395	histone H1 I-1 (RN
70	2	40.0			S56769	RNA-directed RNA p
71	2	40.0			C82807	30S ribosomal prot
72	2	40.0			S28196	lysine kallikrein
72	2	40.0			P00613	ferritin 5 - cowpe
72	2	40.0			P00614	ferritin 2 - cowpe
72	2	40.0			P00615	ferritin 1 - cowpe
72	2	40.0			S30980	gene 35 protein -
72	2	40.0			S75519	hypothetical prote
72	2	40.0			E69386	hypothetical prote
72	2	40.0			E69323	hypothetical prote
72	2	40.0			T48971	conserved hypotnet
73	2	40.0			D69319	hypothetical prote
73	2	40.0			T44814	hypothetical prote
73	2	40.0			G64443	hypothetical prote
74	2	40.0			E69028	hypothetical prote
75	2	40.0			T12080	low molecular walg
75	2	40.0			C85636	hypothetical prote
75	2	40.0			A64842	yyed protein - Esc
75	2	40.0			T17673	hypothetical prote
76	2	40.0			B83402	hypothetical prote
76	2	40.0			A75309	hypothetical prote
76	2	40.0			H69328	nifu protein (nifu
77	2	40.0			D85940	hypothetical prote
77	2	40.0			S00970	kcral protein - pl
78	2	40.0			S61468	p83/100 protein -
78	2	40.0			G71720	hypothetical prote
78	2	40.0			T16325	hypothetical prote
79	2	40.0			T30118	hypothetical prote
80	2	40.0			F72306	conserved hypotnet
80	2	40.				

103	5	50.0	376	2	S04497	surface antigen PA	176	5	50.0	573	2	T21653	hypothetical prote
104	5	50.0	389	2	D84068	RNA helicase BH334	177	5	50.0	573	2	S66710	probable membrane
105	5	50.0	391	2	I51097	thyroid hormone re	178	5	50.0	574	1	S76132	protein kinase pkn
106	5	50.0	395	2	D83782	aspartate aminotra	179	5	50.0	578	2	T33916	hypothetical prote
107	5	50.0	410	2	D70599	hypothetical prote	180	5	50.0	580	2	C96597	Robisco subunit b1
108	5	50.0	415	2	T20335	hypothetical prote	181	5	50.0	583	2	S01301	Iamin L-III - Afri
109	5	50.0	416	2	G69748	conserved hypochet	182	5	50.0	583	2	T30131	hypothetical prote
110	5	50.0	418	2	F83986	transposer BH2694	183	5	50.0	603	2	S06059	gene NDI Intron 4
111	5	50.0	421	2	T14773	hypothetical prote	184	5	50.0	604	2	S25203	srmr protein - str
112	5	50.0	422	2	G70984	probable pap45 pro	185	5	50.0	612	2	G71972	threonine--trna 11
113	5	50.0	423	2	S73020	hypothetical prote	186	5	50.0	612	2	C64535	threonine--trna 11
114	5	50.0	428	2	S28468	mannose-1-phosphat	187	5	50.0	615	2	T37981	probable exocyst c
115	5	50.0	435	2	T19687	hypothetical prote	188	5	50.0	637	2	S66953	hypothetical prote
116	5	50.0	440	2	D64616	N-acetyluramoyl-L	189	5	50.0	641	1	T03095	homeoprotein Sal1
117	5	50.0	443	2	E71135	hypothetical prote	190	5	50.0	643	1	DJEC3G	DNA-directed DNA p
118	5	50.0	445	2	D71977	phosphoglucosamine	191	5	50.0	643	2	G85544	hypothetical prote
119	5	50.0	445	2	C38537	urec protein - Hel	192	5	50.0	646	2	G69671	hypothetical prote
120	5	50.0	447	2	T34592	probable lipoprote	193	5	50.0	651	2	T21175	hypothetical prote
121	5	50.0	451	2	B96774	hypothetical prote	194	5	50.0	654	1	HMIVC8	hemagglutinin prec
122	5	50.0	452	2	T38962	hypothetical prote	195	5	50.0	655	2	S07412	hemagglutinin-este
123	5	50.0	453	1	F64623	amidase - Helicoba	196	5	50.0	662	2	T20570	hypothetical prote
124	5	50.0	453	1	A71891	glu-trna amidotran	197	5	50.0	668	2	C71365	probable excinucle
125	5	50.0	460	2	T23087	hypothetical prote	198	5	50.0	668	2	H86729	exclnuclease ABC s
126	5	50.0	461	2	T42513	id-myo-inositol-tr	199	5	50.0	670	2	T34548	hypothetical prote
127	5	50.0	465	2	H82345	mannose-1-phosphat	200	5	50.0	691	2	H81313	ATP-dependent DNA
128	5	50.0	469	2	H71897	probable probable	201	5	50.0	700	2	T13577	hypothetical prote
129	5	50.0	470	2	T15946	hypothetical prote	202	5	50.0	701	1	S33709	DHR39-short protel
130	5	50.0	471	2	JC1403	glutamate--ammonia	203	5	50.0	707	2	JC2218	procollagen C-endo
131	5	50.0	473	2	D70405	glutamate--trna 11	204	5	50.0	713	2	A28706	calpastatin, cardl
132	5	50.0	473	2	S75141	glutamate--ammonia	205	5	50.0	730	1	BMH01	procollagen C-endo
133	5	50.0	476	2	B44997	merozoite surface	206	5	50.0	739	2	T29407	hypothetical prote
134	5	50.0	477	2	A75545	amidophosphoribosy	207	5	50.0	746	2	T19287	hypothetical prote
135	5	50.0	478	2	A32555	major merozoite su	208	5	50.0	750	1	H70628	probable pknG prot
136	5	50.0	482	2	A44997	merozoite surface	209	5	50.0	752	2	S51866	hPR1 protein - yea
137	5	50.0	484	2	D65230	hypothetical 52.9	210	5	50.0	763	2	T44735	serine/threonine-s
138	5	50.0	484	2	A86116	hypothetical prote	211	5	50.0	771	1	T26176	pyrroloquinoline q
139	5	50.0	490	2	PQ0164	sucrose phosphoryl	212	5	50.0	775	2	E83400	pyruvate,water dlk
140	5	50.0	492	2	T43859	uroporphyrinogen I	213	5	50.0	792	2	S20554	phosphoenolpyruvat
141	5	50.0	493	2	T12044	probable legumain	214	5	50.0	792	2	E85778	probable steroid/th
142	5	50.0	496	2	T30976	hypothetical prote	215	5	50.0	806	1	H70647	nuclear F7E22.2 [1
143	5	50.0	498	2	D64878	probable glutamate	216	5	50.0	808	1	S33708	connectin 1 - chic
144	5	50.0	498	2	G85755	glutamate--ammonia	217	5	50.0	811	2	PN0689	protein F7E22.2 [1
145	5	50.0	501	2	T27513	hypothetical prote	218	5	50.0	815	2	H96494	hypothetical prote
146	5	50.0	504	2	G02474	interferon regulat	219	5	50.0	816	2	T17257	verpocollin - yeast
147	5	50.0	505	2	T01667	gag polyprotein -	220	5	50.0	817	2	S51342	conserved hypochet
148	5	50.0	505	2	B64560	poly E-rich protei	221	5	50.0	822	2	G69010	procollagen C-endo
149	5	50.0	507	2	G01614	zinc finger protei	222	5	50.0	823	1	A58788	translational Initia
150	5	50.0	509	1	S04346	steroid 17alpha-mo	223	5	50.0	871	2	H81430	protein T16E15.12
151	5	50.0	516	2	T09364	cytochrome P450 ho	224	5	50.0	871	2	D86355	pyruvate dehydroge
152	5	50.0	519	2	S23796	modifier-3 protein	225	5	50.0	887	2	E81847	pyruvate dehydroge
153	5	50.0	519	2	T45038	hypothetical prote	226	5	50.0	887	2	E81094	SGDI protein - yea
154	5	50.0	528	2	E96795	unknown protein F2	227	5	50.0	899	2	S51341	hypothetical prote
155	5	50.0	530	2	D83281	probable MFS trans	228	5	50.0	912	2	H71931	hypothetical prote
156	5	50.0	532	2	S40963	hypothetical prote	229	5	50.0	919	2	C86578	topc/gen secretion
157	5	50.0	537	2	D86520	CTP synthetase (lm	230	5	50.0	919	2	F72045	type III secretion
158	5	50.0	537	2	A72103	CTP synthetase - C	231	5	50.0	925	2	T33732	probable excinucle
159	5	50.0	537	2	E81568	lymphoid-restrict	232	5	50.0	958	2	S47179	hypothetical prote
160	5	50.0	539	2	I49065	hypothetical prote	233	5	50.0	969	2	A75634	McrB-related prote
161	5	50.0	539	2	T02508	hypothetical prote	234	5	50.0	980	2	S71090	peroxisome biogene
162	5	50.0	542	2	T29707	hypothetical prote	235	5	50.0	982	2	T43699	DNA mismatch repai
163	5	50.0	543	2	T00513	cytochrome P450 ho	236	5	50.0	986	1	B58788	procollagen C-endo
164	5	50.0	547	2	B56573	nuclear pore compl	237	5	50.0	990	2	T12678	hypothetical prote
165	5	50.0	550	2	C86704	conserved hypochet	238	5	50.0	991	2	I49540	procollagen C-endo
166	5	50.0	553	2	C75318	hypothetical prote	239	5	50.0	998	2	H75005	ATP-dependent prot
167	5	50.0	557	2	A70480	carbamoyl-phosphat	240	5	50.0	1000	2	B72385	hypothetical prote
168	5	50.0	557	2	B83962	hypothetical prote	241	5	50.0	1001	2	T29105	myosin-B - Toxopla
169	5	50.0	557	2	A00629	protein-tyrosine k	242	5	50.0	1002	2	S70292	leukocyte surface
170	5	50.0	558	2	B86016	probable enzyme z4	243	5	50.0	1021	2	I39207	hypothetical prote
171	5	50.0	558	2	S75104	hypothetical prote	244	5	50.0	1025	2	E86355	hypothetical prote
172	5	50.0	562	2	G84221	NADH dehydrogenase	245	5	50.0	1070	2	T34385	starch synthase ho
173	5	50.0	566	2	C70482	repair excision nu	246	5	50.0	1071	2	T04926	hypothetical prote
174	5	50.0	567	2	B86481	hypothetical prote	247	5	50.0	1073	2	T01955	carbamoyl-phosphat
175	5	50.0	572	1	FOHYIH	retrovirus-related	248	5	50.0	1092	2	T33717	

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OM protein - protein search, using sw model.

Run on: August 15, 2001, 12:34:44 ; Search time 33.87 Seconds
(without alignments)
22.490 Million cell updates/sec

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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	484	2 A1487	protein p60 precur
2	7	70.0	227	2 D81259	probable tonb tran
3	6	60.0	102	2 F83231	hypothetical prote
4	6	60.0	116	2 T37186	probable regulator
5	6	60.0	456	2 H85574	hypothetical prote
6	6	60.0	617	2 S42719	actin-binding prot
7	6	60.0	748	2 H84913	probable ATP-depen
8	6	60.0	985	1 VCLJSP	env polyprotein
9	6	60.0	1133	2 T30302	P-type ATPase - Te
10	6	60.0	1230	2 E64664	outer membrane pro
11	5	50.0	75	2 E75264	hypothetical prote
12	5	50.0	82	2 T29802	hypothetical prote
13	5	50.0	102	2 B56581	major basic nuclea
14	5	50.0	103	1 KARB	Ig kappa-B4 chain
15	5	50.0	104	2 F53275	Ig kappa-1 chain C
16	5	50.0	112	2 T14788	hypothetical prote
17	5	50.0	114	2 T08411	hypothetical prote
18	5	50.0	124	2 B86557	Dnak suppressor [1
19	5	50.0	124	2 A71518	probable dnk supp
20	5	50.0	124	2 G72066	dnk suppressor -
21	5	50.0	124	2 T24876	hypothetical prote
22	5	50.0	131	2 D66684	phophage p11 prote
23	5	50.0	132	2 B81600	conserved hypotnet
24	5	50.0	133	2 T50083	probable cytidine
25	5	50.0	134	2 A81676	conserved hypotnet
26	5	50.0	141	2 E72580	hypothetical prote
27	5	50.0	147	2 G72384	conserved hypotnet
28	5	50.0	147	2 T33327	hypothetical prote
29	5	50.0	155	2 S3162	SRH-21 protein - p

30	5	50.0	157	2 T25638	hypothetical prote
31	5	50.0	161	2 C96568	hypothetical prote
32	5	50.0	174	2 S07291	repressor protein
33	5	50.0	175	2 D66699	hypothetical prote
34	5	50.0	179	2 G84789	hypothetical prote
35	5	50.0	185	2 H86513	elongation factor
36	5	50.0	185	2 G72110	translacion elonga
37	5	50.0	185	2 D96572	protein f12m16.6 f
38	5	50.0	187	2 JC4806	core protein G - p
39	5	50.0	190	2 H75162	anthranilate synth
40	5	50.0	196	2 A41050	repressor protein
41	5	50.0	199	2 F66832	hypothetical prote
42	5	50.0	200	2 F64217	ribosomal protein
43	5	50.0	201	1 IMPPSR	immunity protein -
44	5	50.0	206	2 A71326	probable V-type AT
45	5	50.0	209	2 S04827	gene 40A protein -
46	5	50.0	211	2 T22122	hypothetical prote
47	5	50.0	217	2 S10212	late 33k protein -
48	5	50.0	217	2 T37859	probable transcrip
49	5	50.0	218	2 C68847	transcription regu
50	5	50.0	221	2 H86860	protein serine/chr
51	5	50.0	227	2 T12797	immunity protein d
52	5	50.0	228	2 H71214	hypothetical prote
53	5	50.0	239	2 A27207	lysase kallikrein
54	5	50.0	241	2 S75154	urase accessory p
55	5	50.0	246	2 I40763	hypothetical prote
56	5	50.0	246	2 E81373	hypothetical prote
57	5	50.0	250	2 S62838	hypothetical prote
58	5	50.0	251	2 T45707	CHLOROPHYLL A-B BI
59	5	50.0	252	2 A86449	hypothetical prote
60	5	50.0	253	2 E71198	hypothetical prote
61	5	50.0	253	2 A75159	protein-1-isoaspar
62	5	50.0	254	2 T23323	hypothetical prote
63	5	50.0	260	2 T18909	hypothetical prote
64	5	50.0	263	2 C69887	hypothetical prote
65	5	50.0	271	2 T16590	hypothetical prote
66	5	50.0	276	2 S75249	esterase s110992 -
67	5	50.0	276	2 T29894	hypothetical prote
68	5	50.0	287	2 E75159	hypothetical prote
69	5	50.0	288	2 A81009	hypothetical prote
70	5	50.0	289	2 C70400	ferredoxin oxidore
71	5	50.0	291	2 S42420	replication protei
72	5	50.0	293	2 T09758	myb-related protei
73	5	50.0	293	2 A82690	phosphatidylserine
74	5	50.0	296	2 S46018	probable membrane
75	5	50.0	296	2 G84747	AT-hook DNA-bindin
76	5	50.0	305	2 JN0518	acetyltransferase (E
77	5	50.0	305	2 F83966	dhlydrocorolate deh
78	5	50.0	307	1 S75769	hypothetical prote
79	5	50.0	308	2 E75409	probable antibiocl
80	5	50.0	309	1 A25776	urate oxidase (EC
81	5	50.0	315	2 T25171	hypothetical prote
82	5	50.0	321	2 D70070	transcription regu
83	5	50.0	327	2 JC4195	36k hydrophobic nu
84	5	50.0	327	2 H82554	conserved hypotnet
85	5	50.0	335	2 G75309	lybA protein - Del
86	5	50.0	335	2 T37262	probable tyrosine
87	5	50.0	336	1 B38274	Y box-binding prot
88	5	50.0	337	2 T46742	ornithine carbamoy
89	5	50.0	340	2 D86837	ornithine carbamoy
90	5	50.0	342	2 T45456	probable membrane
91	5	50.0	343	2 T14245	MDH dehydrogenase
92	5	50.0	343	2 H82171	probable multidrug
93	5	50.0	346	2 S56665	tryptophan synthas
94	5	50.0	355	2 C70457	hypothetical prote
95	5	50.0	360	2 T26037	hypothetical prote
96	5	50.0	360	2 S32695	Wnt-2 protein - Ca
97	5	50.0	366	1 MNXRSD	sigma NS protein -
98	5	50.0	366	1 MNXRST	sigma NS protein -
99	5	50.0	366	1 MNXR72	sigma NS protein -
100	5	50.0	367	2 C27401	sigma NS protein -
101	5	50.0	367	2 S46336	env polyprotein -
102	5	50.0	368	2 S06058	MDH dehydrogenase

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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 25-FEB-1999; 99US-0121825.
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PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137228.
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PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
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PR 18-JUN-1999; 99US-0139456.
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PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
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PR 21-JUN-1999; 99US-0139817.
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PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140659.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
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PR 02-JUL-1999; 99US-0142055.
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PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.
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PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
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PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
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PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
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PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
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PR 20-AUG-1999; 99US-0149723.
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PR 23-AUG-1999; 99US-0149930.
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PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.

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Query Match 50.0%; Score 5; DB 21; Length 196;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 PVAPT 5
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Db 32 pvapt 36

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RESULT 49
AAW89834

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ID AAW89834 standard; Protein: 201 AA.

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XX AAW89834;

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DT 18-FEB-1999 (first entry)

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XX Protein encoded by clone c5.
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KW Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis;
KW peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
XX
OS Helicobacter pylori.
XX
PN WO9849314-A2.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-US08487.
XX
PR 14-OCT-1997; 97US-0061958.
PR 25-APR-1997; 97US-0045107.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Chow TP, Fry KE, Lim MY, McAtee CP;
XX WPI; 1999-009433/01.
DR N-PSDB; AAV90768.
XX
PT New Helicobacter pylori antigens and related nucleic acid sequences
PT - useful in serological diagnosis and protective vaccines, providing
PT long-lasting immune response
XX
PS Claim 15; Page 180-181; 402pp; English.
XX
CC The present sequence represents a Helicobacter pylori antigenic protein
CC that is characterised by immunoreactivity with H. pylori-positive
CC antisera. The proteins are highly immunogenic and induce a long-lasting
CC immune response that persists even after antimicrobial treatment. In
CC antibody-detection assays, on sera, plasma, urine, saliva etc., they are
CC highly sensitive and specific. The specification also describes 69
CC previously unrecognised immunogenic cluster families. H. pylori antigens
CC are used to detect H. pylori-specific antibodies, for diagnosing
CC infection or to confirm eradication of infection, and in vaccines to
CC protect against H. pylori infection and related diseases (gastritis,
CC peptic ulcer, gastric adenocarcinoma/lymphoma).
XX
SQ Sequence 201 AA;

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Query Match 50.0%; Score 5; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 6 QEVKK 10
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Db 139 gevkk 143

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RESULT 50
AAG04638

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ID AAG04638 standard; Protein: 217 AA.

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XX AAG04638;

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DT 17-OCT-2000 (first entry)

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XX Arabidopsis thaliana protein fragment SEQ ID NO: 738.

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XX Protein identification: signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

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XX Arabidopsis thaliana.

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XX EP1033405-A2.

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XX 06-SEP-2000.

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XX 25-FEB-2000; 2000EP-0301439.
XX

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XX AC MAG59940;
XX 18-OCT-2000 (first entry)
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XX Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PE 25-FEB-2000; 2000EP-0301439.
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PR 25-MAR-1999; 99US-0126264.
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PR 21-APR-1999; 99US-0130449.
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PR	10-AUG-1999;	99US-0147935.			
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PR	13-AUG-1999;	99US-0148565.			
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PR	16-AUG-1999;	99US-0149368.			

Query Match

Best Local Similarity

Matches

5: Conservative

50.0%;

Score 5;

DB 21;

Length 196;

Pred. No. 3.4e+02;

Mismatches 0;

Indels 0;

Gaps 0;

QY

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pvapt 5

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DB

32

pvapt 36

RESULT

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AAC59940

ID AAC59940 standard; Protein: 196 AA.

CC useful for detecting the presence of HCV in a sample, the primers
CC are also useful for HCV genotyping. Proteins encoded by the cDNAs
CC can be used in vaccines for immunising against HCV infection. The
CC proteins may also be used to detect antibodies against HCV in serum,
CC saliva, lymphocytes or other mononuclear cells. The antibodies may be
CC used in the prevention of HCV infection.

XX Sequence 192 AA;

Query Match 50.0%; Score 5; DB 17; Length 192;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 50 pvapt 54

RESULT 46

AAR33986

ID AAR33986 standard; Protein; 193 AA.

XX AAR33986;

XX 26-JUL-1993 (first entry)

XX HCT27 E1 protein.

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Db 50 pvapt 54

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RESULT 47

AAG55984

ID AAG55984 standard; Protein; 196 AA.

XX AAG55984;

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Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

PD 06-SEP-2000.

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PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

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XX 13-SEP-1999 (first entry)
DT Chlamydia pneumoniae transmembrane protein sequence.
DE
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX Chlamydia pneumoniae.
OS
XX WO9927105-A2.
PN
XX 03-JUN-1999.
PD
XX 20-NOV-1998; 98WO-1B01890.
PE
XX 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
XX (GEST ) GENSET.
PA
XX Grifvals R;
PI
XX WPI; 1999-357842/30.
DR
XX Genome sequence of Chlamydia pneumoniae
PT
XX Page 759-760; Disclosure; 1912pp; English.
PS
XX AAY34584-Y35879 represent the proteins encoded by all the open reading
XX frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
CC
XX
XX Sequence 185 AA;
SQ

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Query Match 50.0%; Score 5; DB 20; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 5 TOEVK 9
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DB 57 tqevk 61

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RESULT 44
 AAR69639
 ID AAR69639 standard; Protein; 192 AA.
 XX
 XX AAR69639;
 DT 14-SEP-1995 (first entry)
 DE Hepatitis C virus envelope 1 protein isolate S18.
 XX
 XX Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate S18;
 KW diagnosis; vaccines; antibodies; antisera; gene inhibition.
 XX
 XX Hepatitis C virus.
 OS
 XX WO9501442-A.
 PN
 XX 12-JAN-1995.
 PD
 XX

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PF 28-JUN-1994; 94WO-US07320.
XX
XX 29-JUN-1993; 93US-0086428.
PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Bukh J, Miller RH, Purcell RH;
PI
XX WPI; 1995-061006/08.
DR N-PSDB; AA083850.
XX
XX Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived
PT oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis
PT and in vaccines
XX
XX Claim 3; Page 84; 186pp; English.
PS
XX AA083850 encodes AAR69639 hepatitis C virus (HCV) envelope 1 (E1)
XX protein isolate S18, both can be used for the diagnosis of HCV
XX infection, and in the prodn. of anti-HCV vaccines; antibodies
CC and antisera. The cDNA may also be used to inhibit the expression
CC of the HCV E1 gene.
CC
XX
XX Sequence 192 AA;
SQ

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Query Match 50.0%; Score 5; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 PVAPT 5
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DB 50 pvapt 54

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RESULT 45
 AAR89510
 ID AAR89510 standard; Protein; 192 AA.
 XX
 XX AAR89510;
 AC
 XX 30-SEP-1996 (first entry)
 DT
 XX Hepatitis C virus isolate S18 envelope 1 protein.
 DE
 XX HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 KW hepatitis.
 KW
 XX Hepatitis C virus.
 OS
 XX WO9605315-A2.
 PN
 XX 22-FEB-1996.
 PD
 XX 15-AUG-1995; 95WO-US10398.
 PE
 XX 15-AUG-1994; 94US-0290665.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US SEC DEPT HEALTH.
 XX
 XX Bukh J, Miller RH, Purcell RH;
 PI
 XX WPI; 1996-139709/14.
 DR N-PSDB; AAT16564.
 XX
 XX DNA and amino acid sequence of HCV envelope 1 and core proteins -
 PT used to determine HCV genotype and as vaccines against HCV infection
 PT
 XX Claim 2; Page 114; 340pp; English.
 PS
 XX AAR89505-R89555 are HCV E1 (envelope-1) proteins derived from 51 HCV
 CC isolates. Isolated cDNA sequences are used for the prodn. of primers
 CC

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Query Match 50.0%; Score 5; DB 21; Length 180;
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OY 1 PVAPT 5
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 Db 16 prvapt 20

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RESULT 42
AAB25268
ID AAB25268 standard; Protein; 181 AA.
XX
AC AAB25268;
XX
DT 27-NOV-2000 (first entry)
XX
DE Eucalyptus grandis cell signalling involved protein SEQ ID NO:587.
XX
KW Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
KW plant cell signalling; modulation; transgenic plant; pathogen; growth;
KW environmental change; development; cell proliferation; differentiation;
KW elongation; survival; disease resistance; nutrient metabolism.
XX
OS Eucalyptus grandis.
XX
PN MO200042171-A1.
XX
PD 20-JUL-2000.
XX
PF 11-JAN-2000; 2000MO-US00724.
XX
PR 12-JAN-1999; 990S-0228986.
PR 01-NOV-1999; 990S-0162866.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PI Strabala TJ, Nieuwenhuizen NJ;
XX
DR WPI; 2000-476052/41.
XX
PT Isolated polynucleotide encoding a polypeptide involved in cell
PT signalling used for generating transgenic plants with modified responses
PT to external signals -
XX
PS Claim 3: Page 263; 527pp; English.
XX
CC AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
CC and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
CC pine (Pinus radiata also known as Monterey pine). The protein sequences
CC are involved in cell signalling. The polynucleotide and protein
CC sequences can be used to modify the response of plant cells to external
CC signals e.g. environmental changes or pathogens during the growth and
CC development of a plant. They can be used to modify cell proliferation,
CC differentiation, elongation and survival, resistance to disease and
CC nutrient metabolism. Examples of modifications which can be produced are
CC altered fruit ripening and senescence of leaves and flowers e.g. to
CC delay senescence and prolong the life of cut flowers or enhance
CC senescence of reproductive organs to engineer sterile plants. Other
CC modifications can be used to delay senescence in selected cell types or
CC organs providing fruit and vegetables which have a longer shelf life
CC between harvest and consumption, or to decrease branching frequency in
CC forest tree species giving long stretches of valuable knot-free clear
CC wood which can be used in solid timber furniture and veneers.
XX
SQ Sequence 181 AA;

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Query Match 50.0%; Score 5; DB 21; Length 181;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PROEV 8
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 Db 162 prgev 166

RESULT 43
 AAY34781
 ID AAY34781 standard; Protein; 185 AA.
 XX
 AC AAY34781;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 pVApT 5
| | | | |
Db 16 pVapT 20

RESULT 41
AAG59941
ID AAG59941 standard; Protein: 160 AA.

XX AAG59941;
AC
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77586.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
KW
XX Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
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PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

Query Match 50.0%; Score 5; DB 21; Length 180;
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Query Match 50.0%; Score 5; DB 21; Length 179;
Best local similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 pvapt 19

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AC AGS5985;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 71882.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match 50.0%; Score 5; DB 21; Length 179;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 15 pvapt 19

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AC AAG59942;
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XX 18-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
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Query Match      50.0%; Score 5; DB 21; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 95 pvapt 99

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RESULT 37
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AC AAM89904;
XX
DT 18-FEB-1999 (first entry)
XX
DE Antigen from cluster 31.
XX
KW Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis;
KW peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
XX
OS Helicobacter pylori.
XX
PN W09849314-A2.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98MO-US08487.
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PR 14-OCT-1997; 97US-0061958.
PR 25-APR-1997; 97US-0045107.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Chow TP, Fry KE, Llm MY, Mcatee CP;
XX
DR WPI; 1999-009433/01.
XX
PT New Helicobacter pylori antigens and related nucleic acid sequences
- useful in serological diagnosis and protective vaccines, providing

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PT Long-lasting immune response
XX
PS Claim 1; Page 240; 402pp; English.
XX
CC The present sequence represents a Helicobacter pylori antigenic protein
CC that is characterised by immunoreactivity with H. pylori-positive
CC antisera. The proteins are highly immunogenic and induce a long-lasting
CC immune response that persists even after antimicrobial treatment. In
CC antibody-detection assays, on sera, plasma, urine, saliva etc., they are
CC highly sensitive and specific. The specification also describes 69
CC previously unrecognised immunogenic cluster families. H. pylori antigens
CC are used to detect H. pylori-specific antibodies, for diagnosing
CC infection or to confirm eradication of infection, and in vaccines to
CC protect against H. pylori infection and related diseases (gastritis,
CC peptic ulcer, gastric adenocarcinoma/lymphoma).
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SQ Sequence 174 AA;

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Query Match      50.0%; Score 5; DB 20; Length 174;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 38
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AC AAG55986;
XX
DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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PN EP1033405-A2.
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termination sequence.

XX Arabidopsis thaliana.

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termination sequence.
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XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX 17-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

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PN EP1033405-A2.

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PD 06-SEP-2000.

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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 24-SEP-1999; 99US-0156559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159331.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.

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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match          50.0%; Score 5; DB 21; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 6 QEVKK 10
Db 63 gevkk 67

```

RESULT 31

```

ID AAY36760 standard; Protein; 135 AA.

```

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AC AAY36760;

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DT 07-OCT-1999 (first entry)

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```

DE Amino acid sequence of a Chlamydia trachomatis protein.

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KW Vaccine; eye disease; conventional trachoma; nongonococcal urethritis; epididymitis; genital disease; perinephritis;

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KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;

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KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis.

```

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XX Chlamydia trachomatis.

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PN WO9928475-A2.

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PD 10-JUN-1999.

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PF 27-NOV-1998; 98WO-IB01939.

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PR 04-NOV-1998; 98US-0107077.

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PR 28-NOV-1997; 97FR-0015041.

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```

PR 17-DEC-1997; 97FR-0016034.

```

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XX (GEST ) GENSET.

```

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PI Griffais R;

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DR WPI; 1999-371125/31.

```

```

XX Genome sequence of Chlamydia trachomatis

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PT Disclosure; Page 662-663; 1755pp; English.

```

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XX AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome

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CC of Chlamydia trachomatis (see AAY36754). The polypeptides can be used as

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CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences

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CC can also be used to control growth of the microorganism. Chlamydia

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CC trachomatis is responsible for a large number of diseases, e.g. eye

```

```

CC diseases such as conventional trachoma, nongonococcal urethritis,

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CC paratrachoma, and inclusion conjunctivitis; genital diseases such as

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```

CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,

```

```

CC perinephritis, Bartholinitis; pneumopathy in breast feeding infants;

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```

CC and venereal lymphogranulomatosis. The polypeptides of the invention

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CC may be of use in treating these diseases.

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XX Sequence 135 AA;

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SQ

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Query Match          50.0%; Score 5; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 6 QEVKK 10
Db 63 gevkk 67

```

C. pneumoniae causes respiratory disease such as pneumonia and
bronchitis and is thought to be a contributing factor in heart
disease, sarcoidosis, sinusitis, purulent otitis media, erythema
nodosum or pharyngitis. The polypeptides encoded by the open reading
frames of the C. pneumoniae genome (see AAI34564-Y35879) can be used in
immunogenic compositions as vaccines. Vectors containing C. pneumoniae
nucleotide sequences can also be used as immunogenic compositions,
especially where the vector directs the expression of a neutralising
epitope of C. pneumoniae.

Sequence 132 AA:

Query Match 50.0%; Score 5; DB 20; Length 132;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QEVKK 10
|||||
Db 39 gevkk 43

RESULT 30
AAG59953
ID AAG59953 standard; Protein: 134 AA.

XX AAG59953;
AC
XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77605.
DE
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
OS
XX EPI033405-A2.
PN
XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 06-MAY-1999; 99US-0132486.
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PR 20-MAY-1999; 99US-0135124.
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PR 25-MAY-1999; 99US-0136021.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 18-JUN-1999; 99US-0139454.
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PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.

PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
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 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160776.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161982.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 50.0%; Score 5; DB 21; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
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Db 68 pvapt 72

RESULT 28

AAW77657
 ID AAW77657 standard; Protein: 130 AA.

XX AC AAW77657;

XX DT 30-OCT-1998 (first entry)

XX DE Staphylococcus aureus protein of unknown function.

XX KM Staphylococcus aureus protein: immune response induction; eye infection;

KM antibody production; T-cell immune response; gastrointestinal infection;

KM respiratory infection; inhibitory; bacterial infection; cardiac infection;

KM central nervous system; kidney infection; urinary tract infection;

KM antimicrobial compound identification; broad spectrum antibiotic;

XX OS Staphylococcus aureus.

XX XX Staphylococcus aureus.

XX XX Staphylococcus aureus.

XX XX Staphylococcus aureus.

XX XX Staphylococcus aureus.

XX XX Staphylococcus aureus.

XX XX Staphylococcus aureus.

XX XX Staphylococcus aureus.

XX XX Staphylococcus aureus.

PI Black MT, Burnham MKR, Hodgson JE, Knowles DJC;
 PI Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M;
 PI Ward JM;

XX XX
 DR MPI: 1998-252940/23.
 DR N-PSDB; AAV53451.
 XX XX
 PT New nucleic acid sequences from Staphylococcus aureus MCH029 -
 PT useful in vaccines and for treatment of bacterial infections of e.g.
 PT respiratory tract and central nervous system
 XX XX
 PS Claim 11; Page 312; 390pp; English.
 XX XX
 CC This sequence represents a Staphylococcus aureus protein of unknown
 CC function, and is encoded by a DNA sequence of the invention.
 CC The DNA sequences were isolated from Staphylococcus aureus MCH029
 CC (NCIMB 40771). Host cells containing the DNA sequences are used to
 CC produce polypeptides or fragments. The proteins are used in the treatment
 CC of disease, for inducing an immune response by administering them, to
 CC produce antibody and/or T-cell immune response. Antagonists of the
 CC proteins are used for the inhibition of bacterial polypeptides.
 CC Conditions which may be treated include bacterial infections, especially
 CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
 CC urinary tract, skin, bones and joints. The proteins can also be used to
 CC identify antimicrobial compounds which are broad spectrum antibiotics,
 CC especially useful in the treatment of H. pylori infection.
 XX XX
 SQ Sequence 130 AA;

Query Match 50.0%; Score 5; DB 19; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPRO 6
 |||||

Db 108 vaptq 112

RESULT 29

AAV35155
 ID AAV35155 standard; Protein: 132 AA.

XX AC AAV35155;

XX DT 13-SEP-1999 (first entry)

XX DE Chlamydia pneumoniae transmembrane protein sequence.

XX KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis;

XX KM vaccine; neutralising epitope.

XX OS Chlamydia pneumoniae.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

XX XX WO9927105-A2.

CC AAV34584-Y35879 represent the proteins encoded by all the open reading
 CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.

PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
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PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
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PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
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PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139763.
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PR 01-JUL-1999; 99US-0142153.
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PR 14-JUL-1999; 99US-0143624.
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PR 06-OCT-1999; 99US-0157865.
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PR 19-JUL-1999; 99US-0144334.
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KW      hybridisation assay; genetic mapping; gene expression control; promoter;
KM      termination sequence; corn.
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OS      Zea mays subsp. mays.
XX      PN
XX      EPI033405-A2.
XX      PD
XX      06-SEP-2000.
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DT 18-OCT-2000 (first entry)

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.

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PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 50.0%; Score 5; DB 21; Length 114;
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Db 43 gevkk 47

RESULT 25

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ID AA659954;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 77606.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS Arabidopsis thaliana.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
Query Match 50.0%; Score 5; DB 21; Length 110;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GEVKK 10
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Db 39 gevkk 43

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AC AAG12210;
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XX 17-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 11234.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay: genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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XX AAG59955;
AC 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 77607.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
XX
XX EPI033405-A2.
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XX 06-SEP-2000.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 50.0%; Score 5; DB 21; Length 110;
Best Local Similarity 100.0%; Pred. No. 26+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

OY 6 OEYK 10
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Db 39 gevkk 43

RESULT 23
AAG59955
ID AAG59955 standard; Protein; 110 AA.

RESULT 21
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ID AAW75784 standard; Protein: 107 AA.
XX
AC AAW75784;
XX
DT 18-JAN-1999 (first entry)
XX
DE Human lymphocyte surface receptor cytoplasmic domain.
XX
XX TAC1; transmembrane activator and CAML-interactor;
XX calcium signal-modulating cyclophilin ligand: human;
XX lymphocyte surface receptor; human: B-cell; B lymphocyte;
XX infection; cancer; rheumatoid arthritis; autoimmune disease;
XX glomerulonephritis; immunosuppressive; graft versus host disease;
XX transplant rejection; therapy; signal transduction.
XX
OS Homo sapiens.
XX
PN WO9839361-A1.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US04270.
XX
PR 03-MAR-1997; 97US-0810572.
XX
PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Bram RJ, Von Bulow G;
XX
DR WPI: 1998-506346/43.
XX N-PSDB: AAV57329.
XX
PT New isolated transmembrane activator protein - used to develop
PT products for treating e.g. infections, cancers, autoimmune and
PT inflammatory conditions, transplant rejection or graft-versus-host
PT disease
XX
PS Claim 6; Page 72; 89p; English.
XX
XX This polypeptide comprises the C-terminal, i.e. cytoplasmic,
XX domain of novel human transmembrane activator and CAML-interactor
XX protein TAC1 (see AAW75783). TAC1 is a lymphocyte receptor protein
XX that is involved in the calcium activation pathway. It is normally
XX present in B-lymphocytes, and to a much lesser extent in immature
XX T-lymphocytes, and can therefore be targeted to specifically
XX regulate B cell responses without affecting T cell activity. The
XX cytoplasmic domain of TAC1 mediates signal transduction via
XX Ca2+-dependent and Ca2+-independent mechanisms and includes the
XX CAML-binding region of TAC1. Methods are claimed for identifying a
XX ligand for TAC1 and for identifying immunosuppressive drugs that
XX selectively block the action of B lymphocytes without affecting
XX mature T lymphocytes. TAC1 can be activated to increase immune
XX system activity, e.g. for treating infections or cancers. It can
XX be blocked to provide immunosuppression, e.g. for treating
XX autoimmune and inflammatory conditions such as immune complex-
XX induced vasculitis, glomerulonephritis, haemolytic anaemia,
XX myasthenia gravis, type II collagen-induced arthritis, experimental
XX allergic and hyperacute xenograft rejection, rheumatoid arthritis,
XX systemic lupus erythematosus, transplant rejection, cancer or
XX graft versus host disease.
XX
SO Sequence 107 AA;

Query Match 50.0%; Score 5; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 APTOE 7

Db 53 aptge 57
IIII
RESULT 22
AAG12211
ID AAG12211 standard; Protein: 110 AA.
XX
AC AAG12211;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11235.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123348.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 23-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134221.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
XX 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
XX 16-JUN-1999; 99US-0139452.
XX 16-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.
XX 18-JUN-1999; 99US-0139454.

CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 125
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAX84933 for described uses).

XX
SQ Sequence 87 AA;

Query Match

Best Local Similarity 50.0%; Score 5; DB 20; Length 87;
Matches 5; Conservative 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
Db 60 pvapt 64

RESULT 19

AAY82898
ID AAY82898 standard; Protein: 101 AA.

AC AAY82898;

DT 24-JUL-2000 (first entry)

DE CUB domain from BMP-1 protein of mouse.

XX BPC-1; oncogene; oncogenic; cancer; prostate; bladder; antibody;
KM antisense; vaccine; detection; prognosis; drug screening; BMP-1;
XX mouse.

OS Mus musculus.

PN WO200009691-A2.

PD 24-FEB-2000.

PF 10-AUG-1999; 99WO-US18250.

PR 10-AUG-1998; 98US-0095982.

XX (UROG-) UROGENESYS INC.

PA (AFAR/) AFAR D E.

PA (HUBE/) HUBERT R S.

PA (LEON/) LEONG K.

PA (RAIT/) RAITANO A B.

PA (SAFE/) SAFRAN D C.

PA (JAKO/) JAKOBOVITS A.

XX Afar DE, Hubert RS, Leong K, Raitano AB, Saffran DC, Jakobovits A;

XX WPI; 2000-206006/18.

XX New isolated BPC-1 polypeptides, useful for developing products for the

XX diagnosis, staging, prognosis and treatment of cancers, particularly

XX prostate or bladder cancer.

XX Disclosure; Figure 3; 79pp; English.

XX BPC-1 polypeptides and polynucleotides can be used for the detection

XX of BPC-1 polypeptides and polynucleotides in biological samples, this

XX is particularly useful for detecting cancers expressing BPC-1, e.g.

XX prostate cancer or bladder cancer. Antibodies directed against BPC-1

XX or antisense polynucleotides can be used for treating such cancers.

XX The BPC-1 polypeptides can also be used in vaccines for treating or

XX inhibiting the development of a cancer expressing BPC-1. The

XX polypeptides and polynucleotides can also be used for detection,

XX prognosis, drug screening and predicting susceptibility to developing

XX cancer. In normal human tissues BPC-1 is only expressed in certain

XX tissues of the brain, however, it is expressed at high levels in

CC prostate cancer cells and bladder cancer cells. The BPC-1 polypeptide
CC comprises a CUB domain which is expressed in prostate and bladder
CC carcinoma cells and which shows sequence similarity with CUB domains
CC from other known proteins. This is a CUB domain from the BMP-1
CC protein of a mouse. It shows 36.3% identity with the
CC BPC-1 CUB domain 3 in 102 residues overlap.

XX
SQ Sequence 101 AA;

Query Match

Best Local Similarity 50.0%; Score 5; DB 21; Length 101;
Matches 5; Conservative 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAPQ 6
Db 23 vapq 27

RESULT 20

AAB72875
ID AAB72875 standard; Protein: 102 AA.

AC AAB72875;

DT 09-MAY-2001 (first entry)

DE Human p53 A76T/V122A mutated peptide.

XX Human; p53 mutation; mutant; mutein; gene therapy; supertransactivating;
KM cancer.

XX Homo sapiens.

OS Synthetic.

PN WO200109325-A2.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-US20538.

PR 30-JUL-1999; 99US-0146634.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Resnick MA, Inga A;

XX WPI; 2001-123321/13.

XX New isolated mutated human p53 polypeptides for inducing toxicity in a

XX cell, treating cancer and identifying compounds that mimic toxic or

XX supertransactivating mutations.

XX Claim 33; Page -: 144pp; English.

XX The present invention provides a number of peptides derived from the

XX human p53 protein and containing specific mutations. These are useful for

XX isolating supertransactivating and toxic p53 mutants, and for inhibiting

XX cell growth and treating cancer. The present sequence is a peptide

XX derived from the wild-type human p53 protein shown in AAB72878.

XX Note: The present sequence is not shown in the specification but is

XX derived from that given in Genbank acc. no. X02469 (see AAB72878).

XX
SQ Sequence 102 AA;

Query Match

Best Local Similarity 50.0%; Score 5; DB 22; Length 102;
Matches 5; Conservative 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
Db 23 pvapt 27

OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 27 /label= unknown
 FT
 XX MO9856804-A1.
 XX
 XX 17-DEC-1998.
 PD
 XX
 PE 11-JUN-1998; 98WO-US12125.
 XX
 PR 02-OCT-1997; 97US-0061060.
 PR 13-JUN-1997; 97US-0049547.
 PR 13-JUN-1997; 97US-0049548.
 PR 13-JUN-1997; 97US-0049549.
 PR 13-JUN-1997; 97US-0049550.
 PR 13-JUN-1997; 97US-0049606.
 PR 13-JUN-1997; 97US-0049607.
 PR 13-JUN-1997; 97US-0049608.
 PR 13-JUN-1997; 97US-0049609.
 PR 13-JUN-1997; 97US-0049610.
 PR 13-JUN-1997; 97US-0049611.
 PR 13-JUN-1997; 97US-0050566.
 PR 13-JUN-1997; 97US-0050901.
 PR 13-JUN-1997; 97US-0052989.
 PR 08-JUL-1997; 97US-0051919.
 PR 18-AUG-1997; 97US-0055984.
 PR 12-SEP-1997; 97US-0058665.
 PR 12-SEP-1997; 97US-0058668.
 PR 12-SEP-1997; 97US-0058669.
 PR 12-SEP-1997; 97US-0058750.
 PR 12-SEP-1997; 97US-0058971.
 PR 12-SEP-1997; 97US-0058972.
 PR 12-SEP-1997; 97US-0058975.
 PR 02-OCT-1997; 97US-0060834.
 PR 02-OCT-1997; 97US-0060841.
 PR 02-OCT-1997; 97US-0060844.
 PR 02-OCT-1997; 97US-0060865.
 PR 02-OCT-1997; 97US-0061059.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Brewer LA, Ebner R, Ferris AM, Feng P, Greene JM, Laflleur DW;
 PI Moore PA, Nl J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
 PI Yu GL;
 XX
 DR WPI: 1999-080881/07.
 DR N-PSDB: AAX04315.
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 11: Page 266; 380pp; English.
 PS
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAX04302) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 86 novel genes and their fragments (nucleic
 CC acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC polypeptides in a sample or by determining the amount of the new
 CC the new polynucleotides. Specific uses are described for each of the 86
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAX04311 for described uses).
 XX
 S0 Sequence 27 AA:

Query Match 50.0%; Score 5; DB 20; Length 27;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; *Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PVAPT 5.
 Db 9 pvaPT 13
 RESULT 18
 ID AAY27569
 AAAY27569 standard; Protein; 87 AA.
 AC AAY27569;
 XX
 DT 30-JUL-1999 (first entry)
 XX
 DE Human secreted protein encoded by gene No. 3.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN MO9924836-A1.
 XX
 PD 20-MAY-1999.
 XX
 PF 04-NOV-1998; 98WO-US23435.
 XX
 PR 17-NOV-1997; 97US-0066100.
 PR 07-NOV-1997; 97US-0064900.
 PR 07-NOV-1997; 97US-0064908.
 PR 07-NOV-1997; 97US-0064911.
 PR 07-NOV-1997; 97US-0064912.
 PR 07-NOV-1997; 97US-0064983.
 PR 07-NOV-1997; 97US-0064984.
 PR 07-NOV-1997; 97US-0064985.
 PR 07-NOV-1997; 97US-0064987.
 PR 07-NOV-1997; 97US-0064988.
 PR 17-NOV-1997; 97US-0066090.
 PR 17-NOV-1997; 97US-0066094.
 PR 17-NOV-1997; 97US-0066095.
 PR 17-NOV-1997; 97US-0066089.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Carter KC, Ebner R, Endress GA, Feng P, Janat F;
 PI Kyaw H, Laflleur DW, Moore PA, Nl J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Wei Y;
 XX
 DR WPI: 1999-337740/28.
 DR N-PSDB: AAX84935.
 XX
 PT New human secreted proteins and coding sequences useful for treating
 PT disorders of the immune system and hyperproliferative disorders
 XX
 PS Claim 11: Page 350; 507pp; English.
 PS
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAX84924) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 125 novel genes and their fragments (nucleic
 CC acid sequences: AAX84933-X85057; amino acid sequences AAY27567-Y27933)
 CC

CC from a human immunodeficiency virus type 1 (HIV-1) protein. The
 CC immunogenic lipopeptide micelles are used in vaccines, especially
 CC against HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma
 CC or Plasmodium falciparum malaria.
 XX
 SQ Sequence 9 AA;

Query Match 50.0%; Score 5; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TQEVK 9
 |||||
 Db 3 tgevK 7

RESULT 15

AAR54624
 ID AAR54624 standard; Protein; 11 AA.

XX
 AC AAR54624;

XX
 DT 16-JUN-1994 (first entry)

XX
 DE Listeria innocua p60 peptide epitope.

XX
 KM Antibodies; immunoassay; conjugate.

XX
 OS Synthetic.

XX
 PN DE4318450-A.

XX
 PD 16-DEC-1993.

XX
 PF 03-JUN-1993; 93DE-4318450.

XX
 PR 11-JUN-1992; 92DE-4219111.

XX
 PR 25-NOV-1992; 92DE-4239567.

XX
 PA (MERE) MERCK PATENT GMBH.

XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Hubert A, Goebel W, Koehler S;

XX
 DR WPI; 1993-406956/51.

XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection

XX
 PS Disclosure; Fig 5; 19pp; German.

XX
 CC The sequence is that of a Listeria innocua p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species.
 CC
 XX
 SQ Sequence 11 AA;

Query Match 50.0%; Score 5; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 29;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QEVKK 10
 |||||
 Db 7 gevK 11

RESULT 16

AAB72848

ID AAB72848 standard; Protein; 11 AA.

XX
 AC AAB72848;

XX
 DT 09-MAY-2001 (first entry)

XX
 DE Human p53 A76r mutated peptide.

XX
 KM Human: p53 mutation; mutant; mutein; gene therapy; supertransactivating;
 KM cancer.

XX
 OS Homo sapiens.

XX
 PN Synthetic.

XX
 PN WO200109325-A2.

XX
 PD 08-FEB-2001.

XX
 PF 28-JUL-2000; 2000WO-US20538.

XX
 PR 30-JUL-1999; 99US-0146634.

XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
 PI Resnick MA, Inga A;

XX
 DR WPI; 2001-123321/13.

XX
 PT New isolated mutated human p53 polypeptides for inducing toxicity in a
 PT cell, treating cancer and identifying compounds that mimic toxic or
 PT supertransactivating mutations -
 PT
 PS Claim 6; Page -: 14pp; English.

XX
 CC The present invention provides a number of peptides derived from the
 CC human p53 protein and containing specific mutations. These are useful for
 CC isolating supertransactivating and toxic p53 mutants, and for inhibiting
 CC cell growth and treating cancer. The present sequence is a peptide
 CC derived from the wild-type human p53 protein shown in AAB72878.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from that given in Genbank acc. no. X02469 (see AAB72878).
 CC
 XX
 SQ Sequence 11 AA;

Query Match 50.0%; Score 5; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPT 5
 |||||
 Db 3 pvapt 7

RESULT 17

AAW78130
 ID AAW78130 standard; Protein; 27 AA.

XX
 AC AAW78130;

XX
 DT 13-APR-1999 (first entry)

XX
 DE Human secreted protein encoded by gene 5 clone HPBDD36.

XX
 KM Human: secreted protein; fusion protein; gene therapy; protein therapy;
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KM inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX

PT separated by peptide spacers that impart hydrophilicity, useful in
PT vaccines -
XX
PS Disclosure: Page 23; 35pp; French.
XX
CC The invention relates to the generation of a lipopeptide comprising at
CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
CC epitope and at least one lipid residue with (i) the epitopes and lipid
CC portion and (ii) the epitopes, being separated independently by peptide
CC spacers. These spacers comprise sequences of amino acids which carry an
CC overall electrical charge in neutral media to ensure that the
CC lipopeptide is hydrophilic. The peptides AAY5301-Y5349 represents
CC examples of peptide epitopes used to generate the lipopeptides. These are
CC used in therapeutic or prophylactic compositions and vaccines to induce
CC specific immune responses against human immunodeficiency, hepatitis B or
CC papilloma viruses; p53 of melanoma or the malaria parasite.
XX
SQ Sequence 9 AA;

Query Match 50.0%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEVR 9
|||||
Db 3 tqevk 7

RESULT 13
AAY40367
ID AAY40367 standard; peptide: 9 AA.
XX
AC AAY40367;
XX
DT 19-NOV-1999 (first entry)
XX
DE Amino acid sequence of a HIV-1 epitope.
XX
KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
KW vaccine; tumor; infection; immune response; cytokine profile;
KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
KW autoimmune disease.
XX
OS Human immunodeficiency virus type 1.
XX
PN FR2774687-A1.
XX
PD 13-AUG-1999.
XX
PF 06-FEB-1998; 98FR-0001439.
XX
PR 06-FEB-1998; 98FR-0001439.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PA (INSP) INST PASTEUR LILLE.
XX
PI Thiam K, Guillet JG, Ver.Waerde C, Auriault C, Gras MH, Loding E;
XX
DR WPI; 1999-510734/43.
XX
PT New lipopeptide comprising C-terminal interferon-gamma fragment with
PT attached lipophilic groups, used as interferon mimic, e.g. for treating
PT cancer or virus infection
XX
PS Disclosure: Page 41; 53pp; French.
XX
CC AAY40123-140379 represent epitopes that are able to activate cytotoxic
CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
CC B epitopes recognized by corresponding antibodies. The epitopes may be
CC used in the composition of the invention. The specification describes a
CC lipopeptide that has a peptide part derived from mammalian interferon

CC gamma (IFN γ) and one or more lipophilic parts comprising a linear or
CC branched, (un)saturated 4-20C hydrocarbonyl chain or a steroid. The
CC lipopeptide mimics the activity of IFN γ . Compositions comprising the
CC lipopeptide are used to treat or prevent any condition that responds
CC to IFN γ , and as adjuvant for vaccines (particularly those directed
CC against tumors, viral or parasitic infections), to stimulate or
CC (re)orient the immune response between types 1 and 2 cytokine profiles.
CC Particular applications are treatment of infections (particularly
CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
CC (particularly of kidney, cutaneous T cells or ovary, chronic
CC myelogenous leukemia or mesothelioma), allergy; and autoimmune
CC diseases.
XX
SQ Sequence 9 AA;

Query Match 50.0%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOEVR 9
|||||
Db 3 tqevk 7

RESULT 14
AAY26859
ID AAY26859 standard; peptide: 9 AA.
XX
AC AAY26859;
XX
DT 14-SEP-1999 (first entry)
XX
DE HIV-derived lipopeptide epitope #129 for mixed micelles.
XX
KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
KW melanoma; Plasmodium falciparum; malaria.
XX
OS Synthetic.
XX
OS Human immunodeficiency virus type 1.
XX
PN FR2771640-A1.
XX
PD 04-JUN-1999.
XX
PF 03-DEC-1997; 97FR-0015246.
XX
PR 03-DEC-1997; 97FR-0015246.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PA (INSP) INST PASTEUR LILLE.
XX
PI Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;
XX
PI Tartar A, Wieruszski JM;
XX
DR WPI; 1999-349509/30.
XX
PT Immunogenic lipopeptide micelles - comprising lipopeptides
PT containing cytotoxic and helper T-lymphocyte epitopes
XX
PS Disclosure: Page 36; 60pp; French.
XX
CC The invention relates to the generation of mixed micelles or
CC microaggregates for inducing an immune response comprise: (a) a first
CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
CC and at least one lipid unit; and (b) a second lipopeptide comprising at
CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
CC different from that of the first lipopeptide. This peptide represents
CC an example of a lipopeptide epitope used in the invention and is derived


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Db      1 pvpapq 6
      |||||
RESULT  8
ID      AAR45168 standard; Protein: 9 AA.
XX
AC      AAR45168;
XX
DT      16-JUN-1994 (first entry)
XX
DE      Listeria p60 peptide epitope.
XX
KW      Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX
OS      Synthetic.
XX
PN      DE4318450-A.
XX
PD      16-DEC-1993.
XX
PE      03-JUN-1993; 93DE-4318450.
XX
PR      11-JUN-1992; 92DE-4219111.
PR      25-NOV-1992; 92DE-4239567.
XX
PA      (MERE ) MERCK PATENT GMBH.
XX
PI      Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
PI      Hofmann G, Buberl A, Goebel W, Koehler S;
XX
DR      WPI; 1993-406956/51.
XX
PT      New primers for PCR detection of Listeria - including individual
PT      species, also new peptide(s) for raising antibodies for
PT      immunochemical detection
XX
PS      Disclosure: Fig 2; 19pp; German.
XX
CC      The sequence is that of a Listeria p60 peptide epitope which
CC      which may be used in the prodn. of antibodies for the detection
CC      of Listeria by immunoassay (partic. ELISA). It may be used as
CC      part of a method that allows determination of individual Listeria
CC      species, esp. L. monocytogenes.
XX
SQ      Sequence 9 AA:

Query Match      60.0%; Score 6; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 3,4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PVAPRQ 6
      |||||
Db      4 pvpapq 9

RESULT  9
AAR45159
ID      AAR45159 standard; Protein: 20 AA.
XX
AC      AAR45159;
XX
DT      16-JUN-1994 (first entry)
XX
DE      Listeria p60 peptide epitope.
XX
KW      Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers

```

```

FT      Region      1..7
FT      /note= "opt. 0-7 amino acid residues"
FT      Region      14..20
FT      /note= "opt. 0-7 amino acid residues"
XX
PN      DE4318450-A.
XX
PD      16-DEC-1993.
XX
PE      03-JUN-1993; 93DE-4318450.
XX
PR      11-JUN-1992; 92DE-4219111.
PR      25-NOV-1992; 92DE-4239567.
XX
PA      (MERE ) MERCK PATENT GMBH.
XX
PI      Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
PI      Hofmann G, Buberl A, Goebel W, Koehler S;
XX
DR      WPI; 1993-406956/51.
XX
PT      New primers for PCR detection of Listeria - including individual
PT      species, also new peptide(s) for raising antibodies for
PT      immunochemical detection
XX
PS      Claim 3; Page 4; 19pp; German.
XX
CC      The sequence is that of a Listeria p60 peptide epitope which
CC      which may be used in the prodn. of antibodies for the detection
CC      of Listeria by immunoassay (partic. ELISA). It may be used as
CC      part of a method that allows determination of individual Listeria
CC      species, esp. L. monocytogenes.
XX
SQ      Sequence 20 AA:

Query Match      60.0%; Score 6; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4,7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PVAPRQ 6
      |||||
Db      8 pvpapq 13

RESULT  10
AAW98275
ID      AAW98275 standard; Protein: 1230 AA.
XX
AC      AAW98275;
XX
DT      31-MAR-1999 (first entry)
XX
DE      H. pylori GHPD 690 protein.
XX
KW      GHPD protein; Helicobacter infection; gastroduodenal disease; gastritis;
KW      peptic ulcer disease.
XX
OS      Helicobacter pylori.
XX
PN      W09843478-A1.
XX
PD      08-OCT-1998.
XX
PE      01-APR-1998; 98WO-US06371.
XX
PR      29-JUL-1997; 97US-0902615.
PR      01-APR-1997; 97US-0833457.
PR      24-JUN-1997; 97US-0881227.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
PA      (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
XX

```

PA (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 XX
 PI Sharma LR, Van Alstyne D;
 DR WPI: 1995-147431/19.
 XX
 XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 PS Claim 47: Fig 7/10: 98pp; English.
 XX
 XX AAR73913 is the *Listeria monocytogenes* protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 CC NB: Identified by matching corresponding MRHAS peptides.
 CC
 SQ Sequence 484 AA:

Query Match 100.0%; Score 10; DB 16; Length 484;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
 |||||
 DB 148 pvapltgevk 157

RESULT 6
 AAR73903
 ID AAR73903 standard; peptide; 7 AA.
 XX
 AC AAR73903;
 XX
 DT 05-DEC-1995 (first entry)
 XX
 DE *Listeria monocytogenes* protein p60 precursor peptide 151-157.
 XX
 KM *Listeria monocytogenes*; protein p60 precursor; vaccine;
 KM meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KM immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KM viral; peptide 151-157.
 XX
 XX *Listeria monocytogenes*.
 OS
 XX
 PN WO9509232-A.
 PN
 XX
 PD 06-APR-1995.
 PD
 XX
 PF 28-SEP-1994; 94WO-CA00516.
 PF
 XX
 PR 28-SEP-1993; 93US-0127499.
 PR
 XX
 PA (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 XX Sharma LR, Van Alstyne D;
 PI
 XX
 DR WPI: 1995-147431/19.
 DR
 XX
 XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX

PS Claim 35; Page 76; 98pp; English.
 XX
 XX AAR73913 is the *Listeria monocytogenes* protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 CC
 SQ Sequence 7 AA:

Query Match 70.0%; Score 7; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PTOEVKK 10
 |||||
 DB 1 ptgevk 7

RESULT 7
 AAR54615
 ID AAR54615 standard; Protein; 6 AA.
 XX
 AC AAR54615;
 XX
 DT 16-JUN-1994 (first entry)
 DT
 XX
 DE *Listeria* p60 peptide epitope.
 DE
 XX
 KM *Listeria monocytogenes*; antibodies; immunoassay; conjugate.
 KM
 XX
 OS Synthetic.
 OS
 PN DE4318450-A.
 PN
 XX
 PD 16-DEC-1993.
 PD
 XX
 PF 03-JUN-1993; 93DE-4318450.
 PF
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR
 XX
 PR 25-NOV-1992; 92DE-4239567.
 PR
 XX
 PA (MERE) MERCK PATENT GMBH.
 PA
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 PI
 XX
 DR WPI: 1993-406956/51.
 DR
 XX
 XX New primers for PCR detection of *Listeria* - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PT
 XX
 PS Disclosure; Page 3; 19pp; German.
 PS
 XX
 CC The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 CC
 SQ Sequence 6 AA:

Query Match 60.0%; Score 6; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTO 6

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
 |||||
 DB 3 PVAPLQEVKK 12

RESULT 3

AA73891
 ID AAR73891 standard; peptide: 21 AA.

XX AAR73891;

XX AC

XX DT 05-DEC-1995 (first entry)

XX DE Listeria monocytogenes protein P60 precursor peptide 144-164.

XX KW Listeria monocytogenes; protein P60 precursor; vaccine;

XX KM meningitis related homologous antigenic sequence; MRHAS; RV-1;

XX OS Listeria monocytogenes.

XX PN WO9509232-A.

XX PD 06-APR-1995.

XX PF 28-SEP-1994; 94WO-CA00516.

XX PR 28-SEP-1993; 93US-0127499.

XX PA (SHAR/) SHARMA L. R.

XX PI (VALS/) VAN ALSTYNE D.

XX PI Sharma LR, Van Alstyne D;

XX DR WPI: 1995-147431/19.

XX PT New peptide(s) and corresp. antibodies for the treatment of

XX PS Claim 34; Page 74; 98pp; English.

XX CC AAR73913 is the Listeria monocytogenes protein P60 precursor. It

XX CC contains the meningitis related antigenic sequences (MRHAS) claimed

XX CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a

XX CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The

XX CC claimed MRHAS peptides may be used in immunoassays to diagnose the

XX CC presence of bacterial and/or viral meningitis agents in a sample,

XX CC or in prophylactic and therapeutic meningitis treatments. The

XX CC peptides may also be used as vaccines against meningitis.

XX SO Sequence 21 AA;

OY 1 PVAPTOEVKK 10
 |||||
 DB 5 PVAPLQEVKK 14

RESULT 4

AA75178
 ID AAR45178 standard; protein: 478 AA.

XX AC AAR45178;

XX XX

DT 16-JUN-1994 (first entry)

XX DE Listeria p60 protein.

XX KW Immunogenic polypeptide; antibodies; immunoassay; conjugate.

XX OS Listeria monocytogenes.

XX PN DE4318450-A.

XX PD 16-DEC-1993.

XX PF 03-JUN-1993; 93DE-4318450.

XX PR 11-JUN-1992; 92DE-4239111.

XX PA 25-NOV-1992; 92DE-4239567.

XX PI (MERE) MERCK PATENT GMBH.

XX PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;

XX PI Hofmann G, Buber A, Goebel W, Koehler S;

XX DR WPI: 1993-406956/51.

XX PT New primers for PCR detection of Listeria - including individual

XX PS Disclosure: Fig 4; 19pp; German.

XX CC The sequence is that of the Listeria p60 protein. Antibodies

XX CC generated against the protein can be used in the detection

XX CC of Listeria by immunoassay (partic. ELISA). The detection method

XX CC allows determination of individual Listeria species, esp.

XX CC L. monocytogenes.

XX SO Sequence 478 AA;

OY 1 PVAPTOEVKK 10
 |||||
 DB 148 PVAPLQEVKK 157

XX AC AAR73913;

XX DT 05-DEC-1995 (first entry)

XX DE Listeria monocytogenes protein P60 precursor.

XX KW Listeria monocytogenes; protein P60 precursor; vaccine;

XX KM meningitis related homologous antigenic sequence; MRHAS; RV-1;

XX OS Listeria monocytogenes.

XX PN WO9509232-A.

XX PD 06-APR-1995.

XX PF 28-SEP-1994; 94WO-CA00516.

XX PR 28-SEP-1993; 93US-0127499.

XX XX

961	4	40.0	124	16	AA075610	VH Fab M556-2 bind
962	4	40.0	124	16	AA075609	VH Fab H4H1-8 bind
963	4	40.0	124	16	AA075608	VH Fab H4H1-7 bind
964	4	40.0	124	16	AA075607	VH Fab H4H1-6 bind
965	4	40.0	124	16	AA075605	VH Fab H4H1-3 bind
966	4	40.0	124	16	AA075606	VH Fab H4H1-5 bind
967	4	40.0	124	16	AA075606	VH Fab M74 binds t
968	4	40.0	124	16	AA075569	VH Fab 3b1 binds t
969	4	40.0	124	16	AA075570	VH Fab 3b3 binds t
970	4	40.0	124	16	AA075572	VH Fab 3b9 binds t
971	4	40.0	124	16	AA075604	VH Fab H4H1-1 bind
972	4	40.0	124	16	AA075638	VH Fab H31 binds t
973	4	40.0	124	16	AA075639	VH Fab H33 binds t
974	4	40.0	124	16	AA075640	VH Fab H101 binds
975	4	40.0	124	16	AA075641	VH Fab H103 binds
976	4	40.0	124	17	AA001306	VH region of HIV n
977	4	40.0	124	17	AA001309	VH region of HIV n
978	4	40.0	124	17	AA001310	VH region of HIV n
979	4	40.0	124	17	AA001311	VH region of HIV n
980	4	40.0	124	17	AA001304	VH region of HIV n
981	4	40.0	124	17	AA001305	VH region of HIV n
982	4	40.0	124	17	AA001246	VH region of HIV n
983	4	40.0	124	17	AA001247	VH region of HIV n
984	4	40.0	124	17	AA001227	VH region of HIV n
985	4	40.0	124	18	AA033607	Human secreted pro
986	4	40.0	124	19	AA056732	Nucellus specific
987	4	40.0	124	20	AA074122	Human prostate tum
988	4	40.0	124	20	AA050146	Antibody F19 human
989	4	40.0	124	20	AA050147	Antibody F19 human
990	4	40.0	124	20	AA050148	Antibody F19 human
991	4	40.0	124	20	AA050149	Antibody F19 human
992	4	40.0	124	20	AA050150	Antibody F19 human
993	4	40.0	124	20	AA060074	Human endometrium
994	4	40.0	124	20	AA037522	Amino acid sequenc
995	4	40.0	124	21	AA010230	Human fetal kidney
996	4	40.0	124	21	AA037466	Arabidopsis thalia
997	4	40.0	124	21	AA095097	Anti-gp120 antibod
998	4	40.0	124	21	AA095098	Anti-gp120 antibod
999	4	40.0	124	21	AA095099	Anti-gp120 antibod
1000	4	40.0	124	21	AA095156	Anti-gp120 HC3 hea

ALIGNMENTS

RESULT 1

AA045173
ID AA045173 standard; Protein; 10 AA.

XX	AA045173;	
AC		
DT	16-JUN-1994 (first entry)	
XX		
DE	Listeria p60 peptide epitope.	
XX		
KW	Listeria monocytogenes; antibodies; immunoassay; conjugate.	
XX		
OS	Synthetic.	
XX		
PN	DE0318450-A.	
XX		
PD	16-DEC-1993.	
XX		
PF	03-JUN-1993: 93DE-4318450.	
XX		
PR	11-JUN-1992: 92DE-4219111.	
XX		
PR	25-NOV-1992: 92DE-4239567.	
XX		
PA	(MERE) MERCK PATENT GMBH.	
XX		
PI	Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;	
XX	Hofmann G, Buber A, Goebel W, Koehler S;	
XX		

DR	WPI: 1993-406956/51.	
XX		
PT	New primers for PCR detection of Listeria - including individual	
XX	species; also new peptide(s) for raising antibodies for	
PT	immunochemical detection	
XX		
PS	Disclosure; Fig 2; 19pp; German.	
XX		
CC	The sequence is that of a Listeria p60 peptide epitope which	
CC	which may be used in the prodn. of antibodies for the detection	
CC	of Listeria by immunoassay (partic. ELISA). It may be used as	
CC	part of a method that allows determination of individual Listeria	
CC	species, esp. L. monocytogenes.	
XX		
SO	Sequence 10 AA;	

QY	1 PVAPTOGVKK 10	
DB	1 PVAPTOGVKK 10	

RESULT 2

AA045172
ID AA045172 standard; Protein; 12 AA.

XX	AA045172;	
AC		
DT	16-JUN-1994 (first entry)	
XX		
DE	Listeria p60 peptide epitope.	
XX		
KW	Listeria monocytogenes; antibodies; immunoassay; conjugate.	
XX		
OS	Synthetic.	
XX		
PN	DE0318450-A.	
XX		
PD	16-DEC-1993.	
XX		
PF	03-JUN-1993: 93DE-4318450.	
XX		
PR	11-JUN-1992: 92DE-4219111.	
XX		
PR	25-NOV-1992: 92DE-4239567.	
XX		
PA	(MERE) MERCK PATENT GMBH.	
XX		
PI	Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;	
XX	Hofmann G, Buber A, Goebel W, Koehler S;	
XX		
DR	WPI: 1993-406956/51.	
XX		
PT	New primers for PCR detection of Listeria - including individual	
PT	species; also new peptide(s) for raising antibodies for	
PT	immunochemical detection	
XX		
PS	Disclosure; Fig 2; 19pp; German.	
XX		
CC	The sequence is that of a Listeria p60 peptide epitope which	
CC	which may be used in the prodn. of antibodies for the detection	
CC	of Listeria by immunoassay (partic. ELISA). It may be used as	
CC	part of a method that allows determination of individual Listeria	
CC	species, esp. L. monocytogenes.	
XX		
SO	Sequence 12 AA;	

Query Match	100.0%;	Score 10;	DB 14;	Length 12;
Best Local Similarity	100.0%;	Pred. No. 0.00024;		
		Matches 10;	Conservative 0;	Mismatches 0;
			Indels 0;	Gaps 0;

815	4	40.0	117	22	AAB69685	Humanised M195 ant	888	4	40.0	121	17	AAR93611	Kaposi's sarcoma a
816	4	40.0	117	22	AAB69697	Humanised AF2 anti	889	4	40.0	121	17	AAR88504	VHmu for antibody
817	4	40.0	117	22	AAB69698	Human Eu antibody	890	4	40.0	121	18	AAW13512	Anti-melanoma anti
818	4	40.0	118	13	AAR22569	Heavy chain VH15.4	891	4	40.0	121	19	AAW53584	Heavy chain of a h
819	4	40.0	118	13	AAR22421	Antibody produced	892	4	40.0	121	19	AAW53991	Anti-CD4 antibody
820	4	40.0	118	13	AAR28742	Heavy chain variab	893	4	40.0	121	20	AAV49236	N-terminal Cbpa se
821	4	40.0	118	14	AAR37611	hIL2R Ab H chain V	894	4	40.0	121	20	AAV32108	Choline binding pr
822	4	40.0	118	15	AAR61096	Human cancer cell	895	4	40.0	121	20	AAV37740	Chlamydia trachoma
823	4	40.0	118	15	AAR54758	Humanised HMFG1 he	896	4	40.0	121	21	AAW53900	Human colon cancer
824	4	40.0	118	15	AAR55126	Mouse-human chimr	897	4	40.0	121	21	AAW51682	Human secreted pro
825	4	40.0	118	15	AAR60305	Chimeric anti HIV	898	4	40.0	121	21	AAW14231	Arabisdopsis thalia
826	4	40.0	118	15	AAR63768	Humanised H chain	899	4	40.0	121	21	AAW18529	Zea mays protein f
827	4	40.0	118	16	AAR77184	Chimeric protein g	900	4	40.0	121	21	AAW33951	Arabisdopsis thalia
828	4	40.0	118	16	AAW27528	Heavy chain variab	901	4	40.0	121	21	AAW61696	Arabisdopsis thalia
829	4	40.0	118	18	AAW13516	Anti-melanoma anti	902	4	40.0	121	21	AAW00034	Human secreted pro
830	4	40.0	118	20	AAV30188	Amino acid sequenc	903	4	40.0	121	21	AAW00049	Human secreted pro
831	4	40.0	118	20	AAV30188	Arabisdopsis thalia	904	4	40.0	121	21	AAW00059	Human secreted pro
832	4	40.0	118	21	AAV71444	Humanised B9 antib	905	4	40.0	121	21	AAW32383	Pluripotent cell m
833	4	40.0	118	21	AAV71444	Human secreted pro	906	4	40.0	121	22	AAW69668	Humanised Fd138-80
834	4	40.0	118	21	AAV99558	Human Lh13 monoclo	907	4	40.0	122	10	AAW93697	Protein encoded by
835	4	40.0	118	21	AAV56679	Anti-integrin Mab	908	4	40.0	122	15	AAW60102	Mab heavy chain v1
836	4	40.0	118	21	AAV56681	Anti-erythropoiet	909	4	40.0	122	16	AAW75407	HIV-3 strain ANT70
837	4	40.0	119	13	AAR24560	Human x mouse modi	910	4	40.0	122	16	AAW76964	HSV-neutralising a
838	4	40.0	119	13	AAR24561	Human x mouse modi	911	4	40.0	122	19	AAW41087	Human matrix metel
839	4	40.0	119	13	AAR24562	Human x mouse modi	912	4	40.0	122	20	AAW90289	Human anti-GPIIb/I
840	4	40.0	119	13	AAR25730	Humanised VH regio	913	4	40.0	122	20	AAW90292	Human anti-GPIIb/I
841	4	40.0	119	14	AAR53364	N-terminally trunc	914	4	40.0	122	21	AAW03720	Human secreted pro
842	4	40.0	119	15	AAW55124	Mouse-human chimr	915	4	40.0	122	21	AAW70603	VH region of human
843	4	40.0	119	15	AAW60303	Chimeric anti HIV	916	4	40.0	122	22	AAW69691	Humanised CMV5 ant
844	4	40.0	119	16	AAR81324	Humanized VLA-4 an	917	4	40.0	123	16	AAW5571	VH Fab 3b4 binds t
845	4	40.0	119	16	AAR81325	Humanized VLA-4 an	918	4	40.0	123	16	AAR81323	Humanized VLA-4 an
846	4	40.0	119	16	AAR81331	Human 2*CL antibod	919	4	40.0	123	17	AAR92992	Humanised antibody
847	4	40.0	119	18	AAW22425	Humanised alpha-4	920	4	40.0	123	18	AAW22413	Humanised alpha-4
848	4	40.0	119	18	AAW22426	Anti-melanoma anti	921	4	40.0	123	18	AAW19881	CEA-specific antib
849	4	40.0	119	18	AAW13536	Anti-melanoma anti	922	4	40.0	123	18	AAW19886	CEA-specific antib
850	4	40.0	119	19	AAW49813	Amino acid sequenc	923	4	40.0	123	18	AAW19887	CEA-specific antib
851	4	40.0	119	19	AAW58503	Human heavy chain	924	4	40.0	123	18	AAW19888	CEA-specific antib
852	4	40.0	119	19	AAW53590	Humanised antibody	925	4	40.0	123	18	AAW19889	CEA-specific antib
853	4	40.0	119	19	AAW53591	Humanised antibody	926	4	40.0	123	19	AAW79228	Heavy chain variab
854	4	40.0	119	19	AAW53992	Anti-CD4 antibody	927	4	40.0	123	19	AAW76129	Human ICR-1.1 V-H
855	4	40.0	119	20	AAW95451	N-terminally trunc	928	4	40.0	123	19	AAW76125	Human ICR-8.1 V-H
856	4	40.0	119	21	AAW56018	Arabisdopsis thalia	929	4	40.0	123	19	AAW71259	Humanised murine a
857	4	40.0	119	21	AAW71241	Humanised antibody	930	4	40.0	123	19	AAW71255	Humanised murine a
858	4	40.0	119	21	AAW00045	Human secreted pro	931	4	40.0	123	20	AAW06264	RSB protein of CF
859	4	40.0	119	21	AAW03931	Human secreted pro	932	4	40.0	123	20	AAW00785	Antibody against I
860	4	40.0	119	21	AAW04052	Human secreted pro	933	4	40.0	123	20	AAW00782	Antibody against I
861	4	40.0	119	21	AAW08893	Human secreted pro	934	4	40.0	123	20	AAW81453	Humanised antibody
862	4	40.0	119	22	AAW56682	Humanized 369 heav	935	4	40.0	123	20	AAW81449	Humanised antibody
863	4	40.0	119	22	AAW20301	Arabisdopsis apopto	936	4	40.0	123	21	AAW13045	Protein sequence o
864	4	40.0	119	22	AAB69680	Humanised CMV5 ant	937	4	40.0	123	21	AAW83049	Humanised ICR-1.1
865	4	40.0	119	22	AAB69692	Human M01 antibody	938	4	40.0	123	21	AAW82444	Humanised ICR-8.1
866	4	40.0	119	22	AAB62774	Human HIV-1 monocl	939	4	40.0	123	21	AAW82448	Humanised ICR-1.1
867	4	40.0	120	15	AAR47491	Humanised anti-CD1	940	4	40.0	123	21	AAW50920	Human fetal brain
868	4	40.0	120	15	AAR54795	SPA-reactive Igm h	941	4	40.0	123	21	AAW50752	Humanised murine a
869	4	40.0	120	15	AAR54796	SPA-reactive Igm h	942	4	40.0	123	21	AAW50756	Humanised murine a
870	4	40.0	120	17	AAW05825	Humanised M291 ant	943	4	40.0	123	21	AAW56714	Amino acid sequenc
871	4	40.0	120	18	AAW29998	Murine monoclonal	944	4	40.0	124	15	AAW45610	Monoclonal antibod
872	4	40.0	120	18	AAW27550	Human Ab heavy cha	945	4	40.0	124	15	AAW43330	Anti-HIV gp120 imm
873	4	40.0	120	18	AAW27551	Human Ab heavy cha	946	4	40.0	124	15	AAW43331	Anti-HIV gp120 imm
874	4	40.0	120	18	AAW27555	Human Ab heavy cha	947	4	40.0	124	15	AAW43332	Anti-HIV gp120 imm
875	4	40.0	120	18	AAW19882	CEA-specific antib	948	4	40.0	124	15	AAW43335	Anti-HIV gp120 imm
876	4	40.0	120	19	AAW44124	Heavy chain variab	949	4	40.0	124	15	AAW43336	Anti-HIV gp120 imm
877	4	40.0	120	20	AAW89350	Humanised 23F2G he	950	4	40.0	124	15	AAW43344	Anti-HIV gp120 imm
878	4	40.0	120	21	AAW27487	Arabisdopsis thalia	951	4	40.0	124	15	AAW43245	Anti-HIV gp120 imm
879	4	40.0	120	21	AAW00030	Human secreted pro	952	4	40.0	124	15	AAW43246	Anti-HIV gp120 imm
880	4	40.0	120	22	AAW67381	CDIFF-4, Incyte ID	953	4	40.0	124	15	AAW43269	Anti-HIV gp120 imm
881	4	40.0	120	22	AAW67381	p24b DNA, Human i	954	4	40.0	124	16	AAW75617	VH Fab M556-13 bin
882	4	40.0	120	22	AAW67347	Human HIV-1 monocl	955	4	40.0	124	16	AAW75616	VH Fab M556-5 bin
883	4	40.0	121	13	AAW52724	Humanised VH regio	956	4	40.0	124	16	AAW75615	VH Fab M556-16 bin
884	4	40.0	121	15	AAW54797	SPA-reactive Igm h	957	4	40.0	124	16	AAW75614	VH Fab M556-15 bin
885	4	40.0	121	16	AAW77874	Humanised mouse DR	958	4	40.0	124	16	AAW75613	VH Fab M556-7 bind
886	4	40.0	121	17	AAW99556	Flrea allergen Cten	959	4	40.0	124	16	AAW75612	VH Fab M556-3 bind
887	4	40.0	121	17	AAW97830	Kaposi's sarcoma a	960	4	40.0	124	16	AAW75611	VH Fab M556-3 bind

669	4	40.0	104	21	AAB42842	Human ORFX ORF2606	742	4	40.0	114	20	AAW95454	N-terminally trunc
670	4	40.0	104	21	AAV94933	Human secreted pro	743	4	40.0	114	21	AAV71550	Humanised antibody
671	4	40.0	105	19	AAV22856	SEQ ID NO. 52 from	744	4	40.0	114	21	AAV50974	Human FVII heavy
672	4	40.0	105	19	AAV22857	SEQ ID NO. 53 from	745	4	40.0	114	21	AAV75983	Murine skin cell p
673	4	40.0	105	19	AAV22858	SEQ ID NO. 54 from	746	4	40.0	114	21	AAV76033	Murine skin cell p
674	4	40.0	105	19	AAV22859	SEQ ID NO. 55 from	747	4	40.0	114	21	AAV55922	Skin cell protein,
675	4	40.0	105	19	AAW40579	Human lambda CL do	748	4	40.0	114	22	AAW55972	OP-1 based morphon
676	4	40.0	105	20	AAV38473	Human secreted pro	749	4	40.0	115	18	AAW12437	Rat quanylin prepr
677	4	40.0	105	20	AAV08746	Human lambda-CL do	750	4	40.0	115	20	AAV42461	Human phospholiest
678	4	40.0	105	20	AAV12366	Human 5' EST secre	751	4	40.0	115	20	AAV39287	Human Kabat subgro
679	4	40.0	105	20	AAW92426	Human lambda prote	752	4	40.0	115	20	AAW84095	Humanised HBV pre-
680	4	40.0	105	21	AAW27001	Human secreted pro	753	4	40.0	115	21	AAW53629	Humanised HBV pre-
681	4	40.0	105	21	AAW00032	Human secreted pro	754	4	40.0	115	21	AAW12169	Humanised HBV pre-
682	4	40.0	105	21	AAW01554	N-ferminal CBPA se	755	4	40.0	115	21	AAW12172	Human secreted pro
683	4	40.0	106	20	AAV49228	Choline binding pr	756	4	40.0	115	21	AAW00036	Human secreted pro
684	4	40.0	106	20	AAV32101	Amino acid sequenc	757	4	40.0	115	21	AAW00051	Humanised VH regio
685	4	40.0	106	20	AAW70803	Human pancreatic c	758	4	40.0	116	13	AAW25726	N-terminally trunc
686	4	40.0	106	21	AAW54282	Uncharacterised hu	759	4	40.0	116	13	AAW53362	Humanised IL2 Mab
687	4	40.0	106	21	AAW23152	Human nucleic acid	760	4	40.0	116	16	AAW66310	Humanised IL2 Mab
688	4	40.0	106	21	AAW21030	Human secreted pro	761	4	40.0	116	17	AAW92218	Humanised IL2 Mab
689	4	40.0	106	21	AAW03722	Human IgG1 lambda	762	4	40.0	116	17	AAW92219	Variable heavy cha
690	4	40.0	106	21	AAV92193	Human secreted pro	763	4	40.0	116	18	AAW27698	Reshaped human AUK
691	4	40.0	107	21	AAW51712	Human OREX ORF2304	764	4	40.0	116	18	AAW22418	Humanized anti-Tac
692	4	40.0	107	21	AAW42540	N. meningitidis BA	765	4	40.0	116	19	AAW37812	Protein SEQ ID NO:
693	4	40.0	107	21	AAW10493	Arbidopsis thaila	766	4	40.0	116	19	AAW58514	N-terminally trunc
694	4	40.0	107	21	AAW09358	Arbidopsis thaila	767	4	40.0	116	20	AAW95453	Eucalyptus grandis
695	4	40.0	107	21	AAW26325	Arbidopsis thaila	768	4	40.0	116	21	AAW18036	Eucalyptus grandis
696	4	40.0	107	21	AAW56019	Human secreted pro	769	4	40.0	116	21	AAW18113	Zea mays protein f
697	4	40.0	107	21	AAW03723	Neisseria meningit	770	4	40.0	116	21	AAW18487	Human secreted pro
698	4	40.0	107	21	AAV74672	Neisseria meningit	771	4	40.0	116	21	AAW00050	Human FVIII antibo
699	4	40.0	107	21	AAV74673	C. albicans Rbtl p	772	4	40.0	116	21	AAV50971	Humanised anti-Tac
700	4	40.0	108	20	AAV05478	Amino acid sequenc	773	4	40.0	116	22	AAW69645	Humanised anti-Tac
701	4	40.0	108	21	AAW19160	A human cullin-int	774	4	40.0	116	22	AAW69646	Humanised M195 ant
702	4	40.0	108	21	AAW08813	Human secreted pro	775	4	40.0	116	22	AAW69672	Human Bu antibody
703	4	40.0	108	21	AAW00033	Human secreted pro	776	4	40.0	116	22	AAW69686	Human antibody Eu
704	4	40.0	108	21	AAW03890	Immunoglobulin C-1	777	4	40.0	117	13	AAW24104	Protein encoded by
705	4	40.0	109	18	AAW37348	Anti-glutathione a	778	4	40.0	117	13	AAW22358	Humanised VH regio
706	4	40.0	109	18	AAW41016	N-ferminal CBPA se	779	4	40.0	117	13	AAW25732	Human heavy chain
707	4	40.0	109	20	AAV49229	Choline binding pr	780	4	40.0	117	14	AAW53363	CDR-grafted anti-R
708	4	40.0	109	20	AAV32102	Secreted peptide c	781	4	40.0	117	15	AAW37476	Heavy chain variab
709	4	40.0	109	20	AAV28574	Human colon cancer	782	4	40.0	117	15	AAW57476	Sequence of the ma
710	4	40.0	109	21	AAW53666	Arbidopsis thaila	783	4	40.0	117	15	AAW53929	Sequence of the ma
711	4	40.0	109	21	AAW58963	Streptococcus pneu	784	4	40.0	117	15	AAW59514	Human immunoglobul
712	4	40.0	110	19	AAW55113	Vitreonectin alpha-	785	4	40.0	117	15	AAW59515	Human immunoglobul
713	4	40.0	110	20	AAW84099	Human PRO1274 prot	786	4	40.0	117	16	AAW66296	Human immunoglobul
714	4	40.0	110	21	AAW24425	Arbidopsis thaila	787	4	40.0	117	16	AAW66333	Human immunoglobul
715	4	40.0	110	21	AAW05562	Arbidopsis thaila	788	4	40.0	117	16	AAW66334	Human immunoglobul
716	4	40.0	110	21	AAW13654	Arbidopsis thaila	789	4	40.0	117	16	AAW66339	Human immunoglobul
717	4	40.0	110	21	AAW18889	Zea mays protein f	790	4	40.0	117	16	AAW66345	Human immunoglobul
718	4	40.0	110	21	AAV99380	Human signal pepti	791	4	40.0	117	16	AAW66316	Human immunoglobul
719	4	40.0	110	21	AAW87273	Human signal pepti	792	4	40.0	117	16	AAW66302	Human immunoglobul
720	4	40.0	110	22	AAW66129	Heavy chain VH13.1	793	4	40.0	117	16	AAW66311	Human immunoglobul
721	4	40.0	111	13	AAW22575	Zea mays protein f	794	4	40.0	117	16	AAW66297	DNA fragment VH9.
722	4	40.0	111	21	AAW12314	Arbidopsis thaila	795	4	40.0	117	17	AAW03950	Murine I308F VH CD
723	4	40.0	111	21	AAW55547	Arbidopsis thaila	796	4	40.0	117	17	AAW92079	Human VHI family p
724	4	40.0	111	21	AAW03420	Human secreted pro	797	4	40.0	117	18	AAW41113	Human VHI gene VH4
725	4	40.0	111	21	AAV92027	Human bone morphog	798	4	40.0	117	18	AAW24777	S. pneumoniae dily
726	4	40.0	111	22	AAW63325	Human breast cancer	799	4	40.0	117	19	AAW38656	Protein SPO ID NO:
727	4	40.0	112	14	AAW43690	Human immunoglobul	800	4	40.0	117	19	AAW58509	Human bladder tumo
728	4	40.0	112	16	AAW66319	Staphylococcus aur	801	4	40.0	117	20	AAW66146	Amino acid sequenc
729	4	40.0	112	19	AAW77607	Soybean PITSLE pr	802	4	40.0	117	20	AAW40381	B. burgdorferi ant
730	4	40.0	112	20	AAW49163	Zea mays protein f	803	4	40.0	117	20	AAV37327	N-B172 polypeptide
731	4	40.0	112	21	AAW19019	Human Fab clone E9	804	4	40.0	117	20	AAW92252	Humanised anti-alp
732	4	40.0	112	22	AAW66407	Human breast cance	805	4	40.0	117	20	AAW95452	Humanised anti-alp
733	4	40.0	112	22	AAW63407	Hepatitis C virus	806	4	40.0	117	20	AAW84097	Protein sequence o
734	4	40.0	113	17	AAW96560	Hepatitis C virus	807	4	40.0	117	20	AAW84141	Arbidopsis thaila
735	4	40.0	113	17	AAW96561	Hepatitis C virus	808	4	40.0	117	21	AAW24952	Human trypsin trunc
736	4	40.0	113	17	AAW96562	Hepatitis C virus	809	4	40.0	117	21	AAW09548	Human trypsin trunc
737	4	40.0	113	17	AAW96564	Human ORFX ORF33 p	810	4	40.0	117	21	AAW02814	Trypsin truncated
738	4	40.0	113	21	AAW40269	Environmental stre	811	4	40.0	117	21	AAW92595	Human Eu antibody
739	4	40.0	113	22	AAW80629	N-terminally trunc	812	4	40.0	117	22	AAW69644	Human Eu antibody
740	4	40.0	114	14	AAW53361	Consensus sequence	813	4	40.0	117	22	AAW69650	
741	4	40.0	114	20	AAW49136		814	4	40.0	117	22	AAW69650	

523	4	40.0	76	21	AAAG01671	Human secreted pro
524	4	40.0	76	22	AAAB5860	Murine TANGO 281 c
525	4	40.0	77	19	AAAB6001	S. pneumoniae derl
526	4	40.0	77	21	AAAB7219	Human secreted pro
527	4	40.0	78	21	AAAB52108	Human secreted pro
528	4	40.0	78	21	AAAB4691	Human 5' EST relat
529	4	40.0	78	22	AAAB87389	Human gene 48 enco
530	4	40.0	78	22	AAAB87412	Human gene 48 enco
531	4	40.0	79	19	AAAB22863	SEQ ID NO. 59 from
532	4	40.0	79	19	AAAB22864	SEQ ID NO. 60 from
533	4	40.0	79	20	AAAB73910	Human prostate tum
534	4	40.0	80	18	AAAB11223	S. pneumoniae ind
535	4	40.0	80	18	AAAB27747	Staphylococcus aur
536	4	40.0	80	21	AAAG00040	Human secreted pro
537	4	40.0	80	21	AAAG00067	Human secreted pro
538	4	40.0	81	20	AAAB28624	Human secreted pro
539	4	40.0	81	20	AAAB9936	Antigen from clust
540	4	40.0	81	21	AAAB73395	Human secreted pro
541	4	40.0	82	21	AAAG21847	Arabidopsis thalia
542	4	40.0	82	21	AAAB4976	Human 5' EST relat
543	4	40.0	84	21	AAAB03948	Human mesenchymal
544	4	40.0	85	12	AAAB14008	HIV-1 hxb2 gag 262
545	4	40.0	85	12	AAAB14458	HIV-1 hxb2 gag 262
546	4	40.0	85	21	AAAG02769	Human secreted pro
547	4	40.0	86	19	AAAB38421	Proteolipid protel
548	4	40.0	86	20	AAAB73904	Human prostate tum
549	4	40.0	86	20	AAAB73929	Human secreted pro
550	4	40.0	86	21	AAAG01952	Human secreted pro
551	4	40.0	86	22	AAAB35252	HIV-1 p24 protein
552	4	40.0	87	17	AAAB93003	Homologous sequenc
553	4	40.0	87	17	AAAB92991	Homologous sequenc
554	4	40.0	87	21	AAAG26156	Zea mays protein f
555	4	40.0	88	21	AAAB76169	Zea mays protein f
556	4	40.0	88	13	AAAB2576	Human secreted pro
557	4	40.0	88	21	AAAG04407	Heavy chain VH6.1
558	4	40.0	88	21	AAAG33200	Arabidopsis thalia
559	4	40.0	88	21	AAAG54249	Zea mays protein f
560	4	40.0	89	14	AAAB34271	Arabidopsis thalia
561	4	40.0	89	19	AAAB41088	Dp-74 Vhl gene hea
562	4	40.0	89	19	AAAB41233	Human matrix metal
563	4	40.0	89	21	AAAG04406	Alpha-v-beta-5 ant
564	4	40.0	89	21	AAAG54248	Arabidopsis thalia
565	4	40.0	90	21	AAAG26155	Arabidopsis thalia
566	4	40.0	91	21	AAAB42378	Zea mays protein f
567	4	40.0	91	21	AAAG37140	Human ORFX ORF2142
568	4	40.0	92	21	AAAB40314	Zea mays protein f
569	4	40.0	92	21	AAAG2776	Human ORFX ORF78 p
570	4	40.0	92	21	AAAG26934	Arabidopsis thalia
571	4	40.0	92	21	AAAG33234	Zea mays protein f
572	4	40.0	92	21	AAAG33943	Zea mays protein f
573	4	40.0	92	21	AAAG36731	Arabidopsis thalia
574	4	40.0	93	19	AAAB22860	SEQ ID NO. 56 from
575	4	40.0	93	19	AAAB75090	Human secreted pro
576	4	40.0	93	21	AAAG04405	Arabidopsis thalia
577	4	40.0	93	21	AAAG3473	Arabidopsis thalia
578	4	40.0	93	21	AAAG54247	Arabidopsis thalia
579	4	40.0	93	21	AAAG03293	Human secreted pro
580	4	40.0	94	19	AAAB22861	SEQ ID NO. 57 from
581	4	40.0	94	19	AAAB75151	Human secreted pro
582	4	40.0	94	19	AAAB75152	Human secreted pro
583	4	40.0	94	21	AAAB51698	Human secreted pro
584	4	40.0	94	21	AAAG00054	Human secreted pro
585	4	40.0	94	21	AAAG00065	Human secreted pro
586	4	40.0	94	22	AAAB54488	Human secreted pro
587	4	40.0	95	20	AAAB74161	Human secreted pro
588	4	40.0	95	20	AAAB74161	Human prostate tum
589	4	40.0	95	21	AAAB60052	Human endometrium
590	4	40.0	95	21	AAAG14413	Arabidopsis thalia
591	4	40.0	95	21	AAAG57203	Arabidopsis thalia
592	4	40.0	95	21	AAAG59156	Arabidopsis thalia
593	4	40.0	95	21	AAAG00038	Human secreted pro
594	4	40.0	96	20	AAAB1621	Human secreted pro
595	4	40.0	96	20	AAAB67917	Human secreted pro
	4	40.0	96	21	AAAG12504	Zea mays protein f
596	4	40.0	96	21	AAAG15817	Arabidopsis thalia
597	4	40.0	96	21	AAAG25016	Arabidopsis thalia
598	4	40.0	96	21	AAAG00039	Human secreted pro
599	4	40.0	96	21	AAAB6644	Partial peptide fr
600	4	40.0	96	21	AAAB6644	Partial peptide fr
601	4	40.0	96	21	AAAB6644	Partial peptide fr
602	4	40.0	96	21	AAAB6644	Partial peptide fr
603	4	40.0	96	21	AAAB6644	Partial peptide fr
604	4	40.0	97	14	AAAB3359	Osteogenic protein
605	4	40.0	97	14	AAAB3387	Murine osteogenic
606	4	40.0	97	15	AAAB37475	Human HV3 VH. Hom
607	4	40.0	97	17	AAAB32078	Human HV3 VH regio
608	4	40.0	97	20	AAAB72248	C. elegans CED-6 p
609	4	40.0	97	20	AAAB9696	Human osteogenic p
610	4	40.0	97	20	AAAB95444	Conserved 6 cystel
611	4	40.0	97	21	AAAG00068	Human secreted pro
612	4	40.0	97	21	AAAB5401	Human 5' EST relat
613	4	40.0	97	22	AAAB5852	Human TANGO 281 cy
614	4	40.0	98	10	AAAB95661	Human osteogenic p
615	4	40.0	98	14	AAAB33701	SP2 IgG VH segment
616	4	40.0	98	14	AAAB34272	Mutated human Vhl
617	4	40.0	98	15	AAAB54800	SPA-reactive Igm h
618	4	40.0	98	16	AAAB72058	DP10 VH region. h
619	4	40.0	98	16	AAAB72059	HV1263 VH region.
620	4	40.0	98	16	AAAB72070	OE7H1.2 VH-1 H cha
621	4	40.0	98	19	AAAB54008	Human Anti-CD4 ant
622	4	40.0	98	21	AAAB40696	Human ORFX ORF460
623	4	40.0	98	21	AAAB50949	Human anti--factor
624	4	40.0	98	21	AAAB50951	Human anti--factor
625	4	40.0	98	21	AAAB50952	Human anti--factor
626	4	40.0	98	21	AAAB50954	Human anti--factor
627	4	40.0	98	21	AAAB50958	Human FVIII antibo
628	4	40.0	99	20	AAAB50970	Human FVIII antibo
629	4	40.0	99	20	AAAB95555	protein encoded by
630	4	40.0	99	21	AAAB18028	plins radicta myic
631	4	40.0	99	21	AAAG41554	Arabidopsis thalia
632	4	40.0	99	21	AAAG00046	Human secreted pro
633	4	40.0	99	21	AAAG00055	Human secreted pro
634	4	40.0	99	21	AAAG00066	Human secreted pro
635	4	40.0	100	15	AAAB47238	Human secreted pro
636	4	40.0	100	17	AAAB03357	Human Immunodefice
637	4	40.0	100	21	AAAG00536	Human secreted pro
638	4	40.0	100	21	AAAG2052	Human secreted pro
639	4	40.0	100	21	AAAB1811	Streptococcus pneu
640	4	40.0	100	22	AAAB31970	Rice glutamate 1-s
641	4	40.0	101	20	AAAB35775	Chlamydia pneumoni
642	4	40.0	101	20	AAAB12050	Human 5' EST secre
643	4	40.0	101	21	AAAB54122	Human pancreatic c
644	4	40.0	102	13	AAAB95682	Human osteogenic p
645	4	40.0	102	13	AAAB25325	Hv region of human
646	4	40.0	102	14	AAAB53360	Osteogenic protein
647	4	40.0	102	18	AAAB36889	Human osteogenic p
648	4	40.0	102	18	AAAB6897	Mutant human osteo
649	4	40.0	102	18	AAAB6872	Human osteogenic p
650	4	40.0	102	18	AAAB56873	Mouse osteogenic p
651	4	40.0	102	18	AAAB18841	Human immunoglobul
652	4	40.0	102	19	AAAB5889	S. pneumoniae derl
653	4	40.0	102	20	AAAB16708	WO9914235 Seq ID N
654	4	40.0	102	20	AAAB19744	SEQ ID NO. 462 from
655	4	40.0	102	20	AAAB94855	Sequence of human.
656	4	40.0	102	20	AAAB89687	Human osteogenic p
657	4	40.0	102	20	AAAB95443	Conserved 7 cystel
658	4	40.0	102	21	AAAG00047	Human secreted pro
659	4	40.0	102	21	AAAG00071	Human secreted pro
660	4	40.0	102	21	AAAB09534	Human OP-1 C-termi
661	4	40.0	102	21	AAAB02800	Human OP-1 C-termi
662	4	40.0	102	21	AAAB02800	Human OP-1 amino a
663	4	40.0	103	18	AAAB1019	Anti-glutathione a
664	4	40.0	103	19	AAAB60484	Human epimorphin N
665	4	40.0	103	20	AAAB9135	Consensus sequence
666	4	40.0	103	20	AAAB9135	Consensus sequence
667	4	40.0	103	21	AAAB41148	Zea mays protein f
668	4	40.0	104	19	AAAG00061	Human secreted pro
	4	40.0	104	19	AAAB22878	SEQ ID NO. 74 from

377	4	40.0	35	21	AAV67809	Peptide #209 for d	450	4	40.0	56	21	AA828299	Human secreted pro
378	4	40.0	37	18	AAW40369	Human breast cancer	451	4	40.0	56	21	AA601731	Human secreted pro
379	4	40.0	37	18	AAW30366	Fragment #2 of bon	452	4	40.0	56	21	AAV87131	Human secreted pro
380	4	40.0	37	20	AAV25880	Human secreted pro	453	4	40.0	56	22	AA855854	Human TANGO 281 PS
381	4	40.0	37	21	AA809516	Human OP-1 finger	454	4	40.0	56	22	AA855862	Mutine TANGO 281 P
382	4	40.0	37	21	AA809559	Op-1 mutant protei	455	4	40.0	57	21	AA654473	Zee mays protein f
383	4	40.0	37	21	AA809562	Human OP-1 mutant	456	4	40.0	58	10	AA801360	Amino acids 455-51
384	4	40.0	37	21	AA809563	Human OP-1 mutant	457	4	40.0	58	10	AA600062	Human secreted pro
385	4	40.0	37	21	AA809565	Human OP-1 mutant	458	4	40.0	59	16	AA873922	B. catarrhalis CD e
386	4	40.0	37	21	AA809566	Human OP-1 mutant	459	4	40.0	59	21	AA856233	Human secreted pro
387	4	40.0	37	21	AA809573	Human OP-1 mutant	460	4	40.0	59	21	AA659293	Arabidopsis thalia
388	4	40.0	37	21	AA840352	Amino acid sequenc	461	4	40.0	59	21	AAV96790	Maize sucrose non-
389	4	40.0	38	14	AA841075	HIV-1 gp120 C-term	462	4	40.0	60	18	AAW28031	Staphylococcus aur
390	4	40.0	38	20	AAV42830	Erythropoietin rec	463	4	40.0	60	18	AAW15568	PRN60. Feline leu
391	4	40.0	39	16	AA866436	PCUS 4-18 (476-49	464	4	40.0	60	19	AAV20977	Human glial fibril
392	4	40.0	39	16	AA866410	PCUS 4-18 (476-49	465	4	40.0	60	19	AAW72727	Proline rich pepti
393	4	40.0	39	18	AAW19025	HIV envelope glyco	466	4	40.0	60	22	AA890561	Human secreted pro
394	4	40.0	39	20	AAV05347	HIV-1 CLUVAC pepi	467	4	40.0	61	20	AAV27507	E. coli beta'-subu
395	4	40.0	39	20	AAV05340	HIV-1 CLUVAC pepi	468	4	40.0	61	21	AA602506	Human secreted pro
396	4	40.0	39	22	AA859899	HIV-1 C5 region of	469	4	40.0	62	18	AAW27824	Staphylococcus aur
397	4	40.0	40	21	AA805912	Human endothelial	470	4	40.0	62	18	AAW27825	Staphylococcus aur
398	4	40.0	40	21	AA805913	Bovine endothelial	471	4	40.0	62	21	AA603233	Human secreted pro
399	4	40.0	41	19	AAV22869	SEQ ID NO. 65 from	472	4	40.0	63	16	AA876366	HSV-neutralising a
400	4	40.0	41	20	AAV42648	A. thaliana D22A73	473	4	40.0	63	16	AA876367	HSV-neutralising a
401	4	40.0	41	20	AAV07893	Human secreted pro	474	4	40.0	63	16	AA876365	HSV-neutralising a
402	4	40.0	42	9	AA806866	Peptide 147 from t	475	4	40.0	63	16	AA876971	HSV-neutralising a
403	4	40.0	42	18	AAW19055	SP10-BAL immunoge	476	4	40.0	63	16	AA876972	HSV-neutralising a
404	4	40.0	42	19	AAW59179	Gela TMP-2 binding	477	4	40.0	63	16	AA876973	HSV-neutralising a
405	4	40.0	42	20	AAV29924	Human CHD1 RAB do	478	4	40.0	63	21	AA858469	Lung cancer associ
406	4	40.0	43	20	AAW91057	Flanking sequence	479	4	40.0	63	21	AA851667	Human secreted pro
407	4	40.0	43	20	AAW91059	Flanking sequence	480	4	40.0	63	21	AA618871	Zee mays protein f
408	4	40.0	43	20	AAW91063	Flanking sequence	481	4	40.0	63	21	AA659038	Arabidopsis thalia
409	4	40.0	43	21	AA827071	Beta-actenin flank	482	4	40.0	64	21	AA655463	Arabidopsis thalia
410	4	40.0	43	21	AA827073	Beta-actenin flank	483	4	40.0	65	19	AA85862	A. pneumoniae deri
411	4	40.0	43	21	AA827077	Beta-actenin flank	484	4	40.0	65	21	AA838595	Human secreted pro
412	4	40.0	44	21	AAV76821	Cytoplasmic tail p	485	4	40.0	65	21	AAV76042	Human skin cell pr
413	4	40.0	44	21	AA821848	Arabidopsis thalia	486	4	40.0	65	22	AA855981	Arabidopsis thalia
414	4	40.0	45	10	AA890818	Non-immunogenic a	487	4	40.0	66	21	AA619536	Arabidopsis thalia
415	4	40.0	45	20	AAV01143	Secreted protein e	488	4	40.0	66	21	AA624624	Arabidopsis thalia
416	4	40.0	45	22	AA887380	Human gene 39 enco	489	4	40.0	66	21	AA634539	Arabidopsis thalia
417	4	40.0	46	19	AAW79183	Fusion immunoglob	490	4	40.0	66	21	AA646116	Arabidopsis thalia
418	4	40.0	47	20	AAV36545	Fragment of human	491	4	40.0	66	21	AA646138	Arabidopsis thalia
419	4	40.0	47	21	AAV83984	Human IL-18 bindin	492	4	40.0	67	20	AAV42644	B Brassica napus D22
420	4	40.0	49	19	AAW46754	Exon trap L75917.	493	4	40.0	67	21	AA853913	Human colon cancer
421	4	40.0	49	20	AAV25728	Human secreted pro	494	4	40.0	69	18	AAW32434	Mycobacterium tube
422	4	40.0	49	21	AA856202	Human secreted pro	495	4	40.0	69	18	AAW32366	Mycobacterium tube
423	4	40.0	50	16	AA871628	HIV gp120-C5. Syn	496	4	40.0	69	19	AAW81569	M. tuberculosis im
424	4	40.0	50	16	AAW29113	Enhanced CCK-B/gas	497	4	40.0	69	19	AAW64306	Mycobacterium tube
425	4	40.0	51	16	AA877798	Transactivation do	498	4	40.0	69	20	AAV39108	M. tuberculosis an
426	4	40.0	51	16	AA877799	Transactivation do	499	4	40.0	69	20	AAV38971	M. tuberculosis re
427	4	40.0	51	18	AAW29108	Enhanced CCK-B/gas	500	4	40.0	70	20	AAW93960	Human 53BP2:IP-2 p
428	4	40.0	51	21	AA619538	Arabidopsis thalia	501	4	40.0	70	21	AA853453	Human colon cancer
429	4	40.0	51	21	AA624626	Arabidopsis thalia	502	4	40.0	70	21	AA615847	Arabidopsis thalia
430	4	40.0	51	21	AA634541	Arabidopsis thalia	503	4	40.0	71	21	AA621088	Arabidopsis thalia
431	4	40.0	51	21	AA646118	Arabidopsis thalia	504	4	40.0	72	16	AA871350	Consensus sequence
432	4	40.0	51	21	AA646140	Arabidopsis thalia	505	4	40.0	72	16	AA871348	Mercury-binding re
433	4	40.0	51	21	AA809325	Hepatitis GB virus	506	4	40.0	72	16	AA871349	Mercury-binding re
434	4	40.0	52	10	AA891361	Amino acids of the	507	4	40.0	72	19	AAV22887	SEQ ID NO. 83 from
435	4	40.0	52	21	AA822870	White shrimp multi	508	4	40.0	72	21	AA602885	Human secreted pro
436	4	40.0	52	21	AA822871	White shrimp multi	509	4	40.0	73	22	AA850534	Mouse C-CAM1 cyto
437	4	40.0	52	21	AAV66682	Membrane-bound pro	510	4	40.0	74	20	AAV03781	S. aureus polypept
438	4	40.0	52	22	AA865205	Human PRO819 (UNO4	511	4	40.0	74	21	AA856214	Human secreted pro
439	4	40.0	52	22	AA850985	Human PRO819 prote	512	4	40.0	74	21	AA637064	Arabidopsis thalia
440	4	40.0	52	22	AA853093	Human angiotensins	513	4	40.0	74	21	AA855678	Arabidopsis thalia
441	4	40.0	53	19	AAV22898	SEQ ID NO. 94 from	514	4	40.0	74	21	AA660223	Arabidopsis thalia
442	4	40.0	54	19	AAV22867	SEQ ID NO. 63 from	515	4	40.0	74	22	AA850533	Human C-CAM1 cyto
443	4	40.0	54	19	AAV22868	SEQ ID NO. 64 from	516	4	40.0	75	18	AAW28213	Staphylococcus aur
444	4	40.0	54	21	AA859095	Breast and ovarian	517	4	40.0	75	20	AAV30854	Human secreted pro
445	4	40.0	54	21	AA600997	Human secreted pro	518	4	40.0	75	20	AAV35810	Chlamydia pneumonia
446	4	40.0	55	8	AA870360	Sequence of immuno	519	4	40.0	75	20	AAV12951	Amino acid sequenc
447	4	40.0	55	19	AAV22865	SEQ ID NO. 62 from	520	4	40.0	75	21	AA618074	Arabidopsis thalia
448	4	40.0	55	19	AAV22865	SEQ ID NO. 61 from	521	4	40.0	76	20	AAV35859	Chlamydia pneumonia
449	4	40.0	55	20	AAV26920	Felv envelope glyc	522	4	40.0	76	20	AAV12175	Human 5' EST secre

231	4	40.0	11	14	AA841809	M137MD1 mutated fr	304	4	40.0	22	14	AA831965	BC8-132. Syntheti
232	4	40.0	11	17	AA897523	Antigenic peptide,	305	4	40.0	22	14	AA841293	peptide fragment F
233	4	40.0	11	19	AAW70126	Peptide produced b	306	4	40.0	22	19	AAW67032	Peptide with N-ter
234	4	40.0	11	19	AAW50203	Peptide from a krl	307	4	40.0	22	20	AAV04034	HIV-1 p24 peptide
235	4	40.0	11	21	AA822972	White shrimp p62 p	308	4	40.0	22	21	AA812539	HIV-1 nucleoprotei
236	4	40.0	11	21	AA809549	Peptide encoded by	309	4	40.0	23	13	AA825941	N-terminal peptide
237	4	40.0	11	21	AA802815	BMP mutant chimeri	310	4	40.0	23	14	AA845164	Listeria p60 pepit
238	4	40.0	11	21	AA892589	Peptide encoded by	311	4	40.0	23	14	AA841294	Peptide fragment F
239	4	40.0	11	22	AA875973	Human kallikrein (312	4	40.0	23	15	AA841332	HIV gp120 epitope
240	4	40.0	12	16	AA883319	Rb-binding random	313	4	40.0	23	15	AA863849	HIV-1 gp120-40 epi
241	4	40.0	12	16	AA868778	Cytotoxic T lympho	314	4	40.0	23	16	AA874046	Rice carbonic-anhy
242	4	40.0	12	21	AA807094	Human peptido-mime	315	4	40.0	23	19	AAW50207	Peptide from a krl
243	4	40.0	13	17	AA896827	Human snRNP-associ	316	4	40.0	23	19	AAW48108	HIV gp120 residues
244	4	40.0	13	19	AAW70128	Peptide produced b	317	4	40.0	23	20	AAV27500	E. coli beta'-subu
245	4	40.0	13	19	AAW50204	Peptide from a krl	318	4	40.0	24	8	AAV71151	Anti-HIV peptide 6
246	4	40.0	13	21	AA822973	White shrimp p62 p	319	4	40.0	24	9	AA808750	Sequence of peptid
247	4	40.0	14	19	AAW79191	Synthetic peptide	320	4	40.0	24	14	AA833838	Cluster peptide PC
248	4	40.0	14	19	AAW56527	Antigenic HIV-1 pe	321	4	40.0	24	16	AA864432	PCUS 4-18 (4/6-49
249	4	40.0	14	21	AA822974	White shrimp p62 p	322	4	40.0	24	19	AAW54933	HIV gp120 envelope
250	4	40.0	14	21	AAV98509	Mouse WPI peptide	323	4	40.0	24	20	AAV05354	HIV-1 CUVAC pepit
251	4	40.0	14	21	AAV98510	Human WPI peptide	324	4	40.0	24	21	AA822976	White shrimp p62 p
252	4	40.0	15	10	AA890224	Antigenic peptide.	325	4	40.0	25	7	AA860708	HIV virus p18 prot
253	4	40.0	15	16	AA879629	Endocarditis speci	326	4	40.0	25	11	AA802316	Peptide derived fr
254	4	40.0	15	16	AA879626	Endocarditis speci	327	4	40.0	25	13	AA827336	Peptide corresp. t
255	4	40.0	15	18	AAW39011	Prostate Specific	328	4	40.0	25	16	AA879982	Signal transductio
256	4	40.0	15	18	AAW30779	SH2 domain binding	329	4	40.0	25	19	AAW82523	HIV-1 p24 epitope
257	4	40.0	15	19	AAW78551	Human prostate spe	330	4	40.0	25	19	AAW82524	HIV-1 p24 epitope
258	4	40.0	15	19	AAW58037	Human prostate spe	331	4	40.0	25	20	AAW82525	HIV-1 p24 epitope
259	4	40.0	15	19	AAW58038	Human prostate spe	332	4	40.0	25	20	AAW81958	Human EMDO-II vari
260	4	40.0	15	19	AAW58039	Human prostate spe	333	4	40.0	26	13	AA824867	Sequence of peptid
261	4	40.0	15	19	AAW58040	Human prostate spe	334	4	40.0	26	14	AA830538	HIV discriminatory
262	4	40.0	15	20	AAV27174	Human SRT peptide	335	4	40.0	26	14	AA830755	HIV discriminatory
263	4	40.0	15	21	AA830407	Nuclear localisati	336	4	40.0	26	14	AA841301	Peptide fragment F
264	4	40.0	15	21	AA814221	HIV USA gp120 clea	337	4	40.0	26	14	AA844111	HIV gp160 epitope.
265	4	40.0	15	21	AA814223	Mutant HIV cleavag	338	4	40.0	26	19	AAW76909	Fusion immunoglob
266	4	40.0	16	18	AAW25388	PLC gamma SH3 doma	339	4	40.0	26	19	AAW50208	Peptide from a krl
267	4	40.0	16	18	AAW09989	HTLV-1 envelope pr	340	4	40.0	26	21	AA822977	White shrimp p62 p
268	4	40.0	16	18	AAW15570	PRN4358. Feline I	341	4	40.0	27	10	AA890819	Non-immunogenic am
269	4	40.0	16	19	AAW76907	Fusion immunoglob	342	4	40.0	27	14	AA830757	HIV discriminatory
270	4	40.0	16	19	AAW50206	Peptide from a krl	343	4	40.0	27	19	AAW79184	HIV gp120 C5 regio
271	4	40.0	16	19	AAW50205	Peptide from a krl	344	4	40.0	27	20	AAV38474	Human secreted pro
272	4	40.0	16	19	AAW37117	HTLV-I envelope an	345	4	40.0	28	15	AA849685	Sequence of trypti
273	4	40.0	16	20	AAV00795	HTLV-I envelope pep	346	4	40.0	29	21	AA833288	Simian immunodef
274	4	40.0	16	20	AA822975	White shrimp p62 p	347	4	40.0	29	22	AA849392	Simian immunodef
275	4	40.0	18	11	AA802317	Peptide derived fr	348	4	40.0	29	22	AA849393	Simian immunodef
276	4	40.0	18	19	AAW79190	Synthetic peptide	349	4	40.0	29	22	AA849394	Simian immunodef
277	4	40.0	18	20	AAW94621	Src homology 3 dom	350	4	40.0	30	12	AA815700	Human tumour-assoc
278	4	40.0	19	11	AA801999	Peptide derived fr	351	4	40.0	30	13	AA827045	Human heavy chain
279	4	40.0	19	11	AA800940	Peptide derived fr	352	4	40.0	30	16	AA885163	Human ONS-M21 anti
280	4	40.0	19	14	AA837695	Retroviral gag pep	353	4	40.0	30	16	AA870657	GLUT4 intracellular
281	4	40.0	19	16	AA876724	gp120 epitope from	354	4	40.0	30	16	AA870658	GLUT4 intracellular
282	4	40.0	19	18	AAW33957	Vasopressin type 2	355	4	40.0	30	17	AA866290	Heavy chain framew
283	4	40.0	20	16	AA868794	Cytotoxic T lympho	356	4	40.0	30	19	AAW76911	Fusion immunoglob
284	4	40.0	20	17	AAW08052	HIV peptide #37.	357	4	40.0	30	19	AAW79211	Framework 1 region
285	4	40.0	20	19	AAW76943	Fusion immunoglob	358	4	40.0	31	17	AA891189	gp120 HTLV-III pep
286	4	40.0	20	19	AAW76875	Fusion immunoglob	359	4	40.0	31	18	AAW24744	Finger 2 domain of
287	4	40.0	20	21	AAV93365	Amino acid sequenc	360	4	40.0	31	19	AAW54936	HIV gp120 envelope
288	4	40.0	20	21	AAV57262	Protein tyrosine p	361	4	40.0	31	20	AAV148370	Human prostate can
289	4	40.0	20	21	AAV66445	HIV A2-binding HIV	362	4	40.0	31	20	AAW82455	Tomato Cu/Zn SOD e
290	4	40.0	20	22	AA849391	Simian immunodef	363	4	40.0	31	21	AAV77377	HIV-1 group O env
291	4	40.0	21	14	AA831614	Peptide ligand for	364	4	40.0	31	21	AAV77378	C-terminal portion
292	4	40.0	21	14	AA834228	HTLV-I gp46 exten	365	4	40.0	32	10	AA891490	Bacteriocalficin-2
293	4	40.0	21	16	AA872664	Cladosporium herba	366	4	40.0	32	18	AAW66676	WT1 derived immuno
294	4	40.0	21	17	AA887131	Conantokin-r (con-	367	4	40.0	32	21	AAV98799	Hepatitis C virus
295	4	40.0	21	17	AA894517	GLU4 insulin sensi	368	4	40.0	33	16	AA869686	Hepatitis C virus
296	4	40.0	21	18	AAW42769	Peptide of the spe	369	4	40.0	33	17	AA889558	Hepatitis C virus
297	4	40.0	21	19	AAW49947	Conantokin peptide	370	4	40.0	34	19	AAV22870	SEO ID NO. 66 from
298	4	40.0	21	19	AAW48174	Conantokin peptide	371	4	40.0	34	19	AAW48443	Human p53 proline-
299	4	40.0	21	20	AAV43600	Peptide fragment o	372	4	40.0	34	20	AAV74105	Human prostate tum
300	4	40.0	21	20	AAW86146	Conantokin-r (con-	373	4	40.0	34	21	AAW53925	Human colon cancer
301	4	40.0	22	11	AAV17925	Synthetic peptide	374	4	40.0	35	19	AAW70114	Peptide produced b
302	4	40.0	22	14	AA843929	Platelet derived g	375	4	40.0	35	21	AAV67806	Peptide #208 for d
303	4	40.0	22	14	AA830539	HIV discriminatory	376	4	40.0	35	21	AAV67808	

85	5	50.0	399	18	AAW3417	Human integrin reg
86	5	50.0	399	20	AAV26927	Human integrin reg
87	5	50.0	404	19	AAW98621	H. pylori GHPO 245
88	5	50.0	421	20	AAV39368	SBHWS1 cytokine s
89	5	50.0	421	21	AAW12445	Human MSB1 protein
90	5	50.0	421	21	AAV53885	A suppressor of cy
91	5	50.0	422	22	AAW6464	protein encoded by
92	5	50.0	428	20	AAV13450	Amino acid sequenc
93	5	50.0	445	19	AAW8793	H. pylori GHPO 125
94	5	50.0	445	19	AAW71558	Helicobacter poly
95	5	50.0	452	18	AAW20598	H. pylori protein.
96	5	50.0	465	21	AAW81876	Streptococcus pneu
97	5	50.0	467	14	AAW41890	Bile acid sulphate
98	5	50.0	469	17	AAW97242	SCR phosphotyrosin
99	5	50.0	473	20	AAW98935	Protein encoded by
100	5	50.0	486	19	AAW37056	HIV-1 breakthrough
101	5	50.0	490	12	AAW15511	Sucrose phosphoryl
102	5	50.0	491	19	AAW37057	HIV-1 breakthrough
103	5	50.0	491	21	AAW69278	HIV-1 non-subtype
104	5	50.0	492	21	AAW69268	HIV-1 non-subtype
105	5	50.0	492	21	AAV69943	HIV synthetic gag
106	5	50.0	494	21	AAW69275	HIV-1 non-subtype
107	5	50.0	496	21	AAW69277	HIV-1 non-subtype
108	5	50.0	497	21	AAW69269	HIV-1 non-subtype
109	5	50.0	497	21	AAW69272	HIV-1 non-subtype
110	5	50.0	498	15	AAW62424	HIV-type virus MWP
111	5	50.0	498	15	AAW51691	HIV-type virus MWP
112	5	50.0	498	20	AAW93076	HIV isolate 5180 g
113	5	50.0	498	20	AAW93077	HIV isolate 5180 g
114	5	50.0	500	21	AAW69274	HIV-1 non-subtype
115	5	50.0	505	9	AAW69285	Sequence encoded b
116	5	50.0	505	19	AAW72992	HIV isolate LAV. MA
117	5	50.0	512	19	AAW68473	HIV-1 strain YBF30
118	5	50.0	515	10	AAW91235	(ENV-80)(GAG-VII)
119	5	50.0	535	22	AAW49707	Small round struct
120	5	50.0	537	20	AAV34628	Protein Involved i
121	5	50.0	559	19	AAW50909	Alteromonas fortis
122	5	50.0	566	20	AAV49068	Amino acid sequenc
123	5	50.0	566	22	AAW31932	Amino acid sequenc
124	5	50.0	605	16	AAW79625	Endocarditis speci
125	5	50.0	612	19	AAW98516	H. pylori GHPO 130
126	5	50.0	649	20	AAW90005	Expressed antigen
127	5	50.0	655	14	AAW31041	srnk polypeptide.
128	5	50.0	662	20	AAV31940	Human rad17 cell c
129	5	50.0	663	20	AAV31941	Human rad17 cell c
130	5	50.0	669	20	AAV31939	Human rad17 cell c
131	5	50.0	670	17	AAW97869	Testis-associated
132	5	50.0	670	20	AAV31937	Human rad17 cell c
133	5	50.0	691	14	AAW38735	Beta-galactosidase
134	5	50.0	707	21	AAV95065	Candida albicans p
135	5	50.0	714	18	AAW55316	M. catarrhalis RI
136	5	50.0	730	9	AAW80618	Human Bone Morpho
137	5	50.0	730	9	AAW13669	C-proteinase encod
138	5	50.0	739	18	AAW25790	Gene 036 product d
139	5	50.0	762	20	AAV00939	Desulfurococcus M1
140	5	50.0	788	19	AAW75919	C-proteinase sequen
141	5	50.0	797	21	AAV70963	Human Ras signalli
142	5	50.0	867	19	AAW98564	H. pylori GHPO 175
143	5	50.0	870	21	AAW10948	L. mexicana casein
144	5	50.0	986	18	AAW13670	C-proteinase encod
145	5	50.0	1006	21	AAW53126	Arbidolopsis thalia
146	5	50.0	1013	19	AAW61539	Human cardiac/brai
147	5	50.0	1013	19	AAW40224	Human tollold-1like
148	5	50.0	1021	18	AAW23281	Allorrection assoc
149	5	50.0	1030	19	AAW53572	Human myosin light
150	5	50.0	1030	19	AAW41378	Human protein p164
151	5	50.0	1036	21	AAW31888	Arbidolopsis thalia
152	5	50.0	1053	21	AAV99357	Human PRO1190 (UNQ
153	5	50.0	1053	22	AAW66106	Protein of the inv
154	5	50.0	1070	21	AAW31887	Arbidolopsis thalia
155	5	50.0	1085	12	AAW11604	P450 17-alpha/P450
156	5	50.0	1096	21	AAW48592	Arbidolopsis thalia
157	5	50.0	1130	21	AAW48591	Arbidolopsis thalia
158	5	50.0	1187	16	AAW66451	Ar-4 protein (enco
159	5	50.0	1210	16	AAW66450	Ar-4 protein (enco
160	5	50.0	1245	13	AAW29029	Bacillus thuringie
161	5	50.0	1245	18	AAW16657	Bacillus thuringie
162	5	50.0	1245	18	AAW13872	B603a toxin. Bac
163	5	50.0	1245	19	AAW73105	B. t. toxin protein
164	5	50.0	1245	21	AAW13894	Bacillus thuringie
165	5	50.0	1245	22	AAW59884	8603 protein. Bac
166	5	50.0	1252	16	AAW80530	B. sphaerictus. Bac
167	5	50.0	1276	21	AAW31886	Arbidolopsis thalia
168	5	50.0	1313	14	AAW36781	A3 maize ACCase.
169	5	50.0	1336	21	AAW48590	Arbidolopsis thalia
170	5	50.0	1409	21	AAW53125	Arbidolopsis thalia
171	5	50.0	1420	21	AAW53124	Arbidolopsis thalia
172	5	50.0	1484	20	AAW89721	Canine ribosome re
173	5	50.0	1566	16	AAW79643	Immunodominant ant
174	5	50.0	1627	12	AAW12789	M. pneumoniae p1 c
175	5	50.0	1627	15	AAW47911	Mycoplasma pneumon
176	5	50.0	1627	16	AAW67538	Cyadhesin p1. My
177	5	50.0	1743	19	AAW98879	H. pylori GHPO 175
178	5	50.0	2237	21	AAW58148	GURAY-3 polypeptel
179	5	50.0	2247	18	AAW27126	Egaine rhinovirus
180	5	50.0	2325	17	AAW05590	Maize acetyl CoA c
181	5	50.0	2325	19	AAW56736	Maize ACCase enzym
182	5	50.0	2325	21	AAW44687	Maize acetyl CoA c
183	5	50.0	2476	20	AAW67738	P1g p105 zone pell
184	5	50.0	2625	21	AAW23832	Shewanella sp. SCR
185	5	50.0	2785	21	AAW57148	Human down-regulat
186	4	40.0	6	21	AAW09551	Peptide encoded by
187	4	40.0	6	21	AAW02817	BMP mutant chimeri
188	4	40.0	6	21	AAV92591	Peptide encoded by
189	4	40.0	6	22	AAW46417	Human IgG heavy ch
190	4	40.0	7	19	AAW48180	Conanotkin peptide
191	4	40.0	7	19	AAW49862	Conanotkin peptide
192	4	40.0	8	14	AAW43520	Sm B/B epitope 16
193	4	40.0	8	17	AAW97521	Antigenic peptide,
194	4	40.0	8	20	AAW41615	Mammalian ion chan
195	4	40.0	8	21	AAV77393	HIV-1 group O env
196	4	40.0	9	14	AAW44262	Residues 68-76 of
197	4	40.0	9	14	AAW54620	Listeria p60 pepti
198	4	40.0	9	14	AAW42578	HIV envelope neutr
199	4	40.0	9	15	AAW57292	Bovine EK tryptic
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201	4	40.0	9	19	AAW79187	M38 murine monoclo
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204	4	40.0	9	20	AAV10315	T cell epitope/MHC
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206	4	40.0	9	20	AAW94619	Sic homology 3 dom
207	4	40.0	9	21	AAW45556	Human B99-1 HLA A3
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210	4	40.0	9	21	AAW98674	WT1 derived immuno
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223	4	40.0	10	19	AAW76876	Fusion Immunoglobu
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225	4	40.0	10	22	AAW75991	Human kallikrein (
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227	4	40.0	10	22	AAW76202	Tumour associated
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:35:47 ; Search time 56.84 Seconds
(without alignments)
10.666 Million cell updates/sec

Title: US-09-372-036-31
Perfect score: 10
Sequence: 1 PVAPQTEVKK 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	100.0	10	AA45173	Listeria p60 pepti
2	100.0	12	AA45172	Listeria p60 pepti
3	100.0	21	AA43891	Listeria monocytog
4	100.0	478	AA45178	Listeria p60 prote
5	100.0	484	AA43913	Listeria monocytog
6	70.0	7	AA473903	Listeria monocytog
7	60.0	6	AA454615	Listeria p60 pepti
8	60.0	6	AA45168	Listeria p60 pepti
9	60.0	20	AA45159	Listeria p60 pepti
10	60.0	1230	AA498275	H. pylori GHP0 690
11	50.0	7	AA421365	Human HDPF-I mutan

12	50.0	9	AA453518	HIV-1 p24 protein
13	50.0	9	AA440367	Amino acid sequenc
14	50.0	20	AA426859	HIV-derived lipope
15	50.0	11	AA454634	Listeria innocua p
16	50.0	11	AA472848	Human p53 A76T mut
17	50.0	27	AA478130	Human secreted pro
18	50.0	87	AA427569	Human secreted pro
19	50.0	101	AA482898	CUB domain from BM
20	50.0	102	AA472875	Human p53 A76T/V12
21	50.0	107	AA475784	Human lymphocyte s
22	50.0	110	AA412211	Arabisidopsis thalia
23	50.0	110	AA459955	Arabisidopsis thalia
24	50.0	114	AA412210	Arabisidopsis thalia
25	50.0	114	AA459954	Arabisidopsis thalia
26	50.0	121	AA454455	Zea mays protein f
27	50.0	125	AA454454	Zea mays protein f
28	50.0	130	AA477657	Staphylococcus aur
29	50.0	132	AA453155	Chlamydia pneumoni
30	50.0	134	AA459953	Arabisidopsis thalia
31	50.0	135	AA436760	Amino acid sequenc
32	50.0	142	AA459889	Arabisidopsis thalia
33	50.0	142	AA453843	Arabisidopsis thalia
34	50.0	148	AA408988	Arabisidopsis thalia
35	50.0	148	AA453842	Arabisidopsis thalia
36	50.0	152	AA454453	Zea mays protein f
37	50.0	174	AA489904	Antigen from clust
38	50.0	179	AA455986	Arabisidopsis thalia
39	50.0	179	AA459942	Arabisidopsis thalia
40	50.0	180	AA455985	Arabisidopsis thalia
41	50.0	180	AA459941	Arabisidopsis thalia
42	50.0	181	AA425268	Eucalyptus grandis
43	50.0	185	AA434781	Chlamydia pneumoni
44	50.0	192	AA486939	Hepatitis C virus
45	50.0	192	AA489510	Hepatitis C virus
46	50.0	193	AA483986	HCT27 El protein.
47	50.0	196	AA455984	Arabisidopsis thalia
48	50.0	196	AA459940	Arabisidopsis thalia
49	50.0	201	AA488834	Protein encoded by
50	50.0	217	AA404638	Arabisidopsis thalia
51	50.0	221	AA450589	Human normal bladd
52	50.0	231	AA404036	HIV-1 (BH10 clone)
53	50.0	240	AA459676	Z. mays MADS-box p
54	50.0	242	AA422390	Antigen ac-1b. El
55	50.0	247	AA459398	Human BR43x2, an l
56	50.0	251	AA408987	Arabisidopsis thalia
57	50.0	251	AA453841	Arabisidopsis thalia
58	50.0	256	AA404637	Arabisidopsis thalia
59	50.0	274	AA421589	Arabisidopsis thalia
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61	50.0	280	AA404636	Arabisidopsis thalia
62	50.0	288	AA479320	Corynebacterium gl
63	50.0	292	AA421588	Arabisidopsis thalia
64	50.0	293	AA475783	Human lymphocyte s
65	50.0	293	AA436312	Human neutrokin-a
66	50.0	293	AA454000	A transmembrane ac
67	50.0	293	AA459341	Arabisidopsis thalia
68	50.0	293	AA471914	Human tumour necro
69	50.0	294	AA421587	Arabisidopsis thalia
70	50.0	295	AA459340	Arabisidopsis thalia
71	50.0	296	AA479319	Corynebacterium gl
72	50.0	303	AA428099	Arabisidopsis thalia
73	50.0	312	AA459327	Murine WDS12 prote
74	50.0	336	AA466021	Arabisidopsis thalia
75	50.0	343	AA416666	Human ORF1430
76	50.0	343	AA466020	Human ORF1430
77	50.0	347	AA466197	Maize DIMBOA biosy
78	50.0	351	AA466019	Arabisidopsis thalia
79	50.0	367	AA405434	Arabisidopsis thalia
80	50.0	368	AA405433	Arabisidopsis thalia
81	50.0	371	AA429193	Amino acid sequenc
82	50.0	381	AA435327	Amino acid sequenc
83	50.0	388	AA404998	Mycobacterium spec
84	50.0	396	AA405432	Arabisidopsis thalia

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Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meliga, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CCCI577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-459-444-19

Query Match 41.7%; Score 5; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QEVK 12
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DB 278 QEVK 282

RESULT 50
US-08-137-627-4
Sequence 4, Application US/08137627
Patent No. 5681737
GENERAL INFORMATION:
APPLICANT: Gee, Pauline
APPLICANT: Maron, Dorothy M.
APPLICANT: Ames, Bruce N.
TITLE OF INVENTION: A DETECTION SYSTEM FOR MUTAGENS THAT
IDENTIFIES MUTAGENIC CHANGES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hoiabach, Test, Albritton & Herbert,
ADDRESSEE: Attn: Karen S. Smith
STREET: 4 Emparadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,627
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Karen S.
REGISTRATION NUMBER: 31,426
REFERENCE/DOCKET NUMBER: A-58312/KSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-627-4

Query Match 41.7%; Score 5; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVA 5
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DB 249 STPVA 253

Search completed: August 15, 2001, 12:33:53
Job time: 58 sec

APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-595A-19

Query Match 41.7%; Score 5; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVKK 12
IIII
Db 278 QEVKK 282

RESULT 48
US-08-459-504B-19
Sequence 19, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwells Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-504B-19

Query Match 41.7%; Score 5; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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IIII
Db 278 QEVKK 282

RESULT 49
US-08-459-444-19
Sequence 19, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.

APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Lauulis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sprull, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-951-715A-19

Query Match 41.7%; Score 5; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 OEYK 12
| | | | |
DB 278 OEYK 282

RESULT 46
US-08-459-448A-19
Sequence 19, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Lauulis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-448A-19

Query Match 41.7%; Score 5; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 OEYK 12
| | | | |
DB 278 OEYK 282

RESULT 47
US-08-459-595A-19
Sequence 19, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.

APPLICANT: PESCHER, PASCALE
APPLICANT: ROMAIN, FELIX
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USES FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0122-0 PCT
CURRENT APPLICATION NUMBER: US/08/875,494
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: PCT/FR96/00166
EARLIER FILING DATE: 1996-02-01
EARLIER APPLICATION NUMBER: 382184
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 325
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-08-875-494-2

Query Match 41.7%; Score 5; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
11111
DB 66 TPVAP 70

RESULT 43
US-08-444-818-152
Sequence 152, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBY Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 152:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-818-152

Query Match 41.7%; Score 5; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
11111
DB 113 PVAPT 117

RESULT 44
US-08-444-818-156
Sequence 156, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBY Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Human 27
US-08-444-818-156

Query Match 41.7%; Score 5; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
11111
DB 113 PVAPT 117

RESULT 45
US-07-951-715A-19
Sequence 19, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Kosziel, Michael G.
APPLICANT: Desai, Nalin M.

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-382-184-2

Query Match 41.7%; Score 5; DB 1; Length 325;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAP 6
|||||
DB 66 TPVAP 70

RESULT 39
US-08-641-356-2
Sequence 2, Application US/08641356
Patent No. 5866130

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,356
FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-641-356-2

Query Match 41.7%; Score 5; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAP 6
|||||
DB 66 TPVAP 70

RESULT 40
US-09-132-528-2
Sequence 2, Application US/09132528A
Patent No. 6221353

GENERAL INFORMATION:
APPLICANT: LAQUEYERRE, Anne
APPLICANT: MARCHAL, Gilles
APPLICANT: PESCHER, Pascale

APPLICANT: ROMAIN, Felix
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0138-0DIY
CURRENT APPLICATION NUMBER: US/09/132,528A
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 08/641,356
EARLIER FILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2

LENGTH: 325
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-132-528-2

Query Match 41.7%; Score 5; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAP 6
|||||
DB 66 TPVAP 70

RESULT 41
US-09-132-528-3
Sequence 3, Application US/09132528A
Patent No. 6221353

GENERAL INFORMATION:
APPLICANT: LAQUEYERRE, Anne
APPLICANT: MARCHAL, Gilles
APPLICANT: PESCHER, Pascale
APPLICANT: ROMAIN, Felix
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0138-0DIY
CURRENT APPLICATION NUMBER: US/09/132,528A
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 08/641,356
EARLIER FILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 3
LENGTH: 325
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-132-528-3

Query Match 41.7%; Score 5; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAP 6
|||||
DB 66 TPVAP 70

RESULT 42
US-08-875-494-2
Sequence 2, Application US/08875494
Patent No. 6221610
GENERAL INFORMATION:
APPLICANT: LAQUEYERRE, ANNE
APPLICANT: MARCHAL, GILLES

ORGANISM: Mycobacterium tuberculosis
US-09-132-528-4

Query Match 41.7%; Score 5; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
DB 27 TPVAP 31

RESULT 36
US-08-875-494-3
Sequence 3, Application US/08875494
Patent No. 6221610
GENERAL INFORMATION:
APPLICANT: LAQUEYERIE, ANNE
APPLICANT: MARCHEL, GILLES
APPLICANT: PESCHER, PASCALE
APPLICANT: ROMAIN, FELIX
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USES FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0122-0 PCT
CURRENT APPLICATION NUMBER: US/08/875,494
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: PCT/FR96/00166
EARLIER FILING DATE: 1996-02-01
EARLIER APPLICATION NUMBER: 382184
EARLIER FILING DATE: 1995-02-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3
LENGTH: 286
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-08-875-494-3

Query Match 41.7%; Score 5; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
DB 27 TPVAP 31

RESULT 37
US-08-810-572A-2
Sequence 2, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 41.7%; Score 5; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APPOE 9
DB 239 APPOE 243

RESULT 38
US-08-382-184-2
Sequence 2, Application US/08382184
Patent No. 5714593
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
US-08-468-544-12

Query Match 41.7%, Score 5, DB 4, Length 264;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TPVPA 5
| | | | |
Db 40 STVPA 44

RESULT 33
US-08-382-184-3
Sequence 3, Application US/08382184
Patent No. 5714593
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-382-184-3

Query Match 41.7%, Score 5, DB 1, Length 286;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TPVAP 6
| | | | |
Db 27 TPVAP 31

RESULT 34
US-08-641-356-3
Sequence 3, Application US/08641356
Patent No. 5866130
GENERAL INFORMATION:
APPLICANT:

APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,356
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-641-356-3

Query Match 41.7%, Score 5, DB 2, Length 286;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TPVAP 6
| | | | |
Db 27 TPVAP 31

RESULT 35
US-09-132-528-4
Sequence 4, Application US/09132528A
Patent No. 6221353
GENERAL INFORMATION:

APPLICANT: LAQUEYERRE, Anne
APPLICANT: MARCHAL, Gilles
APPLICANT: PESCHER, Pascale
APPLICANT: ROMAIN, Felix
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0138-0DIY
CURRENT APPLICATION NUMBER: US/09/132,528A
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 08/641,356
EARLIER FILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 4
LENGTH: 286
TYPE: PRT

APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:
APPLICATION NUMBER: US/07/991,512
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-189-12

Query Match 41.7%; Score 5; DB 3; Length 264;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVA 5
Db 40 STPVA 44

RESULT 31
US-08-465-465-2
Sequence 2, Application US/08465465
Patent No. 6210968
GENERAL INFORMATION:
APPLICANT: Giulio Ratti
TITLE OF INVENTION: RECOMBINANT CHLAMYDIA TRACHOMATIS PCP3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and NO. 6210968-rls
STREET: One Liberty Place - 46th Floor
City: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,465
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,980
FILING DATE: 19-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: CHIR-0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-465-2

Query Match 41.7%; Score 5; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVA 5
Db 40 STPVA 44

RESULT 32
US-08-468-544-12
Sequence 12, Application US/08468544
Patent No. 6248563
GENERAL INFORMATION:
APPLICANT: Ratti, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMD ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
City: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear

AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
SPOZOZOTE 21.5 KB ANTIGEN, AC-6B
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/581,693
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
SEQ ID NO.: 3
LENGTH: 242
5273901-3

Query Match 41.7%; Score 5; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 2,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTQEV 10
|||||
DB 36 PTQEV 40

RESULT 28
5482709-2
Patent No. 5482709
APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,432
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 581,693
FILING DATE: 12-SEP-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
SEQ ID NO.: 2
LENGTH: 242
5482709-2

Query Match 41.7%; Score 5; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 2,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTQEV 10
|||||
DB 36 PTQEV 40

RESULT 29
US-08-969-644-12
Sequence 12, Application US/08969644
Patent No. 6096519
GENERAL INFORMATION:
APPLICANT: Ratelli, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA

TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,152
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-969-644-12

Query Match 41.7%; Score 5; DB 3; Length 264;
Best Local Similarity 100.0%; Pred. No. 2,5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
|||||
DB 40 STPVA 44

RESULT 30
US-08-444-189-12
Sequence 12, Application US/08444189
Patent No. 6110705
GENERAL INFORMATION:
APPLICANT: Ratelli, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA

REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: JH27
US-08-444-818-167

Query Match 41.7%; Score 5; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
|1111|
DB 125 PVAPT 129

RESULT 25
PCT-US95-10398-57
Sequence 57, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BORK, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HERPESVIRUS C VITUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
NUMBER OF INVENTIONS: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

ORIGINAL SOURCE:
ORGANISM: homoplans
INDIVIDUAL ISOLATE: S18
PCT-US95-10398-57

Query Match 41.7%; Score 5; DB 5; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
|1111|
DB 50 PVAPT 54

RESULT 26
US-08-969-721-8
Sequence 8, Application US/08969721
Patent No. 5972339
GENERAL INFORMATION:
APPLICANT: Walker, Bruce D.
TITLE OF INVENTION: METHODS OF ELICITING ANTI-HIV-1
TITLE OF INVENTION: HELPER T CELL RESPONSES
NUMBER OF INVENTIONS: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fastseq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,721
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/732001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-969-721-8

Query Match 41.7%; Score 5; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVR 11
|1111|
DB 178 TOEVR 182

RESULT 27
5273901-3
Patent No. 5273901
APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;

APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
US-08-468-570-57

Query Match 41.7%; Score 5; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
Db 50 PVAPT 54

RESULT 23
US-08-290-665A-57
Sequence 57, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
US-08-290-665A-57

Query Match 41.7%; Score 5; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
Db 50 PVAPT 54

RESULT 24
US-08-444-818-167
Sequence 167, Application US/08444818
Patent No. 615087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Ruter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chilton Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Ailsa A.
REGISTRATION NUMBER: 33,895

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-542-44

Query Match 41.7%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
|||||
DB 50 PVAPT 54

RESULT 20
US-08-231-368-44
Sequence 44, Application US/08231368
Patent No. 5756312
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chilton Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-231-368-44

Query Match 41.7%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
|||||
DB 50 PVAPT 54

RESULT 21
US-08-440-210-44
Sequence 44, Application US/08440210
Patent No. 5766845
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chilton Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,210
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-210-44

Query Match 41.7%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
|||||
DB 50 PVAPT 54

RESULT 22
US-08-468-570-57
Sequence 57, Application US/08468570
Patent No. 5871962
GENERAL INFORMATION:

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 PTOEV 10
| | | | |
Db 43 PTOEV 47

RESULT 17

US-08-086-428B-57

; Sequence 57, Application US/08086428B
; Patent No. 5514359

; GENERAL INFORMATION:

; APPLICANT: BURKH, J., MILLER, R.H. AND

; APPLICANT: PURCELL, R.H.

; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE

; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE

; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN

; NUMBER OF SEQUENCES: 159

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/086.428B

; FILING DATE: 29-JUN-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: RICHARD W. BORK

; REGISTRATION NUMBER: 36,459

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 192 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; ORGANISM: homosapiens

; INDIVIDUAL ISOLATE: S18

US-08-086-428B-57

Query Match 41.7%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PVAPT 7
| | | | |
Db 50 PVAPT 54

RESULT 18

US-08-440-103-44

; Sequence 44, Application US/08440103

; Patent No. 5670152

; GENERAL INFORMATION:

; APPLICANT: Weiner, Amy J.

; APPLICANT: Houghton, Michael

; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/440.103

; FILING DATE: 12-MAY-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/231.368

; FILING DATE:

; APPLICATION NUMBER: US 07/759,575

; FILING DATE: 13-SEP-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McClung, Barbara G.

; REGISTRATION NUMBER: 33,113

; REFERENCE/DOCKET NUMBER: 0205.001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 601-2708

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 192 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-440-103-44

Query Match 41.7%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PVAPT 7
| | | | |
Db 50 PVAPT 54

RESULT 19

US-08-440-542-44

; Sequence 44, Application US/08440542

; Patent No. 5670153

; GENERAL INFORMATION:

; APPLICANT: Weiner, Amy J.

; APPLICANT: Houghton, Michael

; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/440.542

; FILING DATE: 12-MAY-1995

; CLASSIFICATION: 424

RESULT 14
US-09-001-984C-55
; Sequence 55, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001.984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034.003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-55

Query Match 41.7%; Score 5; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAP 6
11111
Db 1 TPVAP 5

RESULT 15
US-08-810-572A-4
; Sequence 4, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810.572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-487-1684
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-4

Query Match 41.7%; Score 5; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APPOE 9
11111
Db 53 APPOE 57

RESULT 16
US-08-497-025-10
; Sequence 10, Application US/08497025
; Patent No. 5646251
; GENERAL INFORMATION:
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Rivas, Alberto
; APPLICANT: Laus, Reiner
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: ALLOREACTION-ASSOCIATED ANTIGEN (AAR):
; TITLE OF INVENTION: A NOVEL MEMBER OF THE IMMUNOGLOBULIN GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497.025
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,212
; FILING DATE: 05-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..118
; OTHER INFORMATION:
; OTHER INFORMATION: /note= "A variable-type
; immunoglobulin-type domain of AAg-h-1."
US-08-497-025-10

Query Match 41.7%; Score 5; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14-20
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-17

Query Match 50.0%; Score 6; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PVAPTQ 8
IIIIII
-
DB 8 PVAPTQ 13

RESULT 13
US-08-456-670B-35
Sequence 35, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria innocua
US-08-456-670B-35

Query Match 41.7%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 QEVKK 12
IIIIII
DB 7 QEVKK 11

ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-26

Query Match 66.7%; Score 8; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPRO 8
Db 2 STPVAPRO 9

RESULT 10
US-08-127-499A-28
Sequence 28, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5330
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-28

Query Match 58.3%; Score 7; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PTOEVKK 12
Db 1 PTOEVKK 7

RESULT 11
US-08-482-847-28
Sequence 28, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5330
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-28

Query Match 58.3%; Score 7; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTOEVKK 12
Db 1 PTOEVKK 7

RESULT 12
US-08-456-670B-17
Sequence 17, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWETTER, WINFRIED
APPLICANT: BURGER, CHRISTA

FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-26

Query Match 100.0%; Score 12; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STPVAPTOEVKK 12
|||||
Db 146 STPVAPTOEVKK 157

RESULT 8
US-08-456-670B-31
Sequence 31, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

Query Match 83.3%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVAPTOEVKK 12
|||||
Db 1 PVAPTOEVKK 10

RESULT 9
US-08-456-670B-26
Sequence 26, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992

APPLICANT: LINNWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ. ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-40

Query Match 100.0%; Score 12; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPTOEVK 12
DB 146 STPVAPTOEVK 157

RESULT 6
US-08-127-499A-26
Sequence 26, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra

TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-26

Query Match 100.0%; Score 12; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPTOEVK 12
DB 146 STPVAPTOEVK 157

RESULT 7
US-08-482-847-26
Sequence 26, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499

Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
|||||
Db 3 STPVAPTOEVKK 14

RESULT 3

US-08-482-847-27

Sequence 27, Application US/08482847

Patent No. 5556757

GENERAL INFORMATION:

APPLICANT: VAN ALSTYNE, Diane

APPLICANT: SHARMA, Lawrence Rajendra

TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR

TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR

TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,847

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/127,499

FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 51916/104/INBI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

US-08-482-847-27

Query Match 100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;

Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
|||||
Db 3 STPVAPTOEVKK 14

RESULT 4

US-08-456-670B-39

Sequence 39, Application US/08456670B

Patent No. 5932415

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED

APPLICANT: PAMELZIK, MARTINA

APPLICANT: LINKEWELER, WINFRIED

APPLICANT: BURGER, CHRISTA

APPLICANT: HOFMANN, GOTTFRIED

APPLICANT: BUBERT, ANDREAS

APPLICANT: GOEBEL, WERNER

APPLICANT: KOHLER, STEFAN

TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

TITLE OF INVENTION: LISTERIAS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD., SUITE 1400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: US

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,670B

FILING DATE: 01-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/412,227

FILING DATE: 27-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/075,248

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4239567.4

FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4219111.4

FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1694D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

TELEX: 64191

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Listeria monocytogenes

STRAIN: EGD

US-08-456-670B-39

Query Match 100.0%; Score 12; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;

Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
|||||
Db 77 STPVAPTOEVKK 88

RESULT 5

US-08-456-670B-40

Sequence 40, Application US/08456670B

Patent No. 5932415

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED

APPLICANT: PAMELZIK, MARTINA

977 4 33.3 236 3 US-08-493-071-15 Sequence 15, Appl
978 4 33.3 236 4 US-09-049-672A-7 Sequence 7, Appl
979 4 33.3 236 4 US-09-049-672A-13 Sequence 13, Appl
980 4 33.3 236 4 US-08-961-083-96 Sequence 96, Appl
981 4 33.3 237 1 US-08-096-946-10 Sequence 10, Appl
982 4 33.3 237 1 US-08-096-946-11 Sequence 11, Appl
983 4 33.3 237 2 US-08-672-564-3 Sequence 3, Appl
984 4 33.3 237 2 US-08-844-024-2 Sequence 2, Appl
985 4 33.3 237 3 US-08-718-547-2 Sequence 2, Appl
986 4 33.3 237 3 US-08-768-859A-16 Sequence 16, Appl
987 4 33.3 237 3 US-08-768-859A-21 Sequence 21, Appl
988 4 33.3 237 3 US-08-767-820A-16 Sequence 16, Appl
989 4 33.3 237 3 US-08-767-820A-21 Sequence 21, Appl
990 4 33.3 237 3 US-08-767-820A-16 Sequence 16, Appl
991 4 33.3 237 3 US-08-622-046B-1 Sequence 1, Appl
992 4 33.3 237 3 US-08-622-046B-7 Sequence 7, Appl
993 4 33.3 237 3 US-08-622-046B-12 Sequence 12, Appl
994 4 33.3 237 4 US-08-944-483-37 Sequence 37, Appl
995 4 33.3 237 4 US-08-944-483-38 Sequence 38, Appl
996 4 33.3 237 4 US-09-100-264-1 Sequence 1, Appl
997 4 33.3 237 4 US-09-100-264-3 Sequence 3, Appl
998 4 33.3 237 4 US-09-100-264-12 Sequence 12, Appl
999 4 33.3 237 5 PCT-US94-07329-10 Sequence 10, Appl
1000 4 33.3 237 5 PCT-US94-07329-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-456-670B-30
; Sequence 30, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, STEFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINXWEILER, WINFRIED
; APPLICANT: BUNGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILDEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4

; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ. ID NO.: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
; US-08-456-670B-30

Query Match 100.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVPAPTOEVKK 12
DB 1 STVPAPTOEVKK 12

RESULT 2
US-08-127-499A-27
; Sequence 27, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ. ID NO.: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-127-499A-27

Query Match 100.0%; Score 12; DB 1; Length 21;

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832	4	33.3	163	4	US-09-006-632-7	Sequence 7, Appli	905	4	33.3	201	2	US-08-916-901-8	Sequence 8, Appli
833	4	33.3	164	1	US-08-033-857A-8	Sequence 8, Appli	906	4	33.3	201	2	US-08-718-270A-13	Sequence 13, Appli
834	4	33.3	164	1	US-08-374-983A-8	Sequence 8, Appli	907	4	33.3	205	2	US-08-829-110-6	Sequence 6, Appli
835	4	33.3	164	2	US-08-824-405-2	Sequence 2, Appli	908	4	33.3	205	2	US-08-748-483-5	Sequence 5, Appli
836	4	33.3	166	2	US-08-483-695-3	Sequence 3, Appli	909	4	33.3	207	2	US-09-022-940-1	Sequence 1, Appli
837	4	33.3	166	2	US-07-965-285-3	Sequence 3, Appli	910	4	33.3	207	3	US-08-996-338-23	Sequence 23, Appli
838	4	33.3	166	2	US-08-487-231-3	Sequence 3, Appli	911	4	33.3	207	3	US-09-216-386-1	Sequence 1, Appli
839	4	33.3	166	2	US-08-631-338-55	Sequence 55, Appli	912	4	33.3	208	2	US-08-531-525-15	Sequence 15, Appli
840	4	33.3	166	4	US-09-201-912-3	Sequence 3, Appli	913	4	33.3	208	2	US-08-531-525-17	Sequence 17, Appli
841	4	33.3	169	1	US-07-841-646-9	Sequence 9, Appli	914	4	33.3	208	2	US-08-844-120-1	Sequence 1, Appli
842	4	33.3	169	1	US-08-147-023-9	Sequence 9, Appli	915	4	33.3	208	2	US-08-718-270A-15	Sequence 15, Appli
843	4	33.3	169	1	US-08-447-570-9	Sequence 9, Appli	916	4	33.3	208	2	US-08-718-270A-17	Sequence 17, Appli
844	4	33.3	169	2	US-08-449-700-9	Sequence 9, Appli	917	4	33.3	208	4	US-08-097-869-6	Sequence 6, Appli
845	4	33.3	169	2	US-08-449-699A-9	Sequence 9, Appli	918	4	33.3	210	1	US-07-667-276A-2	Sequence 2, Appli
846	4	33.3	173	3	US-09-188-579-87	Sequence 87, Appli	919	4	33.3	211	4	US-08-097-869-8	Sequence 8, Appli
847	4	33.3	173	3	US-09-315-444-87	Sequence 87, Appli	920	4	33.3	212	2	US-08-531-525-18	Sequence 18, Appli
848	4	33.3	174	2	US-08-683-262B-45	Sequence 45, Appli	921	4	33.3	212	2	US-08-718-270A-18	Sequence 18, Appli
849	4	33.3	174	2	US-08-683-262B-48	Sequence 48, Appli	922	4	33.3	212	4	US-08-973-462-25	Sequence 25, Appli
850	4	33.3	176	3	US-09-130-663-29	Sequence 29, Appli	923	4	33.3	215	2	US-08-912-129A-58	Sequence 58, Appli
851	4	33.3	176	3	US-08-392-794A-8	Sequence 8, Appli	924	4	33.3	216	2	US-08-929-418-2	Sequence 2, Appli
852	4	33.3	176	3	US-09-432-335-29	Sequence 29, Appli	925	4	33.3	219	2	US-08-902-516-2	Sequence 2, Appli
853	4	33.3	177	1	US-08-450-257-61	Sequence 61, Appli	926	4	33.3	220	2	US-08-726-306A-29	Sequence 29, Appli
854	4	33.3	177	1	US-08-450-246-61	Sequence 61, Appli	927	4	33.3	221	2	US-08-032-848C-13	Sequence 13, Appli
855	4	33.3	177	1	US-08-450-098-61	Sequence 61, Appli	928	4	33.3	221	2	US-08-861-269-6	Sequence 6, Appli
856	4	33.3	177	1	US-08-451-233-61	Sequence 61, Appli	929	4	33.3	221	2	US-09-134-596-6	Sequence 6, Appli
857	4	33.3	177	1	US-08-450-236-61	Sequence 61, Appli	930	4	33.3	221	3	US-09-293-273-6	Sequence 6, Appli
858	4	33.3	178	3	US-09-081-180-2	Sequence 2, Appli	931	4	33.3	222	1	US-08-458-516-22	Sequence 22, Appli
859	4	33.3	178	3	US-09-040-786-2	Sequence 2, Appli	932	4	33.3	224	1	US-08-553-516-2	Sequence 2, Appli
860	4	33.3	178	3	US-08-705-875A-8	Sequence 8, Appli	933	4	33.3	225	2	US-08-886-765-2	Sequence 2, Appli
861	4	33.3	178	3	US-09-122-443-9	Sequence 9, Appli	934	4	33.3	225	2	US-09-074-512-3	Sequence 3, Appli
862	4	33.3	178	4	US-09-147-928-4	Sequence 4, Appli	935	4	33.3	225	4	US-09-115-660-2	Sequence 2, Appli
863	4	33.3	178	4	US-09-220-731-23	Sequence 23, Appli	936	4	33.3	226	1	US-07-929-198-2	Sequence 2, Appli
864	4	33.3	178	4	US-09-220-731-24	Sequence 24, Appli	937	4	33.3	226	1	US-07-929-198-4	Sequence 4, Appli
865	4	33.3	178	4	US-09-221-970-8	Sequence 8, Appli	938	4	33.3	226	1	US-07-929-198-6	Sequence 6, Appli
866	4	33.3	179	2	US-08-621-803-257	Sequence 257, App	939	4	33.3	226	2	US-08-557-146-15	Sequence 15, Appli
867	4	33.3	179	2	US-08-621-803-261	Sequence 261, App	940	4	33.3	226	2	US-09-154-344-15	Sequence 15, Appli
868	4	33.3	180	3	US-09-038-909-4	Sequence 4, Appli	941	4	33.3	226	4	US-08-944-483-13	Sequence 43, Appli
869	4	33.3	181	4	US-08-961-083-114	Sequence 114, App	942	4	33.3	227	4	US-08-944-483-13	Sequence 40, Appli
870	4	33.3	185	2	US-08-865-336-3	Sequence 3, Appli	943	4	33.3	229	4	US-08-751-359-22	Sequence 22, Appli
871	4	33.3	186	1	US-08-928-443-3	Sequence 3, Appli	944	4	33.3	230	1	US-08-118-469A-3	Sequence 3, Appli
872	4	33.3	186	3	US-09-129-055-3	Sequence 3, Appli	945	4	33.3	230	1	US-08-909-119-3	Sequence 3, Appli
873	4	33.3	187	1	US-08-450-257-62	Sequence 62, Appli	946	4	33.3	230	2	US-08-844-120-3	Sequence 3, Appli
874	4	33.3	187	1	US-08-450-246-62	Sequence 62, Appli	947	4	33.3	230	2	US-09-022-940-3	Sequence 3, Appli
875	4	33.3	187	1	US-08-450-098-62	Sequence 62, Appli	948	4	33.3	230	2	US-09-022-940-5	Sequence 5, Appli
876	4	33.3	187	1	US-08-451-233-62	Sequence 62, Appli	949	4	33.3	230	3	US-09-216-001-3	Sequence 3, Appli
877	4	33.3	187	1	US-08-450-236-62	Sequence 62, Appli	950	4	33.3	230	3	US-09-216-386-3	Sequence 3, Appli
878	4	33.3	188	3	US-09-122-443-14	Sequence 14, Appli	951	4	33.3	230	3	US-09-216-386-5	Sequence 5, Appli
879	4	33.3	189	1	US-08-026-758-18	Sequence 18, Appli	952	4	33.3	230	4	US-08-878-862-3	Sequence 3, Appli
880	4	33.3	189	4	US-08-779-764A-28	Sequence 28, Appli	953	4	33.3	232	1	US-08-278-091-8	Sequence 8, Appli
881	4	33.3	190	4	US-09-221-970-14	Sequence 14, Appli	954	4	33.3	232	1	US-08-483-859-8	Sequence 8, Appli
882	4	33.3	192	1	US-08-086-428B-58	Sequence 53, Appli	955	4	33.3	232	1	US-08-472-173-8	Sequence 8, Appli
883	4	33.3	192	1	US-08-086-428B-58	Sequence 58, Appli	956	4	33.3	232	2	US-08-487-167-8	Sequence 8, Appli
884	4	33.3	192	1	US-08-086-428B-85	Sequence 85, Appli	957	4	33.3	232	2	US-08-482-816-8	Sequence 8, Appli
885	4	33.3	192	2	US-08-468-570-53	Sequence 53, Appli	958	4	33.3	232	2	US-08-296-149-8	Sequence 8, Appli
886	4	33.3	192	2	US-08-468-570-58	Sequence 58, Appli	959	4	33.3	232	2	US-08-801-499-8	Sequence 8, Appli
887	4	33.3	192	2	US-08-468-570-85	Sequence 85, Appli	960	4	33.3	232	2	US-08-978-404B-45	Sequence 45, Appli
888	4	33.3	192	2	US-08-290-665A-53	Sequence 53, Appli	961	4	33.3	232	2	US-08-615-271-8	Sequence 8, Appli
889	4	33.3	192	2	US-08-290-665A-58	Sequence 58, Appli	962	4	33.3	232	2	US-09-074-660-8	Sequence 8, Appli
890	4	33.3	192	2	US-08-290-665A-85	Sequence 85, Appli	963	4	33.3	232	3	US-09-074-669-8	Sequence 8, Appli
891	4	33.3	192	4	US-09-475-316A-23	Sequence 23, Appli	964	4	33.3	232	3	US-09-106-658-8	Sequence 8, Appli
892	4	33.3	192	5	PCT-US94-05795-3	Sequence 3, Appli	965	4	33.3	232	4	US-09-106-666A-8	Sequence 8, Appli
893	4	33.3	192	5	PCT-US95-10398-53	Sequence 53, Appli	966	4	33.3	232	4	US-09-106-467-8	Sequence 8, Appli
894	4	33.3	192	5	PCT-US95-10398-58	Sequence 58, Appli	967	4	33.3	232	6	5204259-1	Patent No. 5204259
895	4	33.3	192	5	PCT-US95-10398-85	Sequence 85, Appli	968	4	33.3	233	4	US-08-523-894-6	Sequence 6, Appli
896	4	33.3	194	5	US-08-621-803-255	Sequence 255, App	969	4	33.3	234	1	US-08-287-959-10	Sequence 10, Appli
897	4	33.3	194	3	US-09-032-372-13	Sequence 12, Appli	970	4	33.3	234	3	US-08-487-550-2	Sequence 2, Appli
898	4	33.3	194	3	US-09-078-317-12	Sequence 12, Appli	971	4	33.3	235	1	US-08-458-516-23	Sequence 23, Appli
899	4	33.3	195	2	US-08-621-803-263	Sequence 263, App	972	4	33.3	235	2	US-08-378-929-12	Sequence 12, Appli
900	4	33.3	196	4	US-09-383-586-11	Sequence 11, Appli	973	4	33.3	235	4	US-09-049-672A-10	Sequence 10, Appli
901	4	33.3	198	1	US-08-097-827-2	Sequence 2, Appli	974	4	33.3	235	4	US-09-049-672A-12	Sequence 12, Appli
902	4	33.3	198	1	US-08-494-574-2	Sequence 2, Appli	975	4	33.3	235	4	US-09-329-350-31	Sequence 31, Appli
903	4	33.3	201	2	US-08-531-525-13	Sequence 13, Appli	976	4	33.3	236	3	US-08-487-550-10	Sequence 10, Appli

685	4	33.3	135	1	US-08-477-728-19	Sequence 19, Appl	758	4	33.3	139	5	PCT-US93-07231-5	Sequence 5, Appl1
686	4	33.3	135	1	US-08-474-040-19	Sequence 19, Appl	759	4	33.3	139	5	PCT-US93-07231-6	Sequence 5, Appl1
687	4	33.3	135	1	US-08-487-200-19	Sequence 19, Appl	760	4	33.3	139	5	PCT-US93-08742-5	Sequence 5, Appl1
688	4	33.3	135	1	US-08-137-117D-100	Sequence 100, App	761	4	33.3	139	5	PCT-US93-08742-6	Sequence 6, Appl1
689	4	33.3	135	1	US-08-137-117D-102	Sequence 102, App	762	4	33.3	139	5	PCT-US93-08808-5	Sequence 5, Appl1
690	4	33.3	135	1	US-08-137-117D-112	Sequence 112, App	763	4	33.3	139	5	PCT-US93-08808-6	Sequence 6, Appl1
691	4	33.3	135	2	US-08-436-717-100	Sequence 100, App	764	4	33.3	139	5	PCT-US93-08885-5	Sequence 5, Appl1
692	4	33.3	135	2	US-08-436-717-102	Sequence 102, App	765	4	33.3	139	5	PCT-US93-08885-6	Sequence 6, Appl1
693	4	33.3	135	2	US-08-436-717-112	Sequence 112, App	766	4	33.3	139	5	PCT-US94-13181-10	Sequence 10, Appl
694	4	33.3	135	2	US-08-303-5698-31	Sequence 31, App	767	4	33.3	140	5	PCT-US94-13181-12	Sequence 12, Appl
695	4	33.3	135	2	US-08-621-751A-16	Sequence 16, Appl	768	4	33.3	140	5	US-08-836-561-63	Sequence 28, Appl
696	4	33.3	135	3	US-08-484-537-19	Sequence 19, Appl	769	4	33.3	140	3	US-08-836-561-74	Sequence 63, Appl
697	4	33.3	136	3	US-08-649-100-41	Sequence 41, Appl	770	4	33.3	140	3	US-08-836-561-77	Sequence 74, Appl
698	4	33.3	136	5	US-08-646-265A-99	Sequence 99, Appl	771	4	33.3	140	3	US-08-836-561-83	Sequence 83, Appl
699	4	33.3	136	5	PCT-US93-11611-11	Sequence 11, Appl	772	4	33.3	140	4	US-08-569-147-82	Sequence 82, Appl
700	4	33.3	137	2	US-08-477-281A-96	Sequence 96, Appl	773	4	33.3	140	5	US-08-579-378A-12	Sequence 12, Appl
701	4	33.3	137	2	US-08-472-281A-96	Sequence 96, Appl	774	4	33.3	140	5	PCT-US93-11612-12	Sequence 12, Appl
702	4	33.3	137	2	US-08-477-989A-96	Sequence 96, Appl	775	4	33.3	141	1	US-08-461-284-4	Sequence 4, Appl
703	4	33.3	137	3	US-08-513-968-38	Sequence 38, Appl	776	4	33.3	141	1	US-08-462-939-4	Sequence 4, Appl1
704	4	33.3	138	3	US-08-513-968-44	Sequence 44, Appl	777	4	33.3	141	1	US-08-253-877C-4	Sequence 4, Appl1
705	4	33.3	139	1	US-07-718-274A-2	Sequence 2, Appl	778	4	33.3	141	2	US-08-452-164A-4	Sequence 4, Appl1
706	4	33.3	139	1	US-08-163-877-10	Sequence 10, Appl	779	4	33.3	142	2	US-08-561-521-17	Sequence 17, Appl
707	4	33.3	139	1	US-08-149-106-2	Sequence 2, Appl1	780	4	33.3	142	2	US-08-476-176B-12	Sequence 12, Appl
708	4	33.3	139	1	US-08-298-021-2	Sequence 2, Appl1	781	4	33.3	142	2	US-08-476-176B-14	Sequence 14, Appl
709	4	33.3	139	1	US-08-278-729A-5	Sequence 5, Appl1	782	4	33.3	142	2	US-08-476-176B-16	Sequence 16, Appl
710	4	33.3	139	1	US-08-278-729A-6	Sequence 6, Appl1	783	4	33.3	142	2	US-08-476-176B-18	Sequence 18, Appl
711	4	33.3	139	1	US-08-155-343A-5	Sequence 5, Appl1	784	4	33.3	142	3	US-08-127-721A-12	Sequence 12, Appl
712	4	33.3	139	1	US-08-155-343A-6	Sequence 6, Appl1	785	4	33.3	142	3	US-08-127-721A-14	Sequence 14, Appl
713	4	33.3	139	1	US-08-406-672-5	Sequence 5, Appl1	786	4	33.3	142	3	US-08-127-721A-16	Sequence 16, Appl
714	4	33.3	139	1	US-08-406-672-6	Sequence 6, Appl1	787	4	33.3	142	3	US-08-127-721A-18	Sequence 18, Appl
715	4	33.3	139	1	US-08-643-563A-5	Sequence 5, Appl1	788	4	33.3	142	3	US-08-485-246A-12	Sequence 12, Appl
716	4	33.3	139	1	US-08-643-563A-6	Sequence 6, Appl1	789	4	33.3	142	3	US-08-485-246A-14	Sequence 14, Appl
717	4	33.3	139	1	US-08-643-763A-5	Sequence 5, Appl1	790	4	33.3	142	3	US-08-485-246A-16	Sequence 16, Appl
718	4	33.3	139	1	US-08-643-763A-6	Sequence 6, Appl1	791	4	33.3	142	3	US-08-485-246A-18	Sequence 18, Appl
719	4	33.3	139	1	US-08-462-623-5	Sequence 5, Appl1	792	4	33.3	142	5	PCT-US95-01219-11	Sequence 17, Appl
720	4	33.3	139	1	US-08-462-623-6	Sequence 6, Appl1	793	4	33.3	144	3	US-08-545-809A-100	Sequence 100, App
721	4	33.3	139	1	US-08-451-953A-5	Sequence 5, Appl1	794	4	33.3	146	1	US-08-276-852-155	Sequence 155, App
722	4	33.3	139	1	US-08-451-953A-6	Sequence 6, Appl1	795	4	33.3	146	1	US-08-899-575-155	Sequence 155, App
723	4	33.3	139	1	US-08-360-914B-10	Sequence 10, Appl	796	4	33.3	146	1	US-08-899-575-155	Sequence 155, App
724	4	33.3	139	1	US-08-253-877C-19	Sequence 19, Appl	797	4	33.3	146	5	PCT-US95-08743-155	Sequence 155, App
725	4	33.3	139	1	US-08-202-047-7	Sequence 7, Appl1	798	4	33.3	147	1	US-08-217-918A-4	Sequence 4, Appl1
726	4	33.3	139	1	US-08-202-047-9	Sequence 9, Appl1	799	4	33.3	147	1	US-08-259-372A-8	Sequence 8, Appl1
727	4	33.3	139	1	US-08-202-047-11	Sequence 11, Appl	800	4	33.3	147	1	US-08-468-671-8	Sequence 8, Appl1
728	4	33.3	139	1	US-08-741-589A-10	Sequence 10, Appl	801	4	33.3	147	2	US-08-824-405-12	Sequence 12, Appl
729	4	33.3	139	2	US-08-656-588-8	Sequence 8, Appl1	802	4	33.3	148	1	US-08-166-195A-51	Sequence 51, Appl
730	4	33.3	139	2	US-08-445-468A-5	Sequence 5, Appl1	803	4	33.3	148	2	US-08-436-772-51	Sequence 51, Appl
731	4	33.3	139	2	US-08-445-468A-6	Sequence 6, Appl1	804	4	33.3	148	2	US-08-436-883B-51	Sequence 51, Appl
732	4	33.3	139	2	US-08-452-164A-19	Sequence 19, Appl	805	4	33.3	151	2	US-08-122-050-8	Sequence 8, Appl1
733	4	33.3	139	2	US-08-461-397A-5	Sequence 5, Appl1	806	4	33.3	153	3	US-08-851-843A-177	Sequence 177, App
734	4	33.3	139	2	US-08-461-397A-6	Sequence 6, Appl1	807	4	33.3	153	4	US-08-974-549A-296	Sequence 296, App
735	4	33.3	139	2	US-08-912-088-5	Sequence 5, Appl1	808	4	33.3	154	2	US-08-330-394A-29	Sequence 29, App
736	4	33.3	139	2	US-08-912-088-6	Sequence 6, Appl1	809	4	33.3	156	1	US-07-766-682A-3	Sequence 3, Appl1
737	4	33.3	139	2	US-08-603-024-18	Sequence 18, Appl	810	4	33.3	156	2	US-08-330-394A-22	Sequence 22, Appl
738	4	33.3	139	3	US-08-278-730A-5	Sequence 5, Appl1	811	4	33.3	156	4	US-08-928-941D-4	Sequence 4, Appl1
739	4	33.3	139	3	US-08-278-730A-6	Sequence 6, Appl1	812	4	33.3	156	4	US-08-928-941D-36	Sequence 36, Appl1
740	4	33.3	139	3	US-08-964-690-7	Sequence 7, Appl1	813	4	33.3	158	1	US-08-611-107-4	Sequence 4, Appl1
741	4	33.3	139	3	US-08-964-690-9	Sequence 9, Appl1	814	4	33.3	158	2	US-08-422-560A-4	Sequence 4, Appl1
742	4	33.3	139	3	US-08-964-690-11	Sequence 11, Appl	815	4	33.3	158	4	US-08-468-793-4	Sequence 4, Appl1
743	4	33.3	139	3	US-08-445-467-5	Sequence 5, Appl1	816	4	33.3	161	1	US-08-450-257-56	Sequence 56, Appl
744	4	33.3	139	3	US-08-445-467-6	Sequence 6, Appl1	817	4	33.3	161	1	US-08-450-246-56	Sequence 56, Appl
745	4	33.3	139	3	US-08-443-676-1	Sequence 1, Appl1	818	4	33.3	161	1	US-08-450-098-56	Sequence 56, Appl
746	4	33.3	139	3	US-08-480-515A-5	Sequence 5, Appl1	819	4	33.3	161	1	US-08-451-233-56	Sequence 56, Appl
747	4	33.3	139	3	US-08-480-515A-6	Sequence 6, Appl1	820	4	33.3	161	1	US-08-450-236-56	Sequence 56, Appl
748	4	33.3	139	4	US-08-933-983-21	Sequence 21, Appl	821	4	33.3	161	2	US-08-621-803-249	Sequence 249, App
749	4	33.3	139	4	US-08-414-033A-5	Sequence 5, Appl1	822	4	33.3	161	2	US-08-621-803-249	Sequence 249, App
750	4	33.3	139	4	US-08-414-033A-6	Sequence 6, Appl1	823	4	33.3	161	4	US-09-271-970-2	Sequence 2, Appl1
751	4	33.3	139	4	US-08-271-556A-3	Sequence 3, Appl1	824	4	33.3	162	1	US-08-048-164A-2	Sequence 2, Appl1
752	4	33.3	139	4	US-08-271-556A-4	Sequence 4, Appl1	825	4	33.3	162	1	US-08-460-462-2	Sequence 2, Appl1
753	4	33.3	139	4	US-08-305-223-494	Sequence 494, App	826	4	33.3	162	1	US-08-460-457-2	Sequence 2, Appl1
754	4	33.3	139	5	PCT-US92-01968-5	Sequence 5, Appl1	827	4	33.3	162	1	US-08-460-458-2	Sequence 2, Appl1
755	4	33.3	139	5	PCT-US92-01968-6	Sequence 6, Appl1	828	4	33.3	162	2	US-08-460-455-2	Sequence 2, Appl1
756	4	33.3	139	5	PCT-US93-07190-5	Sequence 5, Appl1	829	4	33.3	162	2	US-08-330-394A-2	Sequence 2, Appl1
757	4	33.3	139	5	PCT-US93-07190-6	Sequence 6, Appl1	830	4	33.3	162	3	US-08-383-045-2	Sequence 2, Appl1

539	4	33.3	119	4	US-08-484-537-89	Sequence 89, Appl	612	4	33.3	124	1	US-08-276-852-67	Sequence 67, Appl
540	4	33.3	119	4	US-09-156-316-9	Sequence 9, Appl	613	4	33.3	124	1	US-08-276-852-68	Sequence 68, Appl
541	4	33.3	119	4	US-08-624-635-13	Sequence 13, Appl	614	4	33.3	124	1	US-08-276-852-125	Sequence 125, Appl
542	4	33.3	119	4	US-09-145-060-18	Sequence 18, Appl	615	4	33.3	124	1	US-08-276-852-126	Sequence 126, Appl
543	4	33.3	119	5	PCT-US94-00657-18	Sequence 18, Appl	616	4	33.3	124	1	US-08-276-852-127	Sequence 127, Appl
544	4	33.3	119	5	PCT-US94-07762-12	Sequence 12, Appl	617	4	33.3	124	1	US-08-276-852-130	Sequence 130, Appl
545	4	33.3	119	5	PCT-US94-07799-12	Sequence 12, Appl	618	4	33.3	124	1	US-08-276-852-131	Sequence 131, Appl
546	4	33.3	119	5	PCT-US95-01219-10	Sequence 10, Appl	619	4	33.3	124	1	US-08-276-852-132	Sequence 132, Appl
547	4	33.3	119	5	PCT-US95-01219-12	Sequence 12, Appl	620	4	33.3	124	1	US-08-899-575-66	Sequence 66, Appl
548	4	33.3	119	5	PCT-US95-01219-13	Sequence 13, Appl	621	4	33.3	124	1	US-08-899-575-67	Sequence 67, Appl
549	4	33.3	119	5	PCT-US95-11235-65	Sequence 65, Appl	622	4	33.3	124	1	US-08-899-575-68	Sequence 68, Appl
550	4	33.3	120	2	US-08-652-816A-19	Sequence 19, Appl	623	4	33.3	124	1	US-08-899-575-125	Sequence 125, Appl
551	4	33.3	120	2	US-08-428-197-12	Sequence 12, Appl	624	4	33.3	124	1	US-08-899-575-126	Sequence 126, Appl
552	4	33.3	120	2	US-08-428-197-13	Sequence 13, Appl	625	4	33.3	124	1	US-08-899-575-130	Sequence 130, Appl
553	4	33.3	120	3	US-08-397-411-10	Sequence 10, Appl	626	4	33.3	124	1	US-08-899-575-137	Sequence 137, Appl
554	4	33.3	120	5	PCT-US93-10555-12	Sequence 12, Appl	627	4	33.3	124	1	US-08-899-575-131	Sequence 131, Appl
555	4	33.3	120	5	PCT-US93-10555-13	Sequence 13, Appl	628	4	33.3	124	1	US-08-899-575-132	Sequence 132, Appl
556	4	33.3	121	1	US-07-634-278-53	Sequence 53, Appl	629	4	33.3	124	1	US-08-899-575-66	Sequence 66, Appl
557	4	33.3	121	1	US-08-477-728-53	Sequence 53, Appl	630	4	33.3	124	1	US-08-899-575-67	Sequence 67, Appl
558	4	33.3	121	1	US-08-264-093-3	Sequence 3, Appl	631	4	33.3	124	1	US-08-899-575-68	Sequence 68, Appl
559	4	33.3	121	1	US-08-478-039-64	Sequence 64, Appl	632	4	33.3	124	1	US-08-899-575-125	Sequence 125, Appl
560	4	33.3	121	1	US-08-474-040-53	Sequence 53, Appl	633	4	33.3	124	1	US-08-899-575-126	Sequence 126, Appl
561	4	33.3	121	1	US-08-487-200-53	Sequence 53, Appl	634	4	33.3	124	1	US-08-899-575-127	Sequence 127, Appl
562	4	33.3	121	1	US-08-476-349A-64	Sequence 64, Appl	635	4	33.3	124	1	US-08-899-575-130	Sequence 130, Appl
563	4	33.3	121	1	US-08-202-047-23	Sequence 23, Appl	636	4	33.3	124	1	US-08-899-575-131	Sequence 131, Appl
564	4	33.3	121	2	US-08-420-235B-23	Sequence 23, Appl	637	4	33.3	124	1	US-08-899-575-132	Sequence 132, Appl
565	4	33.3	121	2	US-08-237-081B-41	Sequence 41, Appl	638	4	33.3	124	1	PCT-US95-08743-66	Sequence 66, Appl
566	4	33.3	121	2	US-08-428-197-14	Sequence 14, Appl	639	4	33.3	124	5	PCT-US95-08743-67	Sequence 67, Appl
567	4	33.3	121	2	US-08-964-680-20	Sequence 20, Appl	640	4	33.3	124	5	PCT-US95-08743-68	Sequence 68, Appl
568	4	33.3	121	4	US-08-983-607-20	Sequence 20, Appl	641	4	33.3	124	5	PCT-US95-08743-125	Sequence 125, Appl
569	4	33.3	121	4	US-08-793-624-23	Sequence 23, Appl	642	4	33.3	124	5	PCT-US95-08743-126	Sequence 126, Appl
570	4	33.3	121	4	US-08-484-537-53	Sequence 53, Appl	643	4	33.3	124	5	PCT-US95-08743-127	Sequence 127, Appl
571	4	33.3	121	4	US-08-579-378A-8	Sequence 8, Appl	644	4	33.3	124	5	PCT-US95-08743-130	Sequence 130, Appl
572	4	33.3	121	5	PCT-US93-10555-14	Sequence 14, Appl	645	4	33.3	124	5	PCT-US95-08743-131	Sequence 131, Appl
573	4	33.3	121	5	PCT-US93-11612-8	Sequence 8, Appl	646	4	33.3	124	5	PCT-US95-08743-132	Sequence 132, Appl
574	4	33.3	121	5	PCT-US95-10194-23	Sequence 23, Appl	647	4	33.3	125	1	US-08-276-852-124	Sequence 124, Appl
575	4	33.3	121	5	PCT-US95-13658-4	Sequence 4, Appl	648	4	33.3	125	1	US-08-276-852-128	Sequence 128, Appl
576	4	33.3	122	1	US-07-634-278-88	Sequence 88, Appl	649	4	33.3	125	1	US-08-276-852-129	Sequence 129, Appl
577	4	33.3	122	1	US-08-477-728-88	Sequence 88, Appl	650	4	33.3	125	1	US-08-899-575-124	Sequence 124, Appl
578	4	33.3	122	1	US-08-474-040-88	Sequence 88, Appl	651	4	33.3	125	1	US-08-899-575-128	Sequence 128, Appl
579	4	33.3	122	1	US-08-487-200-88	Sequence 88, Appl	652	4	33.3	125	1	US-08-899-575-129	Sequence 129, Appl
580	4	33.3	122	4	US-08-484-537-88	Sequence 88, Appl	653	4	33.3	125	1	US-08-899-575-124	Sequence 124, Appl
581	4	33.3	122	5	PCT-US95-00067-2	Sequence 2, Appl	654	4	33.3	125	1	US-08-899-575-128	Sequence 128, Appl
582	4	33.3	122	6	PCT-US95-00067-2	Sequence 2, Appl	655	4	33.3	125	1	US-08-899-575-129	Sequence 129, Appl
583	4	33.3	123	1	US-08-497-312-17	Sequence 17, Appl	656	4	33.3	125	2	US-08-665-202-56	Sequence 56, Appl
584	4	33.3	123	1	US-08-477-877B-94	Sequence 94, Appl	657	4	33.3	125	2	US-08-665-202-58	Sequence 58, Appl
585	4	33.3	123	1	US-08-482-882-53	Sequence 53, Appl	658	4	33.3	125	2	US-08-665-202-59	Sequence 59, Appl
586	4	33.3	123	1	US-08-482-882-86	Sequence 86, Appl	659	4	33.3	125	4	US-09-199-149-3	Sequence 3, Appl
587	4	33.3	123	2	US-08-483-389-53	Sequence 53, Appl	660	4	33.3	125	5	PCT-US95-08743-124	Sequence 124, Appl
588	4	33.3	123	2	US-08-483-389-86	Sequence 86, Appl	661	4	33.3	125	5	PCT-US95-08743-129	Sequence 129, Appl
589	4	33.3	123	2	US-08-472-281A-94	Sequence 94, Appl	662	4	33.3	126	5	PCT-US95-08743-129	Sequence 129, Appl
590	4	33.3	123	2	US-08-487-113D-53	Sequence 53, Appl	663	4	33.3	126	5	PCT-US95-08743-129	Sequence 129, Appl
591	4	33.3	123	2	US-08-487-113D-86	Sequence 86, Appl	664	4	33.3	126	1	US-08-276-852-123	Sequence 123, Appl
592	4	33.3	123	2	US-08-561-521-11	Sequence 11, Appl	665	4	33.3	126	1	US-08-899-575-123	Sequence 123, Appl
593	4	33.3	123	2	US-08-473-503-53	Sequence 53, Appl	666	4	33.3	126	1	US-08-899-575-123	Sequence 123, Appl
594	4	33.3	123	2	US-08-473-503-86	Sequence 86, Appl	667	4	33.3	126	5	PCT-US95-08743-123	Sequence 123, Appl
595	4	33.3	123	2	US-08-652-816A-1	Sequence 1, Appl	668	4	33.3	128	1	US-08-276-852-56	Sequence 56, Appl
596	4	33.3	123	2	US-08-652-816A-6	Sequence 6, Appl	669	4	33.3	128	1	US-08-276-852-58	Sequence 58, Appl
597	4	33.3	123	2	US-08-652-816A-7	Sequence 7, Appl	670	4	33.3	128	1	US-08-478-039-63	Sequence 63, Appl
598	4	33.3	123	2	US-08-652-816A-8	Sequence 8, Appl	671	4	33.3	128	1	US-08-476-349A-63	Sequence 63, Appl
599	4	33.3	123	2	US-08-652-816A-9	Sequence 9, Appl	672	4	33.3	128	1	US-08-899-575-56	Sequence 56, Appl
600	4	33.3	123	2	US-08-483-932-53	Sequence 53, Appl	673	4	33.3	128	1	US-08-899-575-58	Sequence 58, Appl
601	4	33.3	123	2	US-08-483-932-86	Sequence 86, Appl	674	4	33.3	128	1	US-08-202-047-72	Sequence 22, Appl
602	4	33.3	123	2	US-08-477-989B-94	Sequence 94, Appl	675	4	33.3	128	1	US-08-899-575-56	Sequence 56, Appl
603	4	33.3	123	2	US-08-720-420A-53	Sequence 53, Appl	676	4	33.3	128	1	US-08-899-575-58	Sequence 58, Appl
604	4	33.3	123	2	US-08-720-420A-86	Sequence 86, Appl	677	4	33.3	128	3	US-08-964-690-22	Sequence 22, Appl
605	4	33.3	123	3	US-08-714-017-53	Sequence 53, Appl	678	4	33.3	128	5	US-09-199-149-12	Sequence 12, Appl
606	4	33.3	123	3	US-08-714-017-86	Sequence 86, Appl	679	4	33.3	128	5	PCT-US95-08743-56	Sequence 56, Appl
607	4	33.3	123	3	US-08-475-680-53	Sequence 53, Appl	680	4	33.3	129	1	US-08-313-075A-52	Sequence 52, Appl
608	4	33.3	123	3	US-08-475-680-56	Sequence 56, Appl	681	4	33.3	129	1	US-08-561-521-45	Sequence 45, Appl
609	4	33.3	123	3	US-09-102-528-22	Sequence 22, Appl	682	4	33.3	129	2	US-08-561-521-45	Sequence 45, Appl
610	4	33.3	123	5	PCT-US95-01219-11	Sequence 11, Appl	683	4	33.3	133	4	PCT-US95-01219-45	Sequence 45, Appl
611	4	33.3	124	1	US-08-276-852-66	Sequence 66, Appl	684	4	33.3	135	1	US-08-718-333A-8	Sequence 8, Appl
												US-07-634-278-19	Sequence 19, Appl

393	4	33.3	116	1	US-07-634-278-57	Sequence 57, Appl	466	4	33.3	117	3	US-08-545-809A-110	Sequence 110, App
394	4	33.3	116	1	US-07-634-278-73	Sequence 73, Appl	467	4	33.3	117	3	US-08-545-809A-127	Sequence 127, App
395	4	33.3	116	1	US-08-477-728-5	Sequence 5, Appl1	468	4	33.3	117	3	US-08-545-809A-128	Sequence 128, App
396	4	33.3	116	1	US-08-477-728-6	Sequence 6, Appl1	469	4	33.3	117	3	US-08-545-809A-133	Sequence 133, App
397	4	33.3	116	1	US-08-477-728-57	Sequence 57, Appl	470	4	33.3	117	3	US-08-545-809A-139	Sequence 139, App
398	4	33.3	116	1	US-08-477-728-73	Sequence 73, Appl	471	4	33.3	117	3	US-08-839-765-166	Sequence 166, App
399	4	33.3	116	1	US-08-474-040-6	Sequence 5, Appl1	472	4	33.3	117	4	US-09-136-389-166	Sequence 166, App
400	4	33.3	116	1	US-08-474-040-57	Sequence 57, Appl	473	4	33.3	117	4	US-08-484-537-4	Sequence 4, Appl1
401	4	33.3	116	1	US-08-474-040-57	Sequence 57, Appl	474	4	33.3	117	4	US-08-484-537-15	Sequence 15, Appl
402	4	33.3	116	1	US-08-474-040-73	Sequence 73, Appl	475	4	33.3	117	4	US-08-484-537-72	Sequence 72, Appl
403	4	33.3	116	1	US-08-487-200-5	Sequence 5, Appl1	476	4	33.3	117	4	US-08-484-537-104	Sequence 104, App
404	4	33.3	116	1	US-08-487-200-6	Sequence 6, Appl1	477	4	33.3	117	4	US-08-484-537-105	Sequence 105, App
405	4	33.3	116	1	US-08-487-200-57	Sequence 57, Appl	478	4	33.3	117	4	US-08-646-265A-132	Sequence 132, App
406	4	33.3	116	1	US-08-487-200-73	Sequence 73, Appl	479	4	33.3	117	5	US-09-042-353-232	Sequence 232, App
407	4	33.3	116	1	US-08-656-253-2	Sequence 2, Appl	480	4	33.3	117	5	PCT-US93-11611-6	Sequence 6, Appl1
408	4	33.3	116	1	US-08-488-113B-169	Sequence 169, App	481	4	33.3	117	5	PCT-US93-11611-7	Sequence 7, Appl1
409	4	33.3	116	1	US-08-477-484B-169	Sequence 169, App	482	4	33.3	117	5	PCT-US95-10053-14	Sequence 14, Appl
410	4	33.3	116	1	US-08-107-669D-55	Sequence 55, App	483	4	33.3	117	5	PCT-US96-09448-17	Sequence 17, Appl
411	4	33.3	116	1	US-08-472-788A-86	Sequence 86, Appl	484	4	33.3	118	1	US-08-300-386A-64	Sequence 64, Appl
412	4	33.3	116	1	US-08-690-102A-8	Sequence 8, Appl	485	4	33.3	118	1	US-08-477-877B-93	Sequence 93, Appl
413	4	33.3	116	1	US-08-690-102A-9	Sequence 9, Appl	486	4	33.3	118	1	US-08-491-845-14	Sequence 14, Appl
414	4	33.3	116	2	US-08-690-102A-55	Sequence 55, App	487	4	33.3	118	1	US-08-491-845-14	Sequence 14, Appl
415	4	33.3	116	2	US-08-646-360-169	Sequence 169, App	488	4	33.3	118	2	US-08-472-281A-93	Sequence 93, Appl
416	4	33.3	116	2	US-08-561-521-41	Sequence 41, Appl	489	4	33.3	118	2	US-08-491-835-10	Sequence 10, Appl
417	4	33.3	116	2	US-08-561-521-41	Sequence 41, Appl	490	4	33.3	118	2	US-08-428-257A-78	Sequence 78, Appl
418	4	33.3	116	2	US-08-082-842A-86	Sequence 86, Appl	491	4	33.3	118	2	US-08-232-081B-8	Sequence 8, Appl1
419	4	33.3	116	3	US-08-934-841-1	Sequence 1, Appl	492	4	33.3	118	2	US-08-477-989B-93	Sequence 93, Appl
420	4	33.3	116	3	US-08-545-809A-104	Sequence 104, App	493	4	33.3	118	3	US-08-392-734A-4	Sequence 4, Appl1
421	4	33.3	116	3	US-09-393-409-1	Sequence 1, Appl1	494	4	33.3	118	3	US-09-153-733A-12	Sequence 12, Appl
422	4	33.3	116	4	US-08-839-765-169	Sequence 169, App	495	4	33.3	118	3	US-08-946-092A-10	Sequence 10, Appl
423	4	33.3	116	4	US-09-136-389-169	Sequence 169, App	496	4	33.3	118	3	US-08-931-645-64	Sequence 64, Appl
424	4	33.3	116	4	US-08-484-537-5	Sequence 5, Appl1	497	4	33.3	118	3	US-08-513-968-80	Sequence 80, Appl
425	4	33.3	116	4	US-08-484-537-6	Sequence 6, Appl1	498	4	33.3	118	4	US-08-983-607-24	Sequence 24, Appl
426	4	33.3	116	4	US-08-484-537-57	Sequence 57, Appl	499	4	33.3	118	4	US-09-199-149-5	Sequence 5, Appl1
427	4	33.3	116	4	US-09-127-902-8	Sequence 8, Appl1	500	4	33.3	118	4	US-09-172-062-10	Sequence 10, Appl
428	4	33.3	116	4	US-09-127-902-9	Sequence 9, Appl1	501	4	33.3	118	4	US-07-987-264-60	Sequence 60, Appl
429	4	33.3	116	4	US-09-155-107-8	Sequence 8, Appl1	502	4	33.3	118	5	PCT-US94-00666-12	Sequence 12, Appl
430	4	33.3	116	4	US-09-155-107-21	Sequence 21, Appl	503	4	33.3	118	5	PCT-US94-00665-10	Sequence 10, Appl
431	4	33.3	116	5	PCT-US95-01219-41	Sequence 41, Appl	504	4	33.3	118	5	PCT-US95-11235-64	Sequence 64, Appl
432	4	33.3	116	5	PCT-US95-09641-8	Sequence 8, Appl1	505	4	33.3	119	1	US-07-634-278-65	Sequence 65, Appl
433	4	33.3	116	5	PCT-US95-09641-9	Sequence 9, Appl1	506	4	33.3	119	1	US-07-634-278-89	Sequence 89, Appl
434	4	33.3	117	1	US-07-634-278-4	Sequence 4, Appl1	507	4	33.3	119	1	US-08-477-728-65	Sequence 65, Appl
435	4	33.3	117	1	US-07-634-278-15	Sequence 15, Appl	508	4	33.3	119	1	US-08-477-728-89	Sequence 89, Appl
436	4	33.3	117	1	US-07-634-278-72	Sequence 72, Appl	509	4	33.3	119	1	US-08-300-386A-65	Sequence 65, Appl
437	4	33.3	117	1	US-07-634-278-104	Sequence 104, App	510	4	33.3	119	1	US-08-478-039-65	Sequence 65, Appl
438	4	33.3	117	1	US-07-634-278-105	Sequence 105, App	511	4	33.3	119	1	US-08-474-040-65	Sequence 65, Appl
439	4	33.3	117	1	US-08-477-728-4	Sequence 4, Appl1	512	4	33.3	119	1	US-08-474-040-89	Sequence 89, Appl
440	4	33.3	117	1	US-08-477-728-15	Sequence 15, Appl	513	4	33.3	119	1	US-08-487-200-65	Sequence 65, Appl
441	4	33.3	117	1	US-08-477-728-72	Sequence 72, Appl	514	4	33.3	119	1	US-08-487-200-89	Sequence 89, Appl
442	4	33.3	117	1	US-08-477-728-104	Sequence 104, App	515	4	33.3	119	1	US-08-488-113B-160	Sequence 160, App
443	4	33.3	117	1	US-08-477-728-105	Sequence 105, App	516	4	33.3	119	1	US-08-476-349A-65	Sequence 65, App
444	4	33.3	117	1	US-08-474-040-4	Sequence 4, Appl1	517	4	33.3	119	1	US-08-477-484B-160	Sequence 160, App
445	4	33.3	117	1	US-08-474-040-15	Sequence 15, Appl	518	4	33.3	119	1	US-08-107-669D-24	Sequence 24, Appl
446	4	33.3	117	1	US-08-474-040-72	Sequence 72, Appl	519	4	33.3	119	1	US-08-472-788A-24	Sequence 24, Appl
447	4	33.3	117	1	US-08-474-040-104	Sequence 104, App	520	4	33.3	119	1	US-08-581-529B-12	Sequence 12, Appl
448	4	33.3	117	1	US-08-474-040-105	Sequence 105, App	521	4	33.3	119	1	US-08-491-845-10	Sequence 10, Appl
449	4	33.3	117	1	US-08-487-200-4	Sequence 4, Appl1	522	4	33.3	119	1	US-08-458-516-10	Sequence 10, Appl
450	4	33.3	117	1	US-08-487-200-15	Sequence 15, Appl	523	4	33.3	119	1	US-08-455-555-18	Sequence 18, Appl
451	4	33.3	117	1	US-08-487-200-72	Sequence 72, Appl	524	4	33.3	119	2	US-08-477-531B-24	Sequence 24, Appl
452	4	33.3	117	1	US-08-487-200-104	Sequence 104, App	525	4	33.3	119	2	US-08-525-596B-22	Sequence 22, Appl
453	4	33.3	117	1	US-08-487-200-105	Sequence 105, App	526	4	33.3	119	2	US-08-646-360-160	Sequence 160, App
454	4	33.3	117	1	US-08-488-113B-166	Sequence 166, App	527	4	33.3	119	2	US-08-561-521-10	Sequence 10, Appl
455	4	33.3	117	1	US-08-477-484B-166	Sequence 166, App	528	4	33.3	119	2	US-08-561-521-12	Sequence 12, Appl
456	4	33.3	117	1	US-08-107-669D-52	Sequence 52, App	529	4	33.3	119	2	US-08-561-521-13	Sequence 13, Appl
457	4	33.3	117	1	US-08-477-531B-52	Sequence 52, App	530	4	33.3	119	2	US-08-082-842A-24	Sequence 24, App
458	4	33.3	117	2	US-08-477-531B-52	Sequence 52, App	531	4	33.3	119	2	US-08-581-528A-12	Sequence 12, App
459	4	33.3	117	2	US-08-290-592B-117	Sequence 17, Appl	532	4	33.3	119	3	US-09-097-616-12	Sequence 12, App
460	4	33.3	117	2	US-08-646-360-166	Sequence 166, App	533	4	33.3	119	3	US-09-177-860A-22	Sequence 22, App
461	4	33.3	117	3	US-08-082-842A-52	Sequence 52, App	534	4	33.3	119	4	US-08-931-645-65	Sequence 65, App
462	4	33.3	117	3	US-08-545-809A-90	Sequence 90, Appl	535	4	33.3	119	4	US-08-983-607-50	Sequence 50, App
463	4	33.3	117	3	US-08-545-809A-91	Sequence 91, Appl	536	4	33.3	119	4	US-08-839-765-160	Sequence 160, App
464	4	33.3	117	3	US-08-545-809A-96	Sequence 96, Appl	537	4	33.3	119	4	US-09-136-389-160	Sequence 160, App
465	4	33.3	117	3	US-08-545-809A-105	Sequence 105, App	538	4	33.3	119	4	US-08-484-537-65	Sequence 65, App

247	4	33.3	31	2	US-08-466-953A-25	Sequence 25, Appl	320	4	33.3	87	1	US-08-497-312-16	Sequence 16, Appl
248	4	33.3	31	3	US-08-466-368-16	Sequence 16, Appl	321	4	33.3	94	1	US-07-899-535A-1	Sequence 1, Appl
249	4	33.3	31	5	PCT-US93-00909-4	Sequence 4, Appl	322	4	33.3	94	1	US-08-167-035-23	Sequence 23, Appl
250	4	33.3	31	6	5512648-2	Patent No. 5512648	323	4	33.3	94	1	US-08-208-887A-23	Sequence 23, Appl
251	4	33.3	32	1	US-08-780-836B-2	Sequence 2, Appl	324	4	33.3	94	2	US-08-539-005-23	Sequence 23, Appl
252	4	33.3	33	2	US-08-086-428B-137	Sequence 137, App	325	4	33.3	97	2	US-08-290-592E-16	Sequence 16, Appl
253	4	33.3	33	2	US-08-468-570-137	Sequence 137, App	326	4	33.3	97	5	PCT-US95-10053-13	Sequence 13, Appl
254	4	33.3	33	2	US-08-290-665A-241	Sequence 241, App	327	4	33.3	97	5	PCT-US96-09448-16	Sequence 16, Appl
255	4	33.3	33	5	PCT-US95-10398-241	Sequence 241, App	328	4	33.3	98	1	US-08-211-202-130	Sequence 130, App
256	4	33.3	35	4	US-09-001-984C-11	Sequence 11, Appl	329	4	33.3	98	1	US-08-211-202-140	Sequence 140, App
257	4	33.3	35	4	US-09-001-984C-42	Sequence 42, Appl	330	4	33.3	98	1	US-08-478-039-81	Sequence 81, Appl
258	4	33.3	37	1	US-08-463-660-8	Sequence 8, Appl	331	4	33.3	98	1	US-08-476-349A-81	Sequence 81, Appl
259	4	33.3	37	1	US-08-678-280-8	Sequence 8, Appl	332	4	33.3	98	2	US-08-428-197-17	Sequence 17, Appl
260	4	33.3	38	1	US-08-176-500-85	Sequence 85, Appl	333	4	33.3	98	2	US-08-665-202-33	Sequence 33, Appl
261	4	33.3	38	1	US-08-471-052A-85	Sequence 85, Appl	334	4	33.3	98	5	PCT-US93-10555-17	Sequence 17, Appl
262	4	33.3	38	1	US-08-169-331-85	Sequence 85, Appl	335	4	33.3	100	3	US-09-034-916-13	Sequence 13, Appl
263	4	33.3	38	2	US-08-471-939-85	Sequence 85, Appl	336	4	33.3	100	4	US-08-973-462-11	Sequence 11, Appl
264	4	33.3	38	2	US-08-471-800-85	Sequence 85, Appl	337	4	33.3	102	1	US-07-834-462-11	Sequence 11, Appl
265	4	33.3	38	2	US-08-146-028-18	Sequence 18, Appl	338	4	33.3	102	1	US-08-053-131-63	Sequence 63, Appl
266	4	33.3	38	2	US-08-471-068-85	Sequence 85, Appl	339	4	33.3	102	1	US-08-335-583C-47	Sequence 47, Appl
267	4	33.3	38	4	US-08-723-425A-18	Sequence 18, Appl	340	4	33.3	102	1	US-08-645-641-63	Sequence 63, Appl
268	4	33.3	38	4	US-09-112-206-18	Sequence 18, Appl	341	4	33.3	102	1	US-07-853-408B-63	Sequence 63, Appl
269	4	33.3	39	2	US-08-453-625-3	Sequence 3, Appl	342	4	33.3	102	2	US-08-096-762-63	Sequence 63, Appl
270	4	33.3	39	2	US-08-455-625-29	Sequence 29, Appl	343	4	33.3	102	2	US-08-800-353-55	Sequence 55, Appl
271	4	33.3	39	4	US-08-455-685-3	Sequence 3, Appl	344	4	33.3	102	2	US-08-308-865-53	Sequence 53, Appl
272	4	33.3	39	4	US-08-455-685-29	Sequence 29, Appl	345	4	33.3	102	2	US-08-808-982-8	Sequence 8, Appl
273	4	33.3	39	5	PCT-US94-05142-29	Sequence 3, Appl	346	4	33.3	102	2	US-08-288-508C-18	Sequence 18, Appl
274	4	33.3	39	5	PCT-US94-05142-29	Sequence 29, Appl	347	4	33.3	102	3	US-08-478-097A-16	Sequence 16, Appl
275	4	33.3	42	3	US-08-924-330A-1	Sequence 1, Appl	348	4	33.3	102	3	US-08-289-222E-27	Sequence 27, Appl
276	4	33.3	42	3	US-09-262-773-202	Sequence 202, App	349	4	33.3	102	4	US-09-054-526B-27	Sequence 27, Appl
277	4	33.3	48	3	US-08-662-259-6	Sequence 6, Appl	350	4	33.3	102	4	US-08-931-858E-161	Sequence 161, App
278	4	33.3	48	3	US-08-762-500-6	Sequence 6, Appl	351	4	33.3	102	4	US-08-981-739-161	Sequence 161, App
279	4	33.3	49	3	US-08-665-259-5	Sequence 5, Appl	352	4	33.3	102	5	PCT-US92-06185-55	Sequence 55, Appl
280	4	33.3	49	3	US-08-762-500-5	Sequence 5, Appl	353	4	33.3	102	5	PCT-US92-10983-63	Sequence 63, Appl
281	4	33.3	50	5	PCT-US91-02942-46	Sequence 46, Appl	354	4	33.3	104	1	US-07-764-731B-8	Sequence 8, Appl
282	4	33.3	50	5	PCT-US91-02942-47	Sequence 47, Appl	355	4	33.3	104	3	US-08-894-173-71	Sequence 71, Appl
283	4	33.3	50	5	PCT-US91-02942-48	Sequence 48, Appl	356	4	33.3	104	4	US-09-398-193-71	Sequence 71, Appl
284	4	33.3	50	5	PCT-US91-02942-49	Sequence 49, Appl	357	4	33.3	105	1	US-08-422-101-9	Sequence 9, Appl
285	4	33.3	50	5	PCT-US91-02942-50	Sequence 50, Appl	358	4	33.3	105	1	US-08-422-091-9	Sequence 9, Appl
286	4	33.3	51	1	US-08-570-157-16	Sequence 16, Appl	359	4	33.3	105	2	US-08-422-092-9	Sequence 9, Appl
287	4	33.3	51	1	US-08-570-157-17	Sequence 17, Appl	360	4	33.3	105	2	US-08-768-800-6	Sequence 6, Appl
288	4	33.3	52	1	US-08-294-189-17	Sequence 17, Appl	361	4	33.3	105	2	US-08-422-093-9	Sequence 9, Appl
289	4	33.3	53	4	US-08-974-549A-184	Sequence 184, App	362	4	33.3	105	3	US-08-422-112-9	Sequence 9, Appl
290	4	33.3	54	2	US-08-400-159-16	Sequence 16, Appl	363	4	33.3	109	1	US-07-829-462-1	Sequence 1, Appl
291	4	33.3	54	3	US-08-611-729A-16	Sequence 16, Appl	364	4	33.3	109	1	US-08-340-812-1	Sequence 1, Appl
292	4	33.3	58	2	US-08-152-721B-19	Sequence 19, Appl	365	4	33.3	109	1	US-08-459-064B-1	Sequence 1, Appl
293	4	33.3	59	1	US-08-306-871-25	Sequence 25, Appl	366	4	33.3	109	2	US-08-460-421A-1	Sequence 1, Appl
294	4	33.3	59	1	US-08-569-959-25	Sequence 25, Appl	367	4	33.3	109	2	US-08-717-169-1	Sequence 1, Appl
295	4	33.3	59	3	US-08-651-136C-66	Sequence 66, Appl	368	4	33.3	109	2	US-08-761-277A-51	Sequence 51, Appl
296	4	33.3	59	3	US-08-468-011A-23	Sequence 23, Appl	369	4	33.3	109	3	US-08-648-322-5	Sequence 5, Appl
297	4	33.3	60	1	US-08-447-925-1	Sequence 1, Appl	370	4	33.3	109	3	US-08-894-173-88	Sequence 88, Appl
298	4	33.3	60	1	US-08-099-354-7	Sequence 7, Appl	371	4	33.3	109	4	US-09-398-193-88	Sequence 88, Appl
299	4	33.3	60	2	US-08-288-059-33	Sequence 33, Appl	372	4	33.3	109	5	PCT-US93-00909-1	Sequence 1, Appl
300	4	33.3	65	4	US-09-188-930-297	Sequence 297, App	373	4	33.3	110	1	US-07-849-389-7	Sequence 7, Appl
301	4	33.3	70	2	US-08-935-450-12	Sequence 12, Appl	374	4	33.3	110	1	US-08-466-886-21	Sequence 21, Appl
302	4	33.3	72	3	US-08-338-579A-106	Sequence 106, App	375	4	33.3	110	1	US-08-466-886-23	Sequence 23, Appl
303	4	33.3	72	3	US-08-338-579A-107	Sequence 107, App	376	4	33.3	110	1	US-08-466-886-25	Sequence 25, Appl
304	4	33.3	75	4	US-08-646-265A-113	Sequence 113, App	377	4	33.3	110	4	US-08-961-083-102	Sequence 102, App
305	4	33.3	80	1	US-08-341-219-23	Sequence 23, Appl	378	4	33.3	110	4	US-08-469-617-21	Sequence 21, Appl
306	4	33.3	80	4	US-08-912-314A-23	Sequence 23, Appl	379	4	33.3	110	4	US-08-469-617-23	Sequence 23, Appl
307	4	33.3	81	2	US-08-469-412A-16	Sequence 16, Appl	380	4	33.3	110	4	US-08-469-617-25	Sequence 25, Appl
308	4	33.3	81	4	US-09-021-715-16	Sequence 16, Appl	381	4	33.3	111	3	US-08-545-809A-111	Sequence 111, App
309	4	33.3	82	1	US-08-225-757B-12	Sequence 12, Appl	382	4	33.3	112	3	US-08-545-809A-113	Sequence 113, App
310	4	33.3	82	1	US-08-446-038B-14	Sequence 14, Appl	383	4	33.3	113	4	US-08-836-075A-70	Sequence 70, Appl
311	4	33.3	82	1	US-08-446-010B-14	Sequence 14, Appl	384	4	33.3	113	4	US-08-836-075A-72	Sequence 72, Appl
312	4	33.3	82	2	US-08-805-445-14	Sequence 14, Appl	385	4	33.3	113	4	US-08-836-075A-74	Sequence 74, Appl
313	4	33.3	82	2	US-08-064-067D-14	Sequence 14, Appl	386	4	33.3	113	4	US-08-836-075A-78	Sequence 78, Appl
314	4	33.3	82	2	US-09-066-208-14	Sequence 14, Appl	387	4	33.3	114	4	US-09-188-930A-161	Sequence 161, App
315	4	33.3	83	1	US-08-370-225-21	Sequence 21, Appl	388	4	33.3	114	4	US-09-188-930-288	Sequence 288, App
316	4	33.3	83	1	US-08-461-859-21	Sequence 21, Appl	389	4	33.3	115	2	US-07-903-029-6	Sequence 6, Appl
317	4	33.3	83	5	PCT-US93-10069-21	Sequence 21, Appl	390	4	33.3	115	2	US-08-478-097A-30	Sequence 30, Appl
318	4	33.3	84	3	US-08-648-322-10	Sequence 10, Appl	391	4	33.3	116	1	US-07-634-278-5	Sequence 5, Appl
319	4	33.3	86	1	US-08-497-312-27	Sequence 27, Appl	392	4	33.3	116	1	US-07-634-278-6	Sequence 6, Appl

101	5	41.7	1013	3	US-08-991-408-2	Sequence 2, Appl1	174	4	33.3	16	2	US-08-102-385G-35	Sequence 35, Appl1
102	5	41.7	1021	1	US-08-497-025-3	Sequence 3, Appl1	175	4	33.3	16	3	US-08-705-875A-14	Sequence 14, Appl1
103	5	41.7	1187	1	US-08-320-559-28	Sequence 28, Appl1	176	4	33.3	16	4	US-08-602-999A-119	Sequence 179, Appl1
104	5	41.7	1187	5	US-08-545-860D-28	Sequence 28, Appl1	177	4	33.3	19	1	US-07-805-437-5	Sequence 5, Appl1
105	5	41.7	1187	5	PCT-US94-0449G-28	Sequence 28, Appl1	178	4	33.3	19	1	US-08-170-596-12	Sequence 12, Appl1
106	5	41.7	1210	1	US-08-320-559-26	Sequence 26, Appl1	179	4	33.3	19	2	US-08-284-391B-39	Sequence 39, Appl1
107	5	41.7	1210	3	US-08-545-860D-26	Sequence 26, Appl1	180	4	33.3	19	5	US-08-284-391B-41	Sequence 41, Appl1
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Pred. No. is the number of results predicted by chance to have a
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DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

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RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

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 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE GAG PROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW396;
 RA Chang K.S., Lin R.-Y., Twu S.-C.;
 RA Lin H.-C., Lin R.-Y., Salmien M.O., Liao S.-K., Wu A.M.,
 RT "Hiv type 1 env gene diversity detected in Taiwan."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U33091; AAD00206.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 DR NON_TER 1 1
 FT NON_TER 91 91
 SO SEQUENCE 91 AA: 10492 MW: 21A08BD402AF874 CRC64;

Query Match
 Best local Similarity 100.0%; Score 5; DB 14; Length 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVK 11
 DB 60 TOEVK 64

RESULT 47

068302 PRELIMINARY; PRT; 95 AA.
 AC 068302;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE GENOME POLYPEPTIDE [CONTAINS: ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35)]
 DE (FRAGMENT).
 GN EL.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepatitis C virus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HCV-BB43;
 RA Songvilal S., Kanistanon D.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: U33396; AAA64862.1; -

DR InterPro: IPR002519; -
 DR Pfam: PF01539; HCV_env; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 95 95
 SO SEQUENCE 95 AA: 10305 MW: 86270AA69397533A CRC64;

Query Match
 Best local Similarity 100.0%; Score 5; DB 14; Length 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
 DB 23 PVAPT 27

RESULT 48

068301 PRELIMINARY; PRT; 102 AA.
 AC 068301;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE GENOME POLYPEPTIDE [CONTAINS: ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35)]
 DE (FRAGMENT).
 GN EL.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepatitis C virus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HCV-BB8;
 RA Songvilal S., Kanistanon D.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: U23395; AAA64861.1; -
 DR InterPro: IPR002519; -
 DR Pfam: PF01539; HCV_env; 1.
 DR Pfam: PF01539; HCV_env; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 102 102
 SO SEQUENCE 102 AA: 11040 MW: 2C560825E0AD043E CRC64;

Query Match
 Best local Similarity 100.0%; Score 5; DB 14; Length 102;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
 DB 24 PVAPT 28

RESULT 49

09IE25 PRELIMINARY; PRT; 108 AA.
 AC 09IE25;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN GP105 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 2.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11709;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Parreira R., Esteves A., Piedade J., Veneno T., Canas-Ferreira F.;
 RT "Intra-individual genetic variability of immunodeficiency virus type 2

RA Nauci A. Jr.;
 RT "HIV-2 genetic variation and DNA load in asymptomatic carriers and
 RL AIDS cases in Guinea-Bissau.";
 DR Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF03894; AAC63160.1; -
 DR InterPro; IPR000777; -
 DR Pfam; PF00516; GP120; 1.
 KW Envelope protein.
 FT NON_TER 1 1
 FT 77 77
 SQ SEQUENCE 77 AA; 9063 MW; 9970B030D95EC9EC CRC64;
 Query Match 41.7%; Score 5; DB 14; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 8 QEVKK 12 *
 Db 59 QEVKK 63
 RESULT 43
 ID Q17728 PRELIMINARY; PRT; 82 AA.
 AC Q17728;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE C06E4.2 PROTEIN.
 GN C06E4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Du Z., Gatlung S.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U41277; AAA82477.1; -
 SQ SEQUENCE 82 AA; 9058 MW; E6CAC722EBB125B6 CRC64;
 Query Match 41.7%; Score 5; DB 5; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 VAPQ 8
 Db 40 VAPQ 44
 RESULT 44

P91335
 ID P91335 PRELIMINARY; PRT; 88 AA.
 AC P91335;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE COSMID F55C7.
 GN F55C7.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BRISTOL N2;
 RA MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Du Z., Le T.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U80436; AAC71107.1; -
 SQ SEQUENCE 88 AA; 9771 MW; 59FB61FED7C0CE3 CRC64;
 Query Match 41.7%; Score 5; DB 5; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 STPVA 5
 Db 31 STPVA 35
 RESULT 45
 ID Q9DR28 PRELIMINARY; PRT; 88 AA.
 AC Q9DR28;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=DD88472;
 RA MEDLINE=21002580; PubMed=11118076;
 RA Abebe A., Pollakis G., Fontanet A.L., Fisseha B., Tegbaru B.,
 RA Kipphuis A., Tesfaye G., Negassa H., Cornelissen M., Goudsmit J.,
 RA Rinke de Wit T.F.;
 RT "Identification of a genetic sub-cluster of HIV-1 subtype C (C')
 RT widespread in Ethiopia.";

RC STRAIN-WISTAR;
 RA MEDLINE-85207604; PubMed-2581948;
 RX Northmann W., Heisig M., Kunz D., Hehrlich P.C.;
 RT "Molecular cloning of cDNA sequences for rat alpha-2-macroglobulin and
 measurement of its transcription during experimental inflammation";
 RL J. Biol. Chem. 260:6200-6205(1985).
 DR EMBL: M84369; AAA41594.1; -
 DR InterPro: IPR001599; -
 DR Pfam: PF00207; A2M; 1.
 FT NON_TER 1 1
 FT NON_TER 23 23
 SO SEQUENCE 23 AA; 2526 MW; E2D721FB1B23876 CRC64;

Query Match 41.7%; Score 5; DB 11; Length 23;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTQE 9
 |||||
 Db 19 APTQE 23

RESULT 39
 O9GL38 PRELIMINARY; PRT; 52 AA.
 AC O9GL38;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DE CALPASTATIN (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chung H.Y., Davis M.E., Hines H.C.;
 RT "PCR-SSCP analysis of the bovine calpastatin gene domain 1 region";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY008267; AAG23869.1; -
 FT NON_TER 1 1
 FT NON_TER 52 52
 SO SEQUENCE 52 AA; 5749 MW; CBD5A7449AFDDA89 CRC64;

Query Match 41.7%; Score 5; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVK 11
 |||||
 Db 4 TOEVK 8

RESULT 40
 O47006 PRELIMINARY; PRT; 62 AA.
 AC O47006;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (T-EMBLrel. 07, Last annotation update)
 DE FLAGELLIN (FRAGMENT).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-045:H23 (ECC6 H23);
 RA Kwang J., Wilson R., Yang S., He T.;
 RL Clin. Diagn. Lab. Immunol. 0:0-0(0).

DR EMBL: U57313; AAB01993.1; -
 FT NON_TER 1 1
 FT NON_TER 62 62
 SO SEQUENCE 62 AA; 6217 MW; 6BF545C9F2134414 CRC64;

Query Match 41.7%; Score 5; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
 |||||
 Db 15 TPVAP 19

RESULT 41
 O9RRH1 PRELIMINARY; PRT; 75 AA.
 AC O9RRH1;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL 7.7 KDA PROTEIN.
 GN DR2520.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R1;
 RX MEDLINE-20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Mofatt K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamachewyan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 radiodurans R1";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE002081; AAF12064.1; -
 DR TIGR: DR2520; -
 KW Hypothetical protein.
 SO SEQUENCE 75 AA; 7704 MW; E8E47B7BBAE33B0E CRC64;

Query Match 41.7%; Score 5; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VAPPO 8
 |||||
 Db 24 VAPPO 28

RESULT 42
 O91692 PRELIMINARY; PRT; 77 AA.
 AC O91692;
 DT 01-NOV-1998 (T-EMBLrel. 08, Created)
 DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 2.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11709;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-6059;
 RA Leitner T., Norrgren H., Marguina S., Aaby P., Melbye M.,
 RA Poulson A.-G., Larsen O., Dias F., Escanilla D., Albert J.;

Query Match 50.0%; Score 6; DB 5; Length 1052;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAP 6
 |||||
 DB 383 STVPAP 388

RESULT 35

025772 PRELIMINARY; PRT; 1230 AA.
 AC 025772;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HYPOTHELICAL 131.8 KDA PROTEIN.
 GN HP1157.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McEnney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.R.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RA "The complete genome sequence of the gastric pathogen Helicobacter
 pylori.";
 RT Nature 388:539-547(1997).
 RL EMBL: AE000621; AAD08205.1; -
 DR EMBL: AE000621; AAD08205.1; -
 DR TIGR: HP1157; -
 DR InterPro: IPR002718; -
 DR Pfam: PF01856; HP_OMP; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 1230 AA; 131847 MW; 4BF1506F1E072410 CRC64;

Query Match 50.0%; Score 6; DB 2; Length 1230;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
 |||||
 DB 173 TOEVKK 178

RESULT 36

09LBC3 PRELIMINARY; PRT; 1653 AA.
 AC 09LBC3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PAA.
 GN PAA.
 OS Streptococcus citreus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1333;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E49;
 RA Tamura H., Kato H.;
 RT "Cell surface antigen I/II - Streptococcus citreus.";

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB042239; BAA95000.1; -
 DR InterPro: IPR001899; -
 DR InterPro: IPR002965; -
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR PRINTS: PRO1217; PRICHEXTENSN.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 SQ SEQUENCE 1653 AA; 180862 MW; 93F28E215BF598DE CRC64;

Query Match 50.0%; Score 6; DB 2; Length 1653;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPTO 8
 |||||
 DB 955 PVAPTO 960

RESULT 37

09PVZ2 PRELIMINARY; PRT; 2037 AA.
 AC 09PVZ2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update)
 DE NUCLEOPORIN CAN.
 GN CAN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99384295; PubMed=10454574;
 RA Askjaer P., Bachl A., Wilm M., Bischoff R., Weeks D.L., Ogniewski V.,
 RA Ohno M., Niehrs C., Kjems J., Matraj I.W., Forrester M.;
 RT "RangRP-regulated interactions of CRM1 with nucleoporins and a
 shuttling DEAD-box helicase.";
 RL Mol. Cell. Biol. 19:6276-6285(1999).
 DR EMBL: AJ243889; CAB53357.1; -
 DR InterPro: IPR000515; -
 DR InterPro: IPR001680; -
 DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBR; UNKNOWN_1.
 DR SMART: SM00320; WD40; 1.
 KW Porin.
 SQ SEQUENCE 2037 AA; 208931 MW; 2250EA49A0435635 CRC64;

Query Match 50.0%; Score 6; DB 13; Length 2037;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAP 6
 |||||
 DB 1052 STVPAP 1057

RESULT 38

063334 PRELIMINARY; PRT; 23 AA.
 AC 063334;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ALPHA-2-MACROGLOBULIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

OX NCBI_TaxID=11963;
 RN [1]
 RP SEQUENCE OF 980-989 FROM N.A.
 RX MEDLINE=88004420; PubMed=2820721;
 RA Fluegel R.M., Rethwilm A., Maurer B., Darai G.;
 RT "Nucleotide sequence analysis of the env gene and its flanking regions
 of the human spumaretrovirus reveals two novel genes.";
 RL EMBO J. 6:2077-2084(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Maurer B., Bannert H., Rethwilm A., Darai G., Fluegel R.M.;
 RL (in) Bolognesi D.P. (eds.):
 Human retroviruses, cancer and AIDS, pp.75-88, Alan Liss Inc.,
 New York (1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101282; PubMed=1846194;
 RA Muranyi W., Fluegel R.M.;
 RT "Analysis of splicing patterns of human spumaretrovirus by polymerase
 chain reaction reveals complex RNA structures.";
 RL J. Virol. 65:727-735(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9135779; PubMed=1651600;
 RA Lochelt M., Zentgraf H., Fluegel R.M.;
 RT "Construction of an infectious DNA clone of the full-length human
 spumaretrovirus genome and mutagenesis of the bel 1 gene.";
 RL Virology 184:43-54(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93348264; PubMed=8394017;
 RA Lochelt M., Muranyi W., Fluegel R.M.;
 RT "Human foamy virus genome possesses an internal, Bel-1-dependent and
 functional promoter.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7317-7321(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9500932; PubMed=7917520;
 RA Weissenberger J., Fluegel R.M.;
 RT "Identification and characterization of the Bel 3 protein of human
 foamy virus.";
 RL AIDS Res. Hum. Retroviruses 10:595-600(1994).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95380275; PubMed=7544460;
 RA Kogel D., Aboud M., Fluegel R.M.;
 RT "Mutational analysis of the reverse transcriptase and ribonuclease H
 domains of the human foamy virus.";
 RL Nucleic Acids Res. 23:2621-2625(1995).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96135216; PubMed=8551561;
 RA Lochelt M., Fluegel R.M.;
 RT "The human foamy virus pol gene is expressed as a Pro-Pol polyprotein
 and not as a Gag-Pol fusion protein.";
 RL J. Virol. 70:1033-1040(1996).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97126112; PubMed=8971036;
 RA Bodem J., Lochelt M., Winkler I., Flower R.P., Delius H.,
 Fluegel R.M.;
 RT "Characterization of the spliced pol transcript of feline foamy virus:
 the splice acceptor site of the pol transcript is located in gag of
 foamy viruses.";
 RL J. Virol. 70:9024-9027(1996).
 RN [10]
 RP SEQUENCE FROM N.A.
 RX Fluegel R.M.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U21247; AAB48113.1; -;
 KM Envelope protein.
 SO SEQUENCE 989 AA; 113890 MM; E0E8338CE44E0A5 CRC64;

Query Match 50.0%; Score 6; DB 14; Length 989;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TOEVRK 12
 |||||
 Db 185 TOEVRK 190
 RESULT 34
 ID QYVS50 PRELIMINARY; PRT; 1052 AA.
 AC QYVS50;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE CG8598 PROTEIN.
 GN CG8598.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Geiniker S.E., Holt R.A., Evans C.A., Gccayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
 RA April J.F., Agdayani A., An H.-J., Andrews-Plamkoc C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokslein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Giodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Morkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassatman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley R.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003559; AAF50579.1; -;
 DR FlyBase: FBgn0035766; CG8598.
 DR InterPro: IPR001969; -;
 DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN.1.
 SO SEQUENCE 1052 AA; 117413 MM; 504AE81BB3B12580 CRC64;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Caligaro S.T., Boube M., Cribbs D.L., Bourbon H.M.;
 RT "tarrans, a novel member of the trithorax-group of homeotic gene
 RT activators, encodes two protein isoforms related to the human cell-
 RT cycle regulator p34(SEI-1).";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF227231; AAF43017.1;
 DR FlyBase: FBgn0040071; tara.
 DR InterPro: IPR000104;
 DR PRINTS: PR00308; ANTIFREZEI.
 SQ SEQUENCE 916 AA; 96272 MW; A67D331E012FA39E CRC64;

Query Match 50.0%; Score 6; DB 5; Length 916;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
 |||||
 DB 718 TPVAPT 723

RESULT 30
 O9NHCO PRELIMINARY; PRT: 916 AA.
 AC O9NHCO;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE TARA 1A ISOFORM.
 CN TARA OR CG6889.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Caligaro S.T., Boube M., Cribbs D.L., Bourbon H.M.;
 RT "tarrans, a novel member of the trithorax-group of homeotic gene
 RT activators from Drosophila, encodes two protein isoforms related to
 RT the human cell-cycle regulator p34(SEI-1).";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF227231; AAF43019.1;
 DR FlyBase: FBgn0040071; tara.
 DR InterPro: IPR000104;
 DR PRINTS: PR00308; ANTIFREZEI.
 SQ SEQUENCE 916 AA; 96242 MW; B76C220F103B98EE CRC64;

Query Match 50.0%; Score 6; DB 5; Length 916;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
 |||||
 DB 718 TPVAPT 723

RESULT 31
 O98830 PRELIMINARY; PRT: 988 AA.
 ID O98830;
 AC O98830;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-FEB-1997 (TREMBLrel. 02, Last annotation update)
 DE PROVIRAL DNA, HSRV1 DELETION VARIANT.
 GN ENV.
 OS Human foamy virus.
 OC Viruses; Retroid viruses; Retroviridae; Spumavirus.

OX NCBI_TaxID=11641;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schmidt M., Herchenröder O., Heeney J.L., Retzlaff A.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Retzlaff A.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y07723; CAA68994.1;
 DR EMBL: Y07724; CAA69000.1;
 DR EMBL: Y07725; CAA69004.1;
 SQ SEQUENCE 988 AA; 113762 MW; 0E9E53BF7D7C6B CRC64;

Query Match 50.0%; Score 6; DB 14; Length 988;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
 |||||
 DB 185 TOEVKK 190

RESULT 32
 O87041 PRELIMINARY; PRT: 988 AA.
 AC O87041;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE SFVCPZ, COMPLETE GENOME.
 CN ENV.
 OS Simian foamy virus.
 OC Viruses; Retroid viruses; Retroviridae; Spumavirus.
 OX NCBI_TaxID=11642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SFVCPZ;
 RX MEDLINE-94240804; PubMed-8184531;
 RA Herchenröder O., Renne R., Loncar D., Cobb E.K., Murthy K.K.,
 RA Schneider J., Mergia A., Luciw P.A.;
 RT "Isolation, cloning, and sequencing of simian foamy viruses from
 RT chimpanzees (SFVCPZ): high homology to human foamy virus (HFV).";
 RL Virology 201:187-199(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SFVCPZ;
 RA Luciw P.A.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U04327; AAA19979.1;
 SQ SEQUENCE 988 AA; 113352 MW; 9A88951475B9C62 CRC64;

Query Match 50.0%; Score 6; DB 14; Length 988;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
 |||||
 DB 185 TOEVKK 190

RESULT 33
 P90288 PRELIMINARY; PRT: 989 AA.
 ID P90288;
 AC P90288;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ENVELOPE PROTEIN.
 OS Human spumaretrovirus (Foamy virus).
 OC Viruses; Retroid viruses; Retroviridae; Spumavirus.

OC Ephyrdoidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRRAIN-BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sultion G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wen R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu P.V., Berman B.P., Bhandari D., Boltsakov S.,
 RA Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Boltsakov S.,
 RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshnell A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kramos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03712; AAF55288.1; -
 DR FLYBASE: FBgn0040071; tara.
 DR InterPro: IPR000104; -
 DR PRINTS: PR00308; ANTIFREEZE1.
 SQ SEQUENCE 904 AA; 94862 MW; 084F49645F5A6998 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 904;
 Best Local Similarity 100.0%; Pred. No. 1,1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
 |||||
 Db 706 TPVAPT 711

RESULT 27
 O9NHCI PRELIMINARY; PRT; 912 AA.
 AC O9NHCI;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE TARA 1B ISOFORM.
 GN TARA OR CG6889.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridae; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC "taranis", a novel trithorax-group of homeotic gene activators, encodes
 RT two protein isoforms related to the human cell-cycle regulator
 RT p34(SER-1).";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF227212; AAF43018.1; -
 DR FLYBASE: FBgn0040071; tara.
 DR InterPro: IPR000104; -
 DR PRINTS: PR00308; ANTIFREEZE1.
 SQ SEQUENCE 912 AA; 95728 MW; 0DBA6C2FE6B8F3E CRC64;

Query Match 50.0%; Score 6; DB 5; Length 912;
 Best Local Similarity 100.0%; Pred. No. 1,1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
 |||||
 Db 714 TPVAPT 719

RESULT 28
 O9NHCI PRELIMINARY; PRT; 912 AA.
 AC O9NHCI;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE TARA 1B ISOFORM.
 GN TARA OR CG6889.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC "taranis", a novel member of the trithorax-group of homeotic gene
 RT activators from *Drosophila*, encodes two protein isoforms related to
 RT the human cell-cycle regulator p34(SER-1).";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF227213; AAF43020.1; -
 DR FLYBASE: FBgn0040071; tara.
 DR InterPro: IPR000104; -
 DR PRINTS: PR00308; ANTIFREEZE1.
 SQ SEQUENCE 912 AA; 95698 MW; 1CAB7D3EFF7F544E CRC64;

Query Match 50.0%; Score 6; DB 5; Length 912;
 Best Local Similarity 100.0%; Pred. No. 1,1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
 |||||
 Db 714 TPVAPT 719

RESULT 29
 O9NHCI PRELIMINARY; PRT; 916 AA.
 AC O9NHCI;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE TARA 1A ISOFORM.
 GN TARA OR CG6889.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

RL Science 287:2185-2195(2000).
 DR EMBL: AE003760; AAF56694.1; -
 DR FlyBase: FBgn0039507; CG3361.
 SQ SEQUENCE 775 AA; 85777 MW; AA3D5C6D6F871160 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 775;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVAP 6
 DB 358 TPVAP 363

RESULT 24
 O9UAG1 PRELIMINARY; PRT; 792 AA.
 AC O9UAG1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SALK-5.
 OS Ephydria fluviatilis.
 CC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 CC Haplosclerida; Spongiillidae; Ephydria.
 CC NCBI_TaxID=31330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99332084; PubMed=10405173;
 RA Suga H., Ono K., Miyata T.;
 RT "Multiple TGF-beta receptor related genes in sponge and ancient gene
 RT duplication before the parazoan-eumetazoan split.";
 RT FEBS Lett. 453:346-350(1999).
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB026828; BAA62605.1; -
 DR InterPro: IPR000719; -
 DR Pfam: PF00069; PKinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR SMART: SM00220; S_TKC; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 792 AA; 85470 MW; CED1CF0CDFCE523 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 792;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 7
 DB 575 TPVAP 580

RESULT 25
 O9V48 PRELIMINARY; PRT; 819 AA.
 AC O9V48;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CG16807 PROTEIN.
 GN CG16807.
 OS Drosophila melanogaster (Fruit Fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Ephydria; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champ M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Broxstein P., Brotlier P.,
 RA Burlis K.C., Busam D.A., Butler H., Caden E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Gang N.S., Gilbert W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.W., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 CC -1- SIMILARITY: CONFINES A RING (C3HC4-CLASS) ZINC FINGER.
 DR EMBL: AE003527; AAF9474.1; -
 DR FlyBase: FBgn0036621; CG16807.
 DR InterPro: IPR000571; -
 DR InterPro: IPR001841; -
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00642; zf-CCCH; 1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 819 AA; 90376 MW; 33D429076EDE7E2E CRC64;

Query Match 50.0%; Score 6; DB 5; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPTO 8
 DB 563 PVAPTO 568

RESULT 26
 O9VEX7 PRELIMINARY; PRT; 904 AA.
 AC O9VEX7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CG6889 PROTEIN.
 GN TARA OR CG6889.
 OS Drosophila melanogaster (Fruit Fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OY 1 STVPAP 6
 |||||
 DB 51 STVPAP 56

RESULT 21

ID 022907

PRELIMINARY; PRT; 748 AA.

AC 022907;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE RNA HELICASE ISOLG.
 GN T08113.17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_COLUMBIA;
 RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
 RA Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
 RA Venter J.C.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
 CC -1- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
 DR EMBL: AC002337; AAB63833.1; -;
 DR EMBL: 26537; Atach:257;26537.
 DR InterPro: IPR000629; -;
 DR InterPro: IPR001410; -;
 DR InterPro: IPR001650; -;
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; helicase_C_1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 DR SMART: SM00490; HELICG; 1.
 KM ATP-binding; Helicase; RNA-binding.
 SO SEQUENCE 748 AA; 81590 MW; 3F2FD0D5722D7364 CRC64;

Query Match 50.0%; Score 6; DB 10; Length 748;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPQ 8
 |||||
 DB 725 PVAPQ 730

RESULT 22

ID 09HF24

PRELIMINARY; PRT; 750 AA.

AC 09HF24;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE REPERSED BY TUP1 PROTEIN 1.
 GN RBT1.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20253093; Pubmed-10790384;
 RA Braun B.R., Johnson A.D.;
 RT "TUP1, CPH1 and EFG1 make independent contributions to filamentation
 in candida albicans.";
 RL Genetics 155:57-67(2000).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE-20435724; Pubmed-10978273;
 RA Braun B.R., Head W.S., Wang M.X., Johnson A.D.;
 RT "Identification and characterization of TUP1-regulated genes in
 Candida albicans.";
 RL Genetics 156:31-44(2000).
 DR EMBL: AF254142; AAG09787.1; -;
 SO SEQUENCE 750 AA; 76351 MW; 3B1C0C8EEAFCD72 CRC64;

Query Match 50.0%; Score 6; DB 3; Length 750;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAP 6
 |||||
 DB 650 STVPAP 655

RESULT 23

ID 09VB49

PRELIMINARY; PRT; 775 AA.

AC 09VB49;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CG3361 PROTEIN.

GN Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;
 RX MEDLINE-20196006; Pubmed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Bailly R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokslein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.E., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshell A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DE 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DR POLYCYSTIC KIDNEY DISEASE-LIKE 2 PROTEIN.
GN PKD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20221369; PubMed=10756092;
RA Guo L., Schreiber T.H., Weremowicz S., Morton C.C., Lee C., Zhou J.;
RT Identification and characterization of a novel polycystin family
RT member, polycystin-12, in mouse and human: sequence, expression,
RT alternative splicing, and chromosomal localization.";
RL Genomics 64:241-251(2000).
DR EMBL, AF182034; AAF65622.1; -
DR InterPro; IPR000636; -
DR InterPro; IPR001682; -
DR InterPro; IPR002111; -
SQ SEQUENCE 624 AA; 73774 MW; 709FFA18542312E4 CRC64;

Query Match 50.0%; Score 6; DB 4; Length 624;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 TQEVKK 12
DB 298 TQEVKK 303

RESULT 19
008484 PRELIMINARY; PRT; 637 AA.
ID 008484
AC 008484; 000028;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE CHROMOSOME XV READING FRAME ORF YOR070C.
OS YOR29-21 OR GYPI.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Bohn C., Bolotin-Fukuhara M., Daignan-Fornier B., Dang D.V.,
RA Valens M.;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97279235; PubMed=9133743;
RA Valens M., Bohn C., Daignan-Fornier B., Dang V., Bolotin-Fukuhara M.;
RT The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the
RT presence of two tRNAs and 24 new open reading frames.";
RL Yeast 13:379-390(1997).
DR EMBL; Z70678; CAAG9263.1; -
DR EMBL; 270678; CAAG9263.1; -
DR SGD; S0005596; GYPI.
DR InterPro; IPR000195; -
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
SQ SEQUENCE 637 AA; 73289 MW; 08C1A26B6ED37E13 CRC64;

Query Match 50.0%; Score 6; DB 3; Length 637;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TPVAPT 7
DB 181 TPVAPT 186

RESULT 20
09WM35 PRELIMINARY; PRT; 652 AA.
ID 09WM35
AC 09WM35;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
DE CG8743 PROTEIN.
GN CG8743
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodt A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
RA Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon R., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL EMBL; AE003516; AAF9118.1; -
DR EMBL; FBgn0036904; CG8743.
DR FlyBase; FBgn0036904; CG8743.
DR InterPro; IPR001682; -
DR InterPro; IPR002111; -
SQ SEQUENCE 652 AA; 74251 MW; 21989FCE490235E4 CRC64;

Query Match 50.0%; Score 6; DB 5; Length 652;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 CC -1. SIMILARITY: BELONGS TO THE ARAC/XYS FAMILY OF TRANSCRIPTIONAL REGULATORS.
 CC EMBL: AL356592; CAB92194.1; -.
 DR InterPro: IPR000005; -.
 DR Pfam: PF00165; HTH_ARAC.1.
 DR PRINTS: PR00032; HTHARAC.
 DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
 DR SMART: SM00342; HTH_ARAC; 1.
 DR DNA-binding; Transcription regulation.
 KW SEQUENCE 289 AA; 31511 MW; F709F9CF93C73F56 CRC64;
 SQ

Query Match 50.0%; Score 6; DB 2; Length 289;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAP 7
 |||||
 DB 37 TPVAP 42

RESULT 12
 O9RW05 PRELIMINARY; PRT; 293 AA.
 AC O9RW05;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL 30.8 KDA PROTEIN.
 GN DR0864.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R1;
 RA MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uitterlinden T., Zaleski C.,
 RA Makarov K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AF001940; AAF10447.1; -.
 DR TIGR: DR0864; -.
 KW Hypothetical protein.
 SQ SEQUENCE 293 AA; 30849 MW; 4FA7BFEFF12A0E83 CRC64;
 RL

Query Match 50.0%; Score 6; DB 2; Length 293;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRPVAP 6
 |||||
 DB 227 SRPVAP 232

RESULT 13
 ID 086673 PRELIMINARY; PRT; 447 AA.
 AC 086673;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE PUTATIVE LIPOPROTEIN.
 GN SC4A2.17C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL031182; CAZ0169.1; -.
 KW Lipoprotein.
 SQ SEQUENCE 447 AA; 46712 MW; 809E0091B7834D80 CRC64;
 SQ

Query Match 50.0%; Score 6; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAP 7
 |||||
 DB 63 TPVAP 68

RESULT 14
 O9XT09 PRELIMINARY; PRT; 460 AA.
 AC O9XT09;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 GN H13N06.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lennard N.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RL

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=96-62333;
 RA Beldi F.J., Barlow K.L., Murphy G., Parry J.V., Clewley J.P.;
 RT "A dual subtype B/E HIV-1 infection with a novel V3 loop crown motif
 among infections acquired in South East Asia and imported into
 England.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AJ224197; CA11887.1; -
 DR InterPro: IPR000721; -
 DR Pfam: PF00607; gag_p24; 1.
 KM Core protein; Polyprotein.
 FT NON_TER 1 1
 FT NON_TER 174 174
 SQ SEQUENCE 174 AA; 19667 MW; D6F18B245B0707DF CRC64;

Query Match
 Best Local Similarity 50.0%; Score 6; DB 14; Length 174;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
 |||||
 Db 154 TOEVKK 159

RESULT 8
 O9FU39 PRELIMINARY; PRT; 237 AA.
 AC O9FU39;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE P0001B06.23 PROTEIN.
 GN P0001B06.23.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
 OC Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 1, PAC
 clone: P0001B06.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF002537; BAB16870.1; -
 SQ SEQUENCE 237 AA; 25810 MW; 972E4F6C57C2E39A CRC64;

Query Match
 Best Local Similarity 50.0%; Score 6; DB 10; Length 237;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
 |||||
 Db 220 TPVAPT 225

RESULT 9
 O9KVZ4 PRELIMINARY; PRT; 274 AA.
 AC O9KVZ4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE BETA-LACTAMASE PRECURSOR.
 GN OXA-23.
 OS Acinetobacter baumannii.

OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RYC 52763/97;
 RX MEDLINE=20277880; PubMed=10817708;
 RA Bou G., Oliver A., Martinez-Beltran J.;
 RT "OXA-24, a novel class D beta-lactamase with carbapenemase activity in
 an Acinetobacter baumannii clinical strain.";
 RL Antimicrob. Agents Chemother. 44:1556-1561(2000).
 DR EMBL: AJ239129; CAB92323.1; -
 KM Signal.
 FT SIGNAL 1 7
 FT SIGNAL POTENTIAL.
 SQ SEQUENCE 274 AA; 30810 MW; 5343DC532A8AB4E6 CRC64;

Query Match
 Best Local Similarity 50.0%; Score 6; DB 2; Length 274;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
 |||||
 Db 197 TOEVKK 202

RESULT 10
 O84512 PRELIMINARY; PRT; 288 AA.
 AC O84512;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 32.2 KDA PROTEIN.
 GN CT504.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/UM-3/CX;
 RX MEDLINE=95000809; PubMed=9784136;
 RA Stephens R.S., Kaiman S., Lammell C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 DR EMBL: AE001323; AAC68105.1; -
 SQ SEQUENCE 288 AA; 32191 MW; 9B5CAE26D04028B5 CRC64;

Query Match
 Best Local Similarity 50.0%; Score 6; DB 2; Length 288;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAP 6
 |||||
 Db 131 STPVAP 136

RESULT 11
 O9KYN4 PRELIMINARY; PRT; 289 AA.
 AC O9KYN4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PUTATIVE ARAC-FAMILY TRANSCRIPTIONAL REGULATOR.
 GN SC9H11.05.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Query Match 58.3%; Score 7; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VAPTOEV 10
DB 39 VAPTOEV 45

RESULT 4
O9PM45 PRELIMINARY; PRT; 227 AA.
AC O9PM45;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PUTATIVE TONB TRANSPORT PROTEIN.
GN TONB2 OR CJI630.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCYC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
BA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
RA Jorgensen K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL: AL139079; CAB3618.1; -
DR InterPro: IPR003538; -
DR PRINTS: PR01374; TONBPROTEIN.
SQ SEQUENCE 227 AA; 26298 MW; 7AEFFB148480DCD CRC64;

Query Match 58.3%; Score 7; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTOEK 11
DB 105 APTOEK 111

RESULT 5
O9HYT7 PRELIMINARY; PRT; 102 AA.
AC O9HYT7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN PA3307.
GN PA3307.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004753; AAG06695.1; -
KM Hypothetical protein.
SQ SEQUENCE 102 AA; 11114 MW; D92FEE4B8B95286B CRC64;

Query Match 50.0%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPQ 8
DB 27 PVAPQ 32

RESULT 6
O9X9T5 PRELIMINARY; PRT; 116 AA.
ID O9X9T5
AC O9X9T5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE PUTATIVE REGULATORY PROTEIN.
GN SC011.16.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K., Harris D.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrett B.G., Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL096823; CAB46971.1; -
SQ SEQUENCE 116 AA; 12228 MW; 4B6986EB74C7E6CD CRC64;

Query Match 50.0%; Score 6; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVK 12
DB 29 TOEVK 34

RESULT 7
O93041 PRELIMINARY; PRT; 174 AA.
ID O93041
AC O93041;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GAG POLYPROTEIN [CONTAINS: CORE PROTEIN(S) P24] (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.


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669 5 41.7 609 14 082672 082672 influenza c
970 5 41.7 609 14 082673 082673 influenza c
971 5 41.7 609 14 082674 082674 influenza c
972 5 41.7 609 14 082675 082675 influenza c
973 5 41.7 620 5 09Y0D4 09Y0D4 penaeus mon
974 5 41.7 620 5 09NEG8 09NEG8 leishmania
975 5 41.7 624 4 09P2U4 09P2U4 homo sapien
976 5 41.7 626 4 09P2U3 09P2U3 homo sapien
977 5 41.7 627 4 09H172 09H172 homo sapien
978 5 41.7 633 2 059526 059526 mycoplasma
979 5 41.7 637 2 P72813 P72813 synechocyst
980 5 41.7 637 2 09W0E6 09W0E6 drosophila
981 5 41.7 641 5 001667 001667 drosophila
982 5 41.7 641 5 09VU01 09VU01 drosophila
983 5 41.7 641 14 091Q72 091Q72 influenza c
984 5 41.7 642 5 09FC03 09FC03 streptomyce
985 5 41.7 645 2 09NPF7 09NPF7 penaeus van
986 5 41.7 645 14 091Q73 091Q73 influenza c
987 5 41.7 645 14 091Q69 091Q69 influenza c
988 5 41.7 646 2 007625 007625 bacillus su
989 5 41.7 646 14 067417 067417 influenza c
990 5 41.7 647 14 067386 067386 influenza c
991 5 41.7 648 14 091Q66 091Q66 influenza c
992 5 41.7 649 14 039661 039661 influenza v
993 5 41.7 649 14 067416 067416 influenza c
994 5 41.7 649 14 067418 067418 influenza c
995 5 41.7 649 14 067419 067419 influenza c
996 5 41.7 649 14 091Q71 091Q71 influenza c
997 5 41.7 649 14 091Q70 091Q70 influenza c
998 5 41.7 650 14 091Q67 091Q67 influenza c
999 5 41.7 651 4 09UF25 09UF25 homo sapien
1000 5 41.7 651 5 018181 018181 caenorhabdt
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ALIGNMENTS

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RESULT 1
O9NRU3 PRELIMINARY: PRT: 86 AA.
AC O9NRU3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE P60 PROTEIN (FRAGMENT).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90256283; PubMed=2111287;
RA Kohler S., Leimister-Wachter M., Chakraborty T., Lottspeich F.,
RA Goebel W.;
RT "The gene coding for protein p60 of Listeria monocytogenes and its use
RT as a specific probe for Listeria monocytogenes.";
RL Infect. Immun. 58:1943-1950(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Park S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF179003; AAD55089.1; -.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9194 MW; 71F649A817D697F6 CRC64;
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Query Match 100.0%; Score 12; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 STPVAPTOEVKK 12

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Db 30 STPVAPTOEVKK 41
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RESULT 2
O03493 PRELIMINARY: PRT: 478 AA.
AC O03493:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094153; PubMed=1459966;
RA Buhert A., Kuhn M., Goebel W., Koehler S.;
RT "Structural and functional properties of the p60 proteins from
RT different Listeria species.";
RL J. Bacteriol. 174:8166-8171(1992).
CC -!- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE
CC INVASION OF NONPROFESSIONAL PHAGOCYtic CELLS BY LISTERIA.
DR EMBL; M80351; AAA25280.1; -.
DR InterPro; IPR00064; -.
DR InterPro; IPR002482; -.
DR Pfam; PF00877; NLPC_P60; 1.
DR Pfam; PF01476; LysM; 2.
DR SMART; SM00257; LysM; 1.
KW Signal.
FT SIGNAL 1 27 BY SIMILARITY.
FT CHAIN 28 478 PROTEIN P60.
SQ SEQUENCE 478 AA; 49997 MW; D46D050507402344 CRC64;
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Query Match 100.0%; Score 12; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 STPVAPTOEVKK 12
Db 146 STPVAPTOEVKK 157
|||||
RESULT 3
O67673 PRELIMINARY: PRT: 94 AA.
AC O67673:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HEXON PROTEIN (FRAGMENT).
OS porcine adenovirus sp.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=47901;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Pring-Akerblom P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95630; CAA64884.1; -.
DR HSSP; P03277; IDHX.
DR InterPro; IPR000736; -.
DR Pfam; PF01065; Adeno_hexon; 1.
KW Hexon protein.
FT NON_TER 1 1
FT NON_TER 94 94
SQ SEQUENCE 94 AA; 10807 MW; 2646FB97DDCC9FD CRC64;
```

823	5	41.7	492	14	Q9WF75	Q9WF75 human immun	896	5	41.7	509	14	056939	056939 human papill
824	5	41.7	492	14	Q9WF72	Q9WF72 human immun	897	5	41.7	509	14	056945	056945 human papill
825	5	41.7	492	14	Q9WF69	Q9WF69 human immun	898	5	41.7	511	2	052569	052569 amycolatops
826	5	41.7	492	14	Q9WF66	Q9WF66 human immun	899	5	41.7	512	5	076725	076725 caenorhabdi
827	5	41.7	492	14	Q9WRK9	Q9WRK9 human immun	900	5	41.7	512	14	091079	091079 human immun
828	5	41.7	492	14	Q9EAL3	Q9EAL3 human immun	901	5	41.7	516	10	Q9SVB0	Q9SVB0 arabisdopsi
829	5	41.7	493	10	024326	024326 phaseolus v	902	5	41.7	516	14	012670	012670 colobus mon
830	5	41.7	493	10	Q9FNR2	Q9FNR2 arabisdopsi	903	5	41.7	516	14	P88804	P88804 human papil
831	5	41.7	493	10	Q9FHL9	Q9FHL9 arabisdopsi	904	5	41.7	517	14	071261	071261 human immun
832	5	41.7	493	14	Q9OMH9	Q9OMH9 human immun	905	5	41.7	517	14	073329	073329 human immun
833	5	41.7	493	14	Q9IV95	Q9IV95 human immun	906	5	41.7	519	5	Q9NEU8	Q9NEU8 caenorhabdi
834	5	41.7	494	14	P90256	P90256 human immun	907	5	41.7	520	11	035731	035731 mus musculu
835	5	41.7	494	14	P90257	P90257 human immun	908	5	41.7	521	2	Q9KJ0D	Q9KJ0D arthrobacte
836	5	41.7	494	14	P90259	P90259 human immun	909	5	41.7	526	4	Q9P280	Q9P280 homo sapien
837	5	41.7	494	14	Q9OS00	Q9OS00 human immun	910	5	41.7	528	10	Q9SRE2	Q9SRE2 arabisdopsi
838	5	41.7	494	14	Q9OC00	Q9OC00 human immun	911	5	41.7	530	2	Q9I008	Q9I008 pseudomonas
839	5	41.7	494	14	Q9QB14	Q9QB14 human immun	912	5	41.7	534	1	Q9E459	Q9E459 methanobact
840	5	41.7	494	14	Q9IW44	Q9IW44 human immun	913	5	41.7	534	2	Q9RJ53	Q9RJ53 streptomyc
841	5	41.7	495	14	Q9OP03	Q9OP03 human immun	914	5	41.7	535	14	Q9QWK6	Q9QWK6 chilita viru
842	5	41.7	495	14	Q9OR22	Q9OR22 human immun	915	5	41.7	535	14	Q9IV39	Q9IV39 human calic
843	5	41.7	495	14	Q9IWS3	Q9IWS3 human immun	916	5	41.7	537	2	Q9Z8U8	Q9Z8U8 chlamydia p
844	5	41.7	495	14	Q76126	Q76126 human immun	917	5	41.7	537	2	Q9JRV7	Q9JRV7 chlamydia p
845	5	41.7	496	5	Q17537	Q17537 caenorhabdi	918	5	41.7	539	10	Q80914	Q80914 arabisdopsi
846	5	41.7	496	14	Q9WSG0	Q9WSG0 human immun	919	5	41.7	539	11	060664	060664 mus musculu
847	5	41.7	496	14	Q9WS51	Q9WS51 human immun	920	5	41.7	540	4	060230	060230 homo sapien
848	5	41.7	496	14	Q9WLH9	Q9WLH9 human immun	921	5	41.7	542	5	Q23446	Q23446 caenorhabdi
849	5	41.7	496	14	Q9QSR1	Q9QSR1 human immun	922	5	41.7	543	10	Q22188	Q22188 arabisdopsi
850	5	41.7	496	14	Q9DKK0	Q9DKK0 human immun	923	5	41.7	544	11	060764	060764 mus musculu
851	5	41.7	497	14	Q41792	Q41792 human immun	924	5	41.7	547	13	Q91349	Q91349 xenopus lae
852	5	41.7	497	14	Q89926	Q89926 human immun	925	5	41.7	548	2	Q9ZEX1	Q9ZEX1 listeria mo
853	5	41.7	497	14	Q9WLJ2	Q9WLJ2 human immun	926	5	41.7	548	2	Q9EXF6	Q9EXF6 listeria mo
854	5	41.7	497	14	Q9WLH1	Q9WLH1 human immun	927	5	41.7	548	5	Q9XXV9	Q9XXV9 bombyx mori
855	5	41.7	497	14	Q9ID96	Q9ID96 human immun	928	5	41.7	549	5	Q24441	Q24441 drosophila
856	5	41.7	498	4	Q9H7A2	Q9H7A2 homo sapien	929	5	41.7	550	2	Q9SAM6	Q9SAM6 escherichia
857	5	41.7	498	14	P88150	P88150 human immun	930	5	41.7	551	2	Q9KZS2	Q9KZS2 streptomyc
858	5	41.7	498	14	Q77372	Q77372 human immun	931	5	41.7	552	5	Q9V152	Q9V152 drosophila
859	5	41.7	498	14	Q79665	Q79665 human immun	932	5	41.7	553	2	Q9RSN4	Q9RSN4 delinococcu
860	5	41.7	498	14	Q9WIR6	Q9WIR6 human immun	933	5	41.7	555	2	Q9SG12	Q9SG12 escherichia
861	5	41.7	498	14	P90239	P90239 human immun	934	5	41.7	555	2	Q9R3X4	Q9R3X4 escherichia
862	5	41.7	498	14	Q9OMW1	Q9OMW1 human immun	935	5	41.7	556	2	Q9SAM3	Q9SAM3 escherichia
863	5	41.7	498	14	Q9QML3	Q9QML3 human immun	936	5	41.7	556	10	Q9ML72	Q9ML72 arabisdopsi
864	5	41.7	498	14	Q9Q6C0	Q9Q6C0 human immun	937	5	41.7	556	10	Q9LFW2	Q9LFW2 arabisdopsi
865	5	41.7	498	14	Q9Q6H6	Q9Q6H6 human immun	938	5	41.7	557	2	Q9R869	Q9R869 aquilex aeo
866	5	41.7	498	14	Q9Q6G9	Q9Q6G9 human immun	939	5	41.7	557	2	Q9K9Z6	Q9K9Z6 bacillus ha
867	5	41.7	498	14	Q9DKH3	Q9DKH3 human immun	940	5	41.7	558	2	P73902	P73902 synecocyst
868	5	41.7	498	14	Q9DH06	Q9DH06 human immun	941	5	41.7	560	2	Q9SAM5	Q9SAM5 escherichia
869	5	41.7	499	11	Q88714	Q88714 mus musculu	942	5	41.7	561	4	Q9Z952	Q9Z952 homo sapien
870	5	41.7	499	14	Q72860	Q72860 human immun	943	5	41.7	562	1	Q9HRL9	Q9HRL9 halobacteri
871	5	41.7	499	14	Q74834	Q74834 human immun	944	5	41.7	567	2	Q93932	Q93932 listeria mo
872	5	41.7	499	14	P89692	P89692 human immun	945	5	41.7	570	2	Q66690	Q66690 aquilex aeo
873	5	41.7	499	14	Q9O712	Q9O712 human immun	946	5	41.7	572	5	Q26042	Q26042 penaeus jap
874	5	41.7	499	14	Q9IW66	Q9IW66 human immun	947	5	41.7	573	3	Q08179	Q08179 saccharomyc
875	5	41.7	500	14	P73537	P73537 synecocyst	948	5	41.7	573	5	Q19963	Q19963 caenorhabdi
876	5	41.7	500	14	P89971	P89971 human immun	949	5	41.7	574	2	Q19963	Q19963 caenorhabdi
877	5	41.7	500	14	Q74806	Q74806 human immun	950	5	41.7	578	5	Q9TVL0	Q9TVL0 caenorhabdi
878	5	41.7	500	14	Q9YX54	Q9YX54 human immun	951	5	41.7	580	10	Q9ZVU7	Q9ZVU7 arabisdopsi
879	5	41.7	500	14	Q9W010	Q9W010 human immun	952	5	41.7	581	2	Q9R0U5	Q9R0U5 delinococcu
880	5	41.7	502	14	Q9Q6X6	Q9Q6X6 human immun	953	5	41.7	583	2	Q9ZNT9	Q9ZNT9 pseudomonas
881	5	41.7	502	14	Q9IDA5	Q9IDA5 human immun	954	5	41.7	583	5	Q17977	Q17977 caenorhabdi
882	5	41.7	502	14	Q9IC78	Q9IC78 chimpanzee	955	5	41.7	584	4	Q9UNR7	Q9UNR7 homo sapien
883	5	41.7	503	10	Q9LD28	Q9LD28 arabisdopsi	956	5	41.7	585	2	P71246	P71246 escherichia
884	5	41.7	503	11	Q9ROM4	Q9ROM4 mus musculu	957	5	41.7	585	2	Q9L736	Q9L736 escherichia
885	5	41.7	503	11	Q9ESZ1	Q9ESZ1 mus musculu	958	5	41.7	585	2	Q9K2Y6	Q9K2Y6 escherichia
886	5	41.7	503	14	Q97058	Q97058 human immun	959	5	41.7	587	10	Q9MOT2	Q9MOT2 arabisdopsi
887	5	41.7	504	2	Q9ZBW5	Q9ZBW5 streptomyc	960	5	41.7	596	10	Q9LSM2	Q9LSM2 arabisdopsi
888	5	41.7	505	2	Q9Z089	Q9Z089 helicobacte	961	5	41.7	599	2	Q9PP00	Q9PP00 campylobact
889	5	41.7	505	4	Q14395	Q14395 homo sapien	962	5	41.7	604	2	Q00509	Q00509 streptomyc
890	5	41.7	505	4	Q9UNR8	Q9UNR8 homo sapien	963	5	41.7	605	1	Q26511	Q26511 methanobact
891	5	41.7	507	4	Q13064	Q13064 homo sapien	964	5	41.7	606	2	Q53561	Q53561 streptococc
892	5	41.7	507	14	Q9O079	Q9O079 chimpanzee	965	5	41.7	609	13	Q13027	Q13027 xenopus lae
893	5	41.7	508	5	Q93227	Q93227 caenorhabdi	966	5	41.7	609	14	Q82659	Q82659 influenza c
894	5	41.7	508	6	Q9GMC8	Q9GMC8 felis silve	967	5	41.7	609	14	Q82670	Q82670 influenza c
895	5	41.7	509	6	Q9GMC7	Q9GMC7 bison bison	968	5	41.7	609	14	Q82671	Q82671 influenza c

677	5	41.7	385	6	O9GL14	O9g114 microptamo	750	5	41.7	469	2	O9ZL71	O9z171 helicobacte
678	5	41.7	385	10	O9%P00	O9%P00 brassica ju	751	5	41.7	469	14	O9JXN9	O9jxn9 human immun
679	5	41.7	385	14	O80627	O80627 human immun	752	5	41.7	469	14	O9END0	O9end0 human immun
680	5	41.7	386	5	P91632	P91632 drosophila	753	5	41.7	469	14	O9ENC2	O9enc2 human immun
681	5	41.7	387	4	O9H8P7	O9h8p7 homo sapien	754	5	41.7	469	14	O9ENC0	O9enc0 human immun
682	5	41.7	388	5	O9VUD1	O9vud1 drosophila	755	5	41.7	469	14	O9ENCO	O9enc0 human immun
683	5	41.7	389	2	O9K7L3	O9k7l3 bacillus ha	756	5	41.7	470	5	O9ENB8	O9enb8 human immun
684	5	41.7	392	4	O9NPL5	O9npl5 homo sapien	757	5	41.7	470	5	O19087	O19087 caenorhabd1
685	5	41.7	392	5	O9VW77	O9vw77 drosophila	758	5	41.7	471	5	O9ENNA4	O9enaa4 human immun
686	5	41.7	393	14	O41549	O41549 human immun	759	5	41.7	472	14	O9ENBA	O9enba4 drosophila
687	5	41.7	394	5	O9VMU4	O9vmu4 drosophila	760	5	41.7	472	14	O9ENB4	O9enb4 human immun
688	5	41.7	394	5	O9XU00	O9xu00 caenorhabd1	761	5	41.7	473	2	O50210	O50210 synechococ
689	5	41.7	395	2	O9KE01	O9ke01 bacillus ha	762	5	41.7	473	14	O9ENB0	O9enb0 human immun
690	5	41.7	398	4	O9UGL3	O9ugl3 homo sapien	763	5	41.7	473	14	O9ENAB	O9enab human immun
691	5	41.7	400	11	O9EOU2	O9eou2 apodemus ag	764	5	41.7	473	14	O9ENAB	O9enab human immun
692	5	41.7	406	3	O9UYD9	O9uyd9 alternaria	765	5	41.7	473	14	O9ENAB	O9enab human immun
693	5	41.7	407	5	O9VBA4	O9vba4 drosophila	766	5	41.7	473	14	O9ENAB	O9enab human immun
694	5	41.7	408	2	O9FD10	O9fd10 salmoneila	767	5	41.7	474	14	O9ENAB	O9enab human immun
695	5	41.7	408	4	O9UGL4	O9ugl4 homo sapien	768	5	41.7	475	2	O9X727	O9x727 escherichia
696	5	41.7	409	2	O9LA43	O9la43 shigella dy	769	5	41.7	475	2	O9F8R9	O9f8r9 escherichia
697	5	41.7	410	2	O05446	O05446 mycobacteri	770	5	41.7	475	2	O9F8R3	O9f8r3 escherichia
698	5	41.7	410	2	O9FAK8	O9fak8 rhizobium l	771	5	41.7	475	2	O9EU22	O9eu22 escherichia
699	5	41.7	410	10	O9MA98	O9ma98 arabidopsis	772	5	41.7	475	10	O9LNM7	O9lnw7 arabidopsis
700	5	41.7	411	2	O9FAK7	O9fak7 rhizobium l	773	5	41.7	476	5	P91292	P91292 caenorhabd1
701	5	41.7	411	5	O9V943	O9v943 drosophila	774	5	41.7	476	5	O03996	O03996 plasmodium
702	5	41.7	411	14	O81814	O81814 hepatitis c	775	5	41.7	477	14	O9EN92	O9en92 human immun
703	5	41.7	414	14	O81329	O81329 hepatitis c	776	5	41.7	477	2	O9RXT6	O9rxt6 delnecoccus
704	5	41.7	414	14	P89958	P89958 hepatitis c	777	5	41.7	478	5	O25684	O25684 plasmodium
705	5	41.7	414	14	P89959	P89959 hepatitis c	778	5	41.7	481	2	O9LA08	O9laq8 clostridium
706	5	41.7	415	14	O81554	O81554 hepatitis c	779	5	41.7	481	14	O77697	O77697 human immun
707	5	41.7	416	2	O31444	O31444 bacillus su	780	5	41.7	481	14	O9IV19	O9iv19 human immun
708	5	41.7	418	2	O9K9F3	O9k9f3 bacillus ha	781	5	41.7	482	5	O44196	O44196 caenorhabd1
709	5	41.7	418	4	O75066	O75066 homo sapien	782	5	41.7	482	5	O9XY38	O9xy38 acanthamoeb
710	5	41.7	418	4	O9NMA8	O9nma8 homo sapien	783	5	41.7	482	5	O03998	O03998 plasmodium
711	5	41.7	421	2	O9ZJ40	O9zj40 neisseria m	784	5	41.7	484	5	O9U9P0	O9u9p0 hydra atten
712	5	41.7	421	2	O9J034	O9j034 neisseria m	785	5	41.7	484	14	O77699	O77699 human immun
713	5	41.7	421	4	O9UNN6	O9unn6 homo sapien	786	5	41.7	484	14	O77700	O77700 human immun
714	5	41.7	421	4	O9UBH9	O9ubh9 homo sapien	787	5	41.7	484	14	O80622	O80622 human immun
715	5	41.7	421	4	O9Y6I7	O9y6i7 homo sapien	788	5	41.7	485	5	O9N4N9	O9nan9 caenorhabd1
716	5	41.7	422	2	P96Z08	P96z08 mycobacteri	789	5	41.7	486	4	O9UCX4	O9ucx4 homo sapien
717	5	41.7	423	1	O93642	O93642 halobacteri	790	5	41.7	486	14	O77804	O77804 human immun
718	5	41.7	423	1	O9HQT5	O9hqt5 halobacteri	791	5	41.7	486	14	O78566	O78566 human immun
719	5	41.7	423	2	O49939	O49939 mycobacteri	792	5	41.7	486	14	O79451	O79451 human immun
720	5	41.7	423	5	O9UIM3	O9uim3 drosophila	793	5	41.7	486	14	O80628	O80628 human immun
721	5	41.7	429	2	O9Z4B1	O9z4b1 escherichia	794	5	41.7	486	14	O80629	O80629 human immun
722	5	41.7	429	2	O9R2H0	O9r2h0 salmonella	795	5	41.7	486	14	O80634	O80634 human immun
723	5	41.7	434	2	O9X6H2	O9x6h2 streptococ	796	5	41.7	487	14	O80621	O80621 human immun
724	5	41.7	434	14	O89933	O89933 human immun	797	5	41.7	488	10	O9LNX1	O9lnx1 arabidopsis
725	5	41.7	435	5	O93322	O93322 caenorhabd1	798	5	41.7	488	14	O79362	O79362 human immun
726	5	41.7	436	14	O9IV79	O9iv79 human immun	799	5	41.7	488	14	O9WT03	O9wt03 human herpe
727	5	41.7	438	5	O9NGI3	O9ngi3 branchiosto	800	5	41.7	489	14	O79350	O79350 human immun
728	5	41.7	439	5	O9V9N5	O9v9n5 drosophila	801	5	41.7	489	14	O79354	O79354 human immun
729	5	41.7	440	2	O25464	O25464 helicobacte	802	5	41.7	489	14	O79360	O79360 human immun
730	5	41.7	443	1	O58579	O58579 pyrococcus	803	5	41.7	489	14	O80306	O80306 human immun
731	5	41.7	444	5	O26861	O26861 trypanosoma	804	5	41.7	489	14	O80307	O80307 human immun
732	5	41.7	444	5	O9VM63	O9vm63 drosophila	805	5	41.7	489	14	O80631	O80631 human immun
733	5	41.7	445	2	O45Z94	O45z94 bacteroides	806	5	41.7	489	14	O80630	O80630 human immun
734	5	41.7	445	2	O9KTI9	O9kti9 bacteroides	807	5	41.7	490	2	O80305	O80305 human immun
735	5	41.7	446	5	O9N3V2	O9n3v2 caenorhabd1	808	5	41.7	490	14	O9RMV1	O9rmv1 bacillus an
736	5	41.7	448	5	O9GMF9	O9gmf9 drosophila	809	5	41.7	490	14	O80623	O80623 human immun
737	5	41.7	448	13	O9Z019	O9z019 xenopus lae	810	5	41.7	490	14	P90073	P90073 human immun
738	5	41.7	452	5	O27696	O27696 musca domes	811	5	41.7	490	14	P90255	P90255 human immun
739	5	41.7	456	11	O9JIT8	O9jit8 mus musculu	812	5	41.7	491	2	O9F5I8	O9f5i8 synechococ
740	5	41.7	459	2	O9ZHC0	O9zhc0 streptococ	813	5	41.7	491	14	O9L181	O9l181 human immun
741	5	41.7	459	14	O9TR53	O9tr53 human papil	814	5	41.7	491	14	O9WLH4	O9wlh4 human immun
742	5	41.7	461	5	O45051	O45051 caenorhabd1	815	5	41.7	491	14	O90EF9	O90ef9 human immun
743	5	41.7	462	10	O9WL43	O9wl43 drosophila	816	5	41.7	491	14	O9QBZ6	O9qbz6 human immun
744	5	41.7	462	10	O9LPM4	O9lpm4 arabidopsis	817	5	41.7	492	2	O9ZND0	O9znd0 clostridium
745	5	41.7	464	2	P74828	P74828 sphingomona	818	5	41.7	492	14	O79351	O79351 human immun
746	5	41.7	465	14	O90729	O90729 human papil	819	5	41.7	492	14	O74452	O74452 human immun
747	5	41.7	467	4	O9NXT1	O9nxt1 homo sapien	820	5	41.7	492	14	O89291	O89291 human immun
748	5	41.7	467	14	O40461	O40461 human immun	821	5	41.7	492	14	O89958	O89958 human immun
749	5	41.7	468	14	O9ENB2	O9enb2 human immun	822	5	41.7	492	14	O89962	O89962 human immun

531	5	41.7	255	14	Q9J6U2	Q9J6U2 human immun	604	5	41.7	315	5	018121	018121 caenorhabdi
532	5	41.7	256	4	Q9X611	Q9X611 streptococc	605	5	41.7	315	5	09XW49	09XW49 caenorhabdi
533	5	41.7	256	4	Q9NUR3	Q9NUR3 homo sapien	606	5	41.7	318	2	066259	066259 actinobacti
534	5	41.7	256	14	Q9J709	Q9J709 human immun	607	5	41.7	318	2	005380	005380 actinobacti
535	5	41.7	256	14	Q9J6U7	Q9J6U7 human immun	608	5	41.7	323	11	Q9R292	Q9R292 mus musculu
536	5	41.7	256	14	Q9J6U6	Q9J6U6 human immun	609	5	41.7	327	2	09PAP3	09PAP3 xylella fas
537	5	41.7	257	14	Q9J7A5	Q9J7A5 human immun	610	5	41.7	327	10	Q9LD07	Q9LD07 oryza sativ
538	5	41.7	257	14	Q9J6W3	Q9J6W3 human immun	611	5	41.7	327	11	Q9QWU6	Q9QWU6 mus musculu
539	5	41.7	257	14	Q9J6P0	Q9J6P0 human immun	612	5	41.7	329	5	09Y205	09Y205 ephydactia f
540	5	41.7	258	2	Q9K410	Q9K410 streptomyce	613	5	41.7	329	5	09Y111	09Y111 drosophila
541	5	41.7	258	14	Q9J6R3	Q9J6R3 human immun	614	5	41.7	330	14	Q72628	Q72628 human immun
542	5	41.7	258	14	Q9J6P4	Q9J6P4 human immun	615	5	41.7	335	2	Q9RXC1	Q9RXC1 delinococcus
543	5	41.7	259	14	Q9J6M3	Q9J6M3 thermoplasm	616	5	41.7	335	2	Q9RSC0	Q9RSC0 delinococcus
544	5	41.7	259	14	Q10736	Q10736 human immun	617	5	41.7	335	5	Q9J4D3	Q9J4D3 caenorhabdi
545	5	41.7	260	5	Q17625	Q17625 caenorhabdi	618	5	41.7	335	5	Q9NEF0	Q9NEF0 caenorhabdi
546	5	41.7	260	7	P79551	P79551 homo sapien	619	5	41.7	335	5	Q9NEF6	Q9NEF6 caenorhabdi
547	5	41.7	261	3	Q9P390	Q9P390 neurospora	620	5	41.7	335	5	Q9N6L3	Q9N6L3 caenorhabdi
548	5	41.7	261	7	Q30096	Q30096 homo sapien	621	5	41.7	337	2	053089	053089 lactobacilli
549	5	41.7	261	7	Q30099	Q30099 homo sapien	622	5	41.7	339	2	Q9RXE8	Q9RXE8 delinococcus
550	5	41.7	261	7	Q30061	Q30061 homo sapien	623	5	41.7	339	14	Q9IE68	Q9IE68 human immun
551	5	41.7	261	7	Q31633	Q31633 homo sapien	624	5	41.7	342	2	Q925F8	Q925F8 mycobacteri
552	5	41.7	261	14	Q9J6R5	Q9J6R5 human immun	625	5	41.7	343	2	Q9RKG7	Q9RKG7 vibrio chol
553	5	41.7	261	14	Q9J6P5	Q9J6P5 human immun	626	5	41.7	343	8	Q92238	Q92238 trichophyto
554	5	41.7	262	14	Q9J6N6	Q9J6N6 human immun	627	5	41.7	344	14	Q9IWA5	Q9IWA5 human immun
555	5	41.7	262	14	Q9J736	Q9J736 human immun	628	5	41.7	347	5	Q9VRJ9	Q9VRJ9 drosophila
556	5	41.7	263	10	P94481	P94481 bacillus su	629	5	41.7	351	5	Q9YSTB	Q9YSTB drosophila
557	5	41.7	263	10	Q9FLK5	Q9FLK5 arabiidopsis	630	5	41.7	351	10	Q23142	Q23142 arabiidopsis
558	5	41.7	264	7	Q28826	Q28826 homo sapien	631	5	41.7	353	5	Q9W418	Q9W418 drosophila
559	5	41.7	264	7	Q28970	Q28970 homo sapien	632	5	41.7	353	14	Q9ENC6	Q9ENC6 human immun
560	5	41.7	264	14	Q10730	Q10730 human immun	633	5	41.7	353	14	Q9ENC4	Q9ENC4 human immun
561	5	41.7	265	14	Q10729	Q10729 human immun	634	5	41.7	354	5	Q9NHF6	Q9NHF6 dictyosteli
562	5	41.7	266	4	Q15795	Q15795 homo sapien	635	5	41.7	355	2	067685	067685 aquifex aeo
563	5	41.7	266	5	Q25732	Q25732 plasmodium	636	5	41.7	356	2	Q9S5G6	Q9S5G6 escherichia
564	5	41.7	267	5	Q16704	Q16704 caenorhabdi	637	5	41.7	359	2	Q9MWN3	Q9MWN3 synecchococ
565	5	41.7	267	14	Q87048	Q87048 semliki for	638	5	41.7	359	8	Q37749	Q37749 cephalospor
566	5	41.7	268	14	Q10735	Q10735 human immun	639	5	41.7	360	4	Q9UGM6	Q9UGM6 homo sapien
567	5	41.7	269	7	Q30155	Q30155 homo sapien	640	5	41.7	362	2	Q9KCG9	Q9KCG9 yerstinia en
568	5	41.7	271	5	Q21382	Q21382 caenorhabdi	641	5	41.7	362	4	Q9UHS5	Q9UHS5 homo sapien
569	5	41.7	273	2	Q05936	Q05936 pseudomonas	642	5	41.7	362	5	Q9NEZ1	Q9NEZ1 caenorhabdi
570	5	41.7	275	4	Q9NRB1	Q9NRB1 homo sapien	643	5	41.7	362	10	Q82054	Q82054 saccharum o
571	5	41.7	276	2	P73137	P73137 synecchocyst	644	5	41.7	363	10	Q9M6B4	Q9M6B4 vllis vlnif
572	5	41.7	276	5	Q94215	Q94215 caenorhabdi	645	5	41.7	366	14	Q86313	Q86313 reovirus sp
573	5	41.7	278	2	Q68435	Q68435 leptospira	646	5	41.7	366	14	Q86314	Q86314 reovirus sp
574	5	41.7	278	2	Q68437	Q68437 leptospira	647	5	41.7	366	14	Q86315	Q86315 reovirus sp
575	5	41.7	282	5	Q9U221	Q9U221 caenorhabdi	648	5	41.7	366	14	Q86316	Q86316 reovirus sp
576	5	41.7	286	2	Q9R640	Q9R640 mycobacteri	649	5	41.7	366	14	Q86317	Q86317 reovirus sp
577	5	41.7	287	1	Q9V1J3	Q9V1J3 pyrococcus	650	5	41.7	366	14	Q86318	Q86318 reovirus sp
578	5	41.7	288	2	Q9JXF2	Q9JXF2 neisseria m	651	5	41.7	366	14	Q86319	Q86319 reovirus sp
579	5	41.7	289	2	Q67230	Q67230 aquifex aeo	652	5	41.7	366	14	Q86320	Q86320 reovirus sp
580	5	41.7	291	2	Q06449	Q06449 serratia ma	653	5	41.7	366	14	Q86323	Q86323 reovirus sp
581	5	41.7	291	2	Q07464	Q07464 salmonella	654	5	41.7	366	14	Q86307	Q86307 reovirus sp
582	5	41.7	293	2	Q92J08	Q92J08 rhodococcus	655	5	41.7	366	14	Q86308	Q86308 reovirus sp
583	5	41.7	293	2	Q9PDL4	Q9PDL4 xylella fas	656	5	41.7	366	14	Q86309	Q86309 reovirus sp
584	5	41.7	293	4	Q14836	Q14836 homo sapien	657	5	41.7	366	14	Q86310	Q86310 reovirus sp
585	5	41.7	293	10	Q49020	Q49020 gossypium h	658	5	41.7	366	14	Q86311	Q86311 reovirus sp
586	5	41.7	296	10	Q22812	Q22812 arabiidopsis	659	5	41.7	366	14	Q86312	Q86312 reovirus sp
587	5	41.7	297	5	Q9VDD4	Q9VDD4 drosophila	660	5	41.7	366	14	Q9ENM1	Q9ENM1 reovirus (c
588	5	41.7	298	2	Q9X9Y6	Q9X9Y6 streptomyce	661	5	41.7	367	14	Q87097	Q87097 chimpanzee
589	5	41.7	298	2	Q9VU90	Q9VU90 drosophila	662	5	41.7	367	14	Q41165	Q41165 paramecium
590	5	41.7	299	2	Q9KPI8	Q9KPI8 vibrio chol	663	5	41.7	368	2	Q9LAD4	Q9LAD4 acinetobact
591	5	41.7	302	10	Q9SAH7	Q9SAH7 arabiidopsis	664	5	41.7	368	2	Q9F010	Q9F010 pseudomonas
592	5	41.7	304	14	Q9J4W8	Q9J4W8 human immun	665	5	41.7	369	5	Q9N405	Q9N405 caenorhabdi
593	5	41.7	305	2	Q9K9W1	Q9K9W1 bacillus ha	666	5	41.7	372	14	Q9PYX0	Q9PYX0 xestia c-n1
594	5	41.7	306	10	Q9SDM3	Q9SDM3 prunus dulc	667	5	41.7	375	10	Q39235	Q39235 arabiidopsis
595	5	41.7	306	10	Q9M5Q3	Q9M5Q3 petunia hyb	668	5	41.7	375	10	Q49349	Q49349 arabiidopsis
596	5	41.7	307	2	Q55410	Q55410 synecchocyst	669	5	41.7	376	5	Q9VB07	Q9VB07 drosophila
597	5	41.7	308	2	Q9RUQ2	Q9RUQ2 delinococcus	670	5	41.7	377	11	Q922K3	Q922K3 cricetus
598	5	41.7	309	5	Q9VUV0	Q9VUV0 drosophila	671	5	41.7	377	2	Q55307	Q55307 streptococc
599	5	41.7	310	11	Q9E047	Q9E047 mus musculu	672	5	41.7	380	1	Q9HRS8	Q9HRS8 halobacteri
600	5	41.7	311	10	Q22805	Q22805 arabiidopsis	673	5	41.7	382	4	Q9H878	Q9H878 homo sapien
601	5	41.7	312	14	Q9WIR5	Q9WIR5 human immun	674	5	41.7	382	5	Q9U3E1	Q9U3E1 caenorhabdi
602	5	41.7	314	10	Q9XFE2	Q9XFE2 pyrus pyrif	675	5	41.7	384	4	Q9S977	Q9S977 homo sapien
603	5	41.7	314	10	Q9XFE2	Q9XFE2 pyrus pyrif	676	5	41.7	384	4	Q9S977	Q9S977 homo sapien

385	5	41.7	222	14	091VJ2	091VJ2 human immun	458	5	41.7	234	14	091VW9	091VW9 human immun
386	5	41.7	222	14	091UV3	091UV3 human immun	459	5	41.7	234	14	091VM6	091VM6 human immun
387	5	41.7	222	14	091UD8	091UD8 human immun	460	5	41.7	235	14	091VZ8	091VZ8 human immun
388	5	41.7	222	14	091DP0	091DP0 human immun	461	5	41.7	235	14	0916O5	0916O5 human immun
389	5	41.7	223	2	09XCL1	09XCL1 streptococ	462	5	41.7	236	10	091LM0	091LM0 plus taeda
390	5	41.7	223	2	09KMN9	09KMN9 vibrio chol	463	5	41.7	236	14	09J758	09J758 human immun
391	5	41.7	223	14	09J730	09J730 human immun	464	5	41.7	237	14	09J725	09J725 human immun
392	5	41.7	223	14	091VQ9	091VQ9 human immun	465	5	41.7	237	14	091VK5	091VK5 human immun
393	5	41.7	223	14	091UW2	091UW2 human immun	466	5	41.7	238	14	09J785	09J785 human immun
394	5	41.7	223	14	091UW0	091UW0 human immun	467	5	41.7	238	14	09J757	09J757 human immun
395	5	41.7	223	14	091UT7	091UT7 human immun	468	5	41.7	239	14	091BJ1	091BJ1 turkey herp
396	5	41.7	224	7	09RFJ3	09RFJ3 streptococ	469	5	41.7	241	2	09X6G8	09X6G8 streptococ
397	5	41.7	224	7	029967	029967 homo sapien	470	5	41.7	241	11	092135	092135 rattus norv
398	5	41.7	224	14	09J792	09J792 human immun	471	5	41.7	241	14	09J6T8	09J6T8 human immun
399	5	41.7	224	14	091VW9	091VW9 human immun	472	5	41.7	243	14	09J6M7	09J6M7 human immun
400	5	41.7	224	14	091VL4	091VL4 human immun	473	5	41.7	244	5	09XEX6	09XEX6 leishmania
401	5	41.7	224	14	091VL1	091VL1 human immun	474	5	41.7	244	14	09J724	09J724 human immun
402	5	41.7	224	14	091VJ9	091VJ9 human immun	475	5	41.7	245	2	084764	084764 chlamydia t
403	5	41.7	224	14	091VJ8	091VJ8 human immun	476	5	41.7	245	14	09J774	09J774 human immun
404	5	41.7	224	14	091UY3	091UY3 human immun	477	5	41.7	245	14	09J723	09J723 human immun
405	5	41.7	224	14	091UV9	091UV9 human immun	478	5	41.7	245	14	09J717	09J717 human immun
406	5	41.7	224	14	091UU2	091UU2 human immun	479	5	41.7	245	14	09J716	09J716 human immun
407	5	41.7	224	14	091DN9	091DN9 human immun	480	5	41.7	245	14	09J704	09J704 human immun
408	5	41.7	225	14	09J6Z9	09J6Z9 human immun	481	5	41.7	246	2	09RG64	09RG64 mycoplasma
409	5	41.7	225	14	09J6R4	09J6R4 human immun	482	5	41.7	246	14	09J721	09J721 human immun
410	5	41.7	225	14	091VR2	091VR2 human immun	483	5	41.7	246	14	09J718	09J718 human immun
411	5	41.7	225	14	091UX9	091UX9 human immun	484	5	41.7	246	14	09J715	09J715 human immun
412	5	41.7	225	14	091UX4	091UX4 human immun	485	5	41.7	246	14	09J714	09J714 human immun
413	5	41.7	225	14	091UV7	091UV7 human immun	486	5	41.7	247	14	09J773	09J773 human immun
414	5	41.7	225	14	091UD5	091UD5 human immun	487	5	41.7	247	14	09J768	09J768 human immun
415	5	41.7	226	14	091VW5	091VW5 human immun	488	5	41.7	247	14	09J6M9	09J6M9 human immun
416	5	41.7	226	14	091VL5	091VL5 human immun	489	5	41.7	248	14	09J719	09J719 human immun
417	5	41.7	226	14	091VK7	091VK7 human immun	490	5	41.7	249	10	065058	065058 picea marie
418	5	41.7	226	14	091VK2	091VK2 human immun	491	5	41.7	249	14	09J708	09J708 human immun
419	5	41.7	226	14	091VK1	091VK1 human immun	492	5	41.7	249	14	09J6V5	09J6V5 human immun
420	5	41.7	226	14	091UP7	091UP7 human immun	493	5	41.7	250	7	019711	019711 homo sapien
421	5	41.7	226	14	091DP7	091DP7 human immun	494	5	41.7	250	7	019714	019714 homo sapien
422	5	41.7	226	14	091DP5	091DP5 human immun	495	5	41.7	250	11	09WV64	09WV64 rattus norv
423	5	41.7	226	14	091DPI	091DPI human immun	496	5	41.7	250	14	09J770	09J770 human immun
424	5	41.7	227	2	031975	031975 bacillus su	497	5	41.7	250	14	09J763	09J763 human immun
425	5	41.7	227	9	037974	037974 bacterioph	498	5	41.7	251	2	09X8B5	09X8B5 bacillus ha
426	5	41.7	227	9	038576	038576 unidentified	499	5	41.7	251	14	09J762	09J762 human immun
427	5	41.7	227	10	092R64	092R64 zea mays (m	500	5	41.7	252	10	09JQL8	09JQL8 arabidopsis
428	5	41.7	227	14	091VP5	091VP5 human immun	501	5	41.7	252	14	09J794	09J794 human immun
429	5	41.7	227	14	091UW8	091UW8 human immun	502	5	41.7	252	14	09J775	09J775 human immun
430	5	41.7	227	14	091UW6	091UW6 human immun	503	5	41.7	252	14	09J767	09J767 human immun
431	5	41.7	227	14	091DO3	091DO3 human immun	504	5	41.7	252	14	09J760	09J760 human immun
432	5	41.7	228	2	09RUB6	09RUB6 delinococcus	505	5	41.7	252	14	09J755	09J755 human immun
433	5	41.7	228	14	09QNX0	09QNX0 human immun	506	5	41.7	252	14	09J749	09J749 human immun
434	5	41.7	228	14	091VR4	091VR4 human immun	507	5	41.7	252	14	09J748	09J748 human immun
435	5	41.7	228	14	091VP2	091VP2 human immun	508	5	41.7	252	14	09J702	09J702 human immun
436	5	41.7	228	14	091VK6	091VK6 human immun	509	5	41.7	252	14	09J700	09J700 human immun
437	5	41.7	228	14	091UV1	091UV1 human immun	510	5	41.7	253	1	059562	059562 pyrococcus
438	5	41.7	228	14	091UV0	091UV0 human immun	511	5	41.7	253	1	09V1J7	09V1J7 pyrococcus
439	5	41.7	228	14	091UW3	091UW3 human immun	512	5	41.7	253	14	09J729	09J729 human immun
440	5	41.7	229	14	09J713	09J713 human immun	513	5	41.7	253	14	09J727	09J727 human immun
441	5	41.7	229	14	091VQ2	091VQ2 human immun	514	5	41.7	253	14	09J726	09J726 human immun
442	5	41.7	229	14	091UW9	091UW9 human immun	515	5	41.7	253	14	09J711	09J711 human immun
443	5	41.7	230	14	091UV5	091UV5 human immun	516	5	41.7	253	14	09J701	09J701 human immun
444	5	41.7	230	14	091VJ5	091VJ5 human immun	517	5	41.7	254	5	021223	021223 caenorhabd1
445	5	41.7	230	14	091UW1	091UW1 human immun	518	5	41.7	254	14	09J795	09J795 human immun
446	5	41.7	230	14	091UT5	091UT5 human immun	519	5	41.7	254	14	09J789	09J789 human immun
447	5	41.7	231	14	091VW3	091VW3 human immun	520	5	41.7	254	14	09J739	09J739 human immun
448	5	41.7	231	14	091UW5	091UW5 human immun	521	5	41.7	254	14	09J732	09J732 human immun
449	5	41.7	232	14	091VP8	091VP8 human immun	522	5	41.7	254	14	09J707	09J707 human immun
450	5	41.7	232	14	091UW9	091UW9 human immun	523	5	41.7	254	14	09J6Z2	09J6Z2 human immun
451	5	41.7	232	14	091UW8	091UW8 human immun	524	5	41.7	254	14	09J6U6	09J6U6 human immun
452	5	41.7	232	14	091UT4	091UT4 human immun	525	5	41.7	254	14	09J6N7	09J6N7 human immun
453	5	41.7	233	14	091VQ0	091VQ0 human immun	526	5	41.7	255	7	019506	019506 homo sapien
454	5	41.7	233	14	091VJ4	091VJ4 human immun	527	5	41.7	255	14	010731	010731 human immun
455	5	41.7	233	14	091UT7	091UT7 human immun	528	5	41.7	255	14	09J746	09J746 human immun
456	5	41.7	233	14	091UT8	091UT8 human immun	529	5	41.7	255	14	09J742	09J742 human immun
457	5	41.7	234	14	091VP0	091VP0 human immun	530	5	41.7	255	14	09J6X0	09J6X0 human immun

239	5	41.7	207	14	Q9MWM3	Q9MWM3	human	limun	312	5	41.7	209	14	Q9IUL7	Q9IUL7	human	limun
240	5	41.7	207	14	Q9MWM2	Q9MWM2	human	limun	313	5	41.7	209	14	Q9IUK7	Q9IUK7	human	limun
241	5	41.7	207	14	Q9MWM1	Q9MWM1	human	limun	314	5	41.7	210	2	Q9XCJ9	Q9XCJ9	human	limun
242	5	41.7	207	14	Q9MWM9	Q9MWM9	human	limun	315	5	41.7	210	2	Q9RNU2	Q9RNU2	streptococ	
243	5	41.7	207	14	Q9MWM8	Q9MWM8	human	limun	316	5	41.7	210	14	Q9J776	Q9J776	human	limun
244	5	41.7	207	14	Q9QNX4	Q9QNX4	human	limun	317	5	41.7	210	14	Q9J6T4	Q9J6T4	human	limun
245	5	41.7	207	14	Q9Q2L6	Q9Q2L6	human	limun	318	5	41.7	210	14	Q9IUX8	Q9IUX8	human	limun
246	5	41.7	207	14	Q9Q2L5	Q9Q2L5	human	limun	319	5	41.7	210	14	Q9IUX1	Q9IUX1	human	limun
247	5	41.7	207	14	Q9Q2K8	Q9Q2K8	human	limun	320	5	41.7	210	14	Q9IUR4	Q9IUR4	human	limun
248	5	41.7	207	14	Q9Q2K5	Q9Q2K5	human	limun	321	5	41.7	210	14	Q9DUW9	Q9DUW9	human	limun
249	5	41.7	207	14	Q9Q2K3	Q9Q2K3	human	limun	322	5	41.7	211	5	Q9XU58	Q9XU58	caenorhabdi	
250	5	41.7	207	14	Q9Q2K2	Q9Q2K2	human	limun	323	5	41.7	211	14	Q9J687	Q9J687	human	limun
251	5	41.7	207	14	Q9Q2K0	Q9Q2K0	human	limun	324	5	41.7	211	14	Q9J688	Q9J688	human	limun
252	5	41.7	207	14	Q9Q2J9	Q9Q2J9	human	limun	325	5	41.7	211	14	Q9J689	Q9J689	human	limun
253	5	41.7	207	14	Q9Q2J8	Q9Q2J8	human	limun	326	5	41.7	211	14	Q9J689	Q9J689	human	limun
254	5	41.7	207	14	Q9Q2J7	Q9Q2J7	human	limun	327	5	41.7	211	14	Q9J689	Q9J689	human	limun
255	5	41.7	207	14	Q9Q2J6	Q9Q2J6	human	limun	328	5	41.7	211	14	Q9J689	Q9J689	human	limun
256	5	41.7	207	14	Q9Q2J5	Q9Q2J5	human	limun	329	5	41.7	211	14	Q9J689	Q9J689	human	limun
257	5	41.7	207	14	Q9Q2J4	Q9Q2J4	human	limun	330	5	41.7	211	14	Q9IYQ3	Q9IYQ3	human	limun
258	5	41.7	207	14	Q9Q2J3	Q9Q2J3	human	limun	331	5	41.7	211	14	Q9IYK4	Q9IYK4	human	limun
259	5	41.7	207	14	Q9Q2J2	Q9Q2J2	human	limun	332	5	41.7	211	14	Q9IUR0	Q9IUR0	human	limun
260	5	41.7	207	14	Q9Q2J1	Q9Q2J1	human	limun	333	5	41.7	211	14	Q9IUN5	Q9IUN5	human	limun
261	5	41.7	207	14	Q9Q2I6	Q9Q2I6	human	limun	334	5	41.7	212	2	Q9S4J5	Q9S4J5	human	limun
262	5	41.7	207	14	Q9Q2I5	Q9Q2I5	human	limun	335	5	41.7	212	11	Q9ERR0	Q9ERR0	human	limun
263	5	41.7	207	14	Q9Q2I3	Q9Q2I3	human	limun	336	5	41.7	212	14	Q9IYQ1	Q9IYQ1	human	limun
264	5	41.7	207	14	Q9Q2I2	Q9Q2I2	human	limun	337	5	41.7	213	14	Q9MWM0	Q9MWM0	human	limun
265	5	41.7	207	14	Q9IUS6	Q9IUS6	human	limun	338	5	41.7	214	14	Q9J7B0	Q9J7B0	human	limun
266	5	41.7	207	14	Q9IUN2	Q9IUN2	human	limun	339	5	41.7	214	14	Q9J7A9	Q9J7A9	human	limun
267	5	41.7	207	14	Q9IUN1	Q9IUN1	human	limun	340	5	41.7	214	14	Q9J7A1	Q9J7A1	human	limun
268	5	41.7	207	14	Q9DV09	Q9DV09	human	limun	341	5	41.7	214	14	Q9J777	Q9J777	human	limun
269	5	41.7	207	14	Q9DV08	Q9DV08	human	limun	342	5	41.7	214	14	Q9IYR3	Q9IYR3	human	limun
270	5	41.7	207	14	Q9DV05	Q9DV05	human	limun	343	5	41.7	215	2	Q9I491	Q9I491	pseudomonas	
271	5	41.7	207	14	Q9DV03	Q9DV03	human	limun	344	5	41.7	215	14	Q9J7B2	Q9J7B2	human	limun
272	5	41.7	207	14	Q9DV01	Q9DV01	human	limun	345	5	41.7	215	14	Q9IUS0	Q9IUS0	human	limun
273	5	41.7	207	14	Q9DV00	Q9DV00	human	limun	346	5	41.7	216	14	Q9J7S9	Q9J7S9	human	limun
274	5	41.7	207	14	Q9DU29	Q9DU29	human	limun	347	5	41.7	216	14	Q9IUK1	Q9IUK1	human	limun
275	5	41.7	207	14	Q9DU25	Q9DU25	human	limun	348	5	41.7	217	14	Q9IYV9	Q9IYV9	human	limun
276	5	41.7	207	14	Q9DU24	Q9DU24	human	limun	349	5	41.7	217	14	Q9IUY0	Q9IUY0	human	limun
277	5	41.7	207	14	Q9DU21	Q9DU21	human	limun	350	5	41.7	217	14	Q9IUY2	Q9IUY2	human	limun
278	5	41.7	207	14	Q9DU20	Q9DU20	human	limun	351	5	41.7	217	14	Q9IUN8	Q9IUN8	human	limun
279	5	41.7	207	14	Q9DU19	Q9DU19	human	limun	352	5	41.7	217	14	Q9IUN3	Q9IUN3	human	limun
280	5	41.7	207	14	Q9DUY3	Q9DUY3	human	limun	353	5	41.7	218	14	Q9J778	Q9J778	human	limun
281	5	41.7	207	14	Q9DUY2	Q9DUY2	human	limun	354	5	41.7	218	14	Q9J754	Q9J754	human	limun
282	5	41.7	207	14	Q9DUY1	Q9DUY1	human	limun	355	5	41.7	218	14	Q9IYV1	Q9IYV1	human	limun
283	5	41.7	207	14	Q9DUY0	Q9DUY0	human	limun	356	5	41.7	218	14	Q9IUX2	Q9IUX2	human	limun
284	5	41.7	207	14	Q9DUX9	Q9DUX9	human	limun	357	5	41.7	218	14	Q9IDR5	Q9IDR5	human	limun
285	5	41.7	207	14	Q9DUX7	Q9DUX7	human	limun	358	5	41.7	219	4	Q9Y656	Q9Y656	homo sapien	
286	5	41.7	207	14	Q9DUX4	Q9DUX4	human	limun	359	5	41.7	219	14	Q9J6V9	Q9J6V9	human	limun
287	5	41.7	207	14	Q9DUX3	Q9DUX3	human	limun	360	5	41.7	219	14	Q9IYV7	Q9IYV7	human	limun
288	5	41.7	207	14	Q9DUW8	Q9DUW8	human	limun	361	5	41.7	219	14	Q9IYV3	Q9IYV3	human	limun
289	5	41.7	207	14	Q9DUW6	Q9DUW6	human	limun	362	5	41.7	219	14	Q9IYV2	Q9IYV2	human	limun
290	5	41.7	207	14	Q9DUW5	Q9DUW5	human	limun	363	5	41.7	219	14	Q9IYX0	Q9IYX0	human	limun
291	5	41.7	207	14	Q9DUW3	Q9DUW3	human	limun	364	5	41.7	219	14	Q9IYV8	Q9IYV8	human	limun
292	5	41.7	207	14	Q9DUW1	Q9DUW1	human	limun	365	5	41.7	219	14	Q9IYV5	Q9IYV5	human	limun
293	5	41.7	207	14	Q9DUV9	Q9DUV9	human	limun	366	5	41.7	219	14	Q9IYV4	Q9IYV4	human	limun
294	5	41.7	207	14	Q9DUV8	Q9DUV8	human	limun	367	5	41.7	219	14	Q9IYK0	Q9IYK0	human	limun
295	5	41.7	207	14	Q9DUV6	Q9DUV6	human	limun	368	5	41.7	220	11	Q9Z1E5	Q9Z1E5	rattus norv	
296	5	41.7	207	14	Q9DUV5	Q9DUV5	human	limun	369	5	41.7	220	14	Q9IYV8	Q9IYV8	human	limun
297	5	41.7	207	14	Q9DUV4	Q9DUV4	human	limun	370	5	41.7	220	14	Q9IYV3	Q9IYV3	human	limun
298	5	41.7	207	14	Q9DOV1	Q9DOV1	human	limun	371	5	41.7	220	14	Q9IYV5	Q9IYV5	human	limun
299	5	41.7	207	14	Q9DOV9	Q9DOV9	human	limun	372	5	41.7	220	14	Q9IYV4	Q9IYV4	human	limun
300	5	41.7	208	2	Q9RBZ7	Q9RBZ7	pseudomonas		373	5	41.7	220	14	Q9IYR3	Q9IYR3	human	limun
301	5	41.7	208	14	Q9J393	Q9J393	human	limun	374	5	41.7	220	14	Q9IDR8	Q9IDR8	human	limun
302	5	41.7	208	14	Q9J394	Q9J394	human	limun	375	5	41.7	220	14	Q9IDP4	Q9IDP4	human	limun
303	5	41.7	208	14	Q9J624	Q9J624	human	limun	376	5	41.7	221	2	P70813	P70813	boirella af	
304	5	41.7	208	14	Q9IUP8	Q9IUP8	human	limun	377	5	41.7	221	14	Q9Q2K7	Q9Q2K7	human	limun
305	5	41.7	208	14	Q9IUL5	Q9IUL5	human	limun	378	5	41.7	221	14	Q9IUX5	Q9IUX5	human	limun
306	5	41.7	209	5	Q9VX73	Q9VX73	human	limun	379	5	41.7	221	14	Q9IYU0	Q9IYU0	human	limun
307	5	41.7	209	14	Q9J7A6	Q9J7A6	human	limun	380	5	41.7	221	14	Q9IYU6	Q9IYU6	human	limun
308	5	41.7	209	14	Q9IUS7	Q9IUS7	human	limun	381	5	41.7	222	14	Q9J7A4	Q9J7A4	human	limun
309	5	41.7	209	14	Q9IUR7	Q9IUR7	human	limun	382	5	41.7	222	14	Q9J621	Q9J621	human	limun
310	5	41.7	209	14	Q9IUR6	Q9IUR6	human	limun	383	5	41.7	222	14	Q9IYV0	Q9IYV0	human	limun
311	5	41.7	209	14	Q9IUR6	Q9IUR6	human	limun	384	5	41.7	222	14	Q9IYV3	Q9IYV3	human	limun

93	5	41.7	130	14	09QKWS	09QKWS human immun	166	5	41.7	185	5	09V916	09V916 drosophila
94	5	41.7	130	14	09QKW1	09QKW1 human immun	167	5	41.7	185	10	09WAI5	09WAI5 arebidopsis
95	5	41.7	131	14	09QL44	09QL44 human immun	168	5	41.7	186	14	09WK89	09WK89 human immun
96	5	41.7	131	14	09QL18	09QL18 human immun	169	5	41.7	186	14	09J6Z5	09J6Z5 human immun
97	5	41.7	131	14	09QL16	09QL16 human immun	170	5	41.7	187	5	09N344	09N344 caenorhabd
98	5	41.7	131	14	09QL08	09QL08 human immun	171	5	41.7	187	14	09IUP3	09IUP3 human immun
99	5	41.7	131	14	09QKX9	09QKX9 human immun	172	5	41.7	190	1	09V1G6	09V1G6 pyrococcus
100	5	41.7	131	14	09QKX7	09QKX7 human immun	173	5	41.7	190	14	093038	093038 human immun
101	5	41.7	131	14	09QKW8	09QKW8 human immun	174	5	41.7	190	14	09J6N5	09J6N5 human immun
102	5	41.7	131	14	09QKW6	09QKW6 human immun	175	5	41.7	191	2	09XCK6	09XCK6 streptococc
103	5	41.7	132	2	09K2C0	09K2C0 chlamydia p	176	5	41.7	192	14	08I390	08I390 hepatitis c
104	5	41.7	132	14	09QL23	09QL23 human immun	177	5	41.7	192	14	09J733	09J733 human immun
105	5	41.7	133	2	087645	087645 methylococc	178	5	41.7	192	14	09J6N9	09J6N9 human immun
106	5	41.7	133	3	09URT5	09URT5 schizosacch	179	5	41.7	193	14	09J7B3	09J7B3 human immun
107	5	41.7	133	14	09OL05	09OL05 human immun	180	5	41.7	193	14	09J5W8	09J5W8 streptococc
108	5	41.7	133	14	09QKX5	09QKX5 human immun	181	5	41.7	195	14	09J769	09J769 human immun
109	5	41.7	134	2	09E0Y9	09E0Y9 chlamydia m	182	5	41.7	195	14	09J731	09J731 human immun
110	5	41.7	137	5	09N3U4	09N3U4 caenorhabd	183	5	41.7	195	14	09J6U1	09J6U1 human immun
111	5	41.7	138	14	09EBV4	09EBV4 foot-and-mo	184	5	41.7	195	14	09IUC4	09IUC4 human immun
112	5	41.7	138	14	09EBV2	09EBV2 foot-and-mo	185	5	41.7	196	14	09J796	09J796 human immun
113	5	41.7	138	14	09EBT3	09EBT3 foot-and-mo	186	5	41.7	197	2	09RKU2	09RKU2 streptomyc
114	5	41.7	140	5	09N5B1	09N5B1 caenorhabd	187	5	41.7	197	14	09ITU4	09ITU4 human immun
115	5	41.7	141	1	09YAL8	09YAL8 aeropyrum p	188	5	41.7	198	14	09J787	09J787 human immun
116	5	41.7	141	3	005690	005690 saccharomyc	189	5	41.7	198	14	09J7L8	09J7L8 human immun
117	5	41.7	142	14	09J6S4	09J6S4 human immun	190	5	41.7	198	14	09IUL3	09IUL3 human immun
118	5	41.7	143	2	007266	007266 mycobacteri	191	5	41.7	198	14	09IUL2	09IUL2 human immun
119	5	41.7	147	2	09WYK3	09WYK3 thermotoga	192	5	41.7	199	2	09K531	09K531 pseudomonas
120	5	41.7	147	5	076560	076560 caenorhabd	193	5	41.7	199	14	09J6Z7	09J6Z7 human immun
121	5	41.7	148	6	09GKP9	09GKP9 bos taurus	194	5	41.7	199	14	09IUP4	09IUP4 human immun
122	5	41.7	148	10	09EP13	09EP13 arebidopsis	195	5	41.7	199	14	09IUM8	09IUM8 human immun
123	5	41.7	149	14	068732	068732 hepatitis c	196	5	41.7	200	14	056247	056247 tobaccoc rat
124	5	41.7	152	14	09J756	09J756 human immun	197	5	41.7	200	14	09J6Q2	09J6Q2 human immun
125	5	41.7	156	6	09N146	09N146 macaca mula	198	5	41.7	200	14	09IUP2	09IUP2 human immun
126	5	41.7	157	2	049991	049991 mycobacteri	199	5	41.7	201	3	P87261	P87261 saccharomyc
127	5	41.7	157	5	09GKJ6	09GKJ6 caenorhabd	200	5	41.7	201	14	09J744	09J744 human immun
128	5	41.7	161	2	09FEC1	09FEC1 streptococc	201	5	41.7	201	14	09IVR7	09IVR7 human immun
129	5	41.7	161	10	09SSS3	09SSS3 arebidopsis	202	5	41.7	201	14	09IUS1	09IUS1 human immun
130	5	41.7	161	14	09J771	09J771 human immun	203	5	41.7	201	14	09IUL1	09IUL1 human immun
131	5	41.7	161	14	09J6U4	09J6U4 human immun	204	5	41.7	202	14	09J7A2	09J7A2 human immun
132	5	41.7	162	14	09J6U0	09J6U0 human immun	205	5	41.7	202	14	09IUT1	09IUT1 human immun
133	5	41.7	163	5	09N3V0	09N3V0 caenorhabd	206	5	41.7	202	14	09IUP6	09IUP6 human immun
134	5	41.7	165	2	052819	052819 rhizobium l	207	5	41.7	202	14	09IUM4	09IUM4 human immun
135	5	41.7	165	14	09J788	09J788 human immun	208	5	41.7	202	14	09IUL9	09IUL9 human immun
136	5	41.7	165	14	09J752	09J752 human immun	209	5	41.7	202	14	09IUL0	09IUL0 human immun
137	5	41.7	166	4	09M4T9	09M4T9 homo sapien	210	5	41.7	203	14	09J6T3	09J6T3 human immun
138	5	41.7	166	10	09M4T9	09M4T9 triticum ae	211	5	41.7	203	14	09IUT5	09IUT5 human immun
139	5	41.7	166	14	09J7A7	09J7A7 human immun	212	5	41.7	203	14	09IUC0	09IUC0 human immun
140	5	41.7	166	14	09J6V7	09J6V7 human immun	213	5	41.7	203	14	09IUP7	09IUP7 human immun
141	5	41.7	167	14	09J6U3	09J6U3 human immun	214	5	41.7	203	14	09IUK9	09IUK9 human immun
142	5	41.7	170	2	005551	005551 listeria mo	215	5	41.7	204	14	09Q2J1	09Q2J1 human immun
143	5	41.7	171	5	09N927	09N927 crypanosoma	216	5	41.7	204	14	09J7A8	09J7A8 human immun
144	5	41.7	172	14	09J784	09J784 human immun	217	5	41.7	204	14	09J797	09J797 human immun
145	5	41.7	172	14	09J6S9	09J6S9 human immun	218	5	41.7	204	14	09J782	09J782 human immun
146	5	41.7	173	14	09J781	09J781 human immun	219	5	41.7	204	14	09J741	09J741 human immun
147	5	41.7	173	14	09J6Z3	09J6Z3 human immun	220	5	41.7	204	14	09J6Q4	09J6Q4 human immun
148	5	41.7	175	5	09V9R6	09V9R6 drosophila	221	5	41.7	204	14	09J6Q3	09J6Q3 human immun
149	5	41.7	175	10	09XHF4	09XHF4 sorghum bic	222	5	41.7	204	14	09IUM7	09IUM7 human immun
150	5	41.7	175	14	09J6W9	09J6W9 human immun	223	5	41.7	204	14	09IUL4	09IUL4 human immun
151	5	41.7	177	10	043478	043478 hordeum vul	224	5	41.7	205	14	09J6P1	09J6P1 human immun
152	5	41.7	177	14	09J791	09J791 human immun	225	5	41.7	205	14	09J6P1	09J6P1 human immun
153	5	41.7	178	14	09J751	09J751 human immun	226	5	41.7	205	14	09IUP5	09IUP5 human immun
154	5	41.7	178	14	09J750	09J750 human immun	227	5	41.7	205	14	09IUP0	09IUP0 human immun
155	5	41.7	178	14	09J747	09J747 human immun	228	5	41.7	205	14	09IUN6	09IUN6 human immun
156	5	41.7	179	10	09ZOD4	09ZOD4 arebidopsis	229	5	41.7	205	14	09IUN0	09IUN0 human immun
157	5	41.7	179	14	09J786	09J786 arebidopsis	230	5	41.7	205	14	09IUM2	09IUM2 human immun
158	5	41.7	179	14	09J6V2	09J6V2 human immun	231	5	41.7	206	2	09I6S1	09I6S1 human immun
159	5	41.7	180	10	09W9M0	09W9M0 arebidopsis	232	5	41.7	206	2	09EX31	09EX31 streptomyc
160	5	41.7	180	14	09J737	09J737 human immun	233	5	41.7	206	14	09J772	09J772 human immun
161	5	41.7	181	14	09J7A3	09J7A3 human immun	234	5	41.7	206	14	09J6W1	09J6W1 human immun
162	5	41.7	181	14	09J793	09J793 human immun	235	5	41.7	206	14	09J6V6	09J6V6 human immun
163	5	41.7	181	14	09J780	09J780 human immun	236	5	41.7	206	14	09IUK3	09IUK3 human immun
164	5	41.7	183	14	09J706	09J706 human immun	237	5	41.7	207	14	09W9W6	09W9W6 human immun
165	5	41.7	184	14	09J6T7	09J6T7 human immun	238	5	41.7	207	14	09W9W4	09W9W4 human immun

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:42:45 ; Search time 58.01 Seconds
(without alignments)
27.369 Million cell updates/sec

Title: US-09-372-036-30
Perfect score: 12
Sequence: 1 STVPAPTOEVKK 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_16:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mmc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-prodent:*
- 12: sp-unclassified:*
- 13: sp-vertebrate:*
- 14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	86	2	09RNU3
2	12	100.0	478	2	003493
3	7	58.3	94	14	067673
4	7	58.3	227	2	09PM45
5	6	50.0	102	2	09HYT7
6	6	50.0	116	2	09X9T5
7	6	50.0	174	14	093041
8	6	50.0	237	10	09FU39
9	6	50.0	274	2	09KVZ4
10	6	50.0	288	2	084512
11	6	50.0	293	2	09KYN4
12	6	50.0	289	2	09RW05
13	6	50.0	447	2	086673
14	6	50.0	460	5	09XT09
15	6	50.0	486	5	026617
16	6	50.0	530	13	09DEV2
17	6	50.0	609	4	09UNJ0
18	6	50.0	624	4	09NZM6
19	6	50.0	637	3	008484

20	50.0	652	5	09VW35	09VW35 drosophila
21	50.0	748	10	022907	022907 arabidopsis
22	50.0	750	3	09HFZ4	09HFZ4 candida alb
23	50.0	775	5	09VB49	09VB49 drosophila
24	50.0	792	5	09UAG1	09UAG1 epiphydactia f
25	50.0	819	5	09VW48	09VW48 drosophila
26	50.0	904	5	09VEX7	09VEX7 drosophila
27	50.0	912	5	09NHCL	09NHCL drosophila
28	50.0	912	5	09NH99	09NH99 drosophila
29	50.0	916	5	09NHCC	09NHCC drosophila
30	50.0	916	5	09NHCO	09NHCO drosophila
31	50.0	988	14	098830	098830 human foamy
32	50.0	988	14	087041	087041 simian foam
33	50.0	989	14	P90288	P90288 human spuma
34	50.0	1052	5	09YS50	09YS50 drosophila
35	50.0	1230	2	025772	025772 helicobacte
36	50.0	1633	2	09LBB3	09LBB3 streptococ
37	50.0	2037	13	09PVZ2	09PVZ2 xenopus lae
38	41.7	23	11	063334	063334 ratius norv
39	41.7	52	6	09GL38	09GL38 bos taurus
40	41.7	62	2	047006	047006 escherichia
41	41.7	75	2	09RRH1	09RRH1 delnococtis
42	41.7	77	14	091692	091692 human immun
43	41.7	82	5	017728	017728 caenorhabdi
44	41.7	88	5	P91335	P91335 caenorhabdi
45	41.7	88	14	09DR28	09DR28 human immun
46	41.7	91	14	09WJ74	09WJ74 human immun
47	41.7	95	14	068302	068302 hepatitis c
48	41.7	102	14	068301	068301 hepatitis c
49	41.7	108	14	091E25	091E25 human immun
50	41.7	112	4	09UG25	09UG25 homo sapien
51	41.7	113	14	093051	093051 human immun
52	41.7	113	14	093052	093052 human immun
53	41.7	113	14	093053	093053 human immun
54	41.7	113	14	09WK43	09WK43 human immun
55	41.7	113	14	09WK42	09WK42 human immun
56	41.7	113	14	09WKA1	09WKA1 human immun
57	41.7	113	14	09WK98	09WK98 human immun
58	41.7	113	14	09WK96	09WK96 human immun
59	41.7	113	14	09WK84	09WK84 human immun
60	41.7	113	14	09WK93	09WK93 human immun
61	41.7	113	14	09WK91	09WK91 human immun
62	41.7	113	14	09WK90	09WK90 human immun
63	41.7	113	14	09WK88	09WK88 human immun
64	41.7	113	14	09WK87	09WK87 human immun
65	41.7	113	14	09WK86	09WK86 human immun
66	41.7	113	14	09WK47	09WK47 human immun
67	41.7	113	14	09WK45	09WK45 human immun
68	41.7	114	10	09SVK9	09SVK9 arabidopsis
69	41.7	115	2	056724	056724 veillonella
70	41.7	115	5	09W2V1	09W2V1 drosophila
71	41.7	117	2	09XOK8	09XOK8 thermotoga
72	41.7	117	5	09VWMO	09VWMO drosophila
73	41.7	121	5	09N3V1	09N3V1 caenorhabdi
74	41.7	121	10	023980	023980 hordem vul
75	41.7	122	5	09VYZ8	09VYZ8 drosophila
76	41.7	124	2	084412	084412 chlamydia t
77	41.7	124	2	09Z818	09Z818 chlamydia p
78	41.7	124	5	094045	094045 caenorhabdi
79	41.7	126	7	029965	029965 homo sapien
80	41.7	126	7	078219	078219 homo sapien
81	41.7	127	2	09X6H1	09X6H1 yersinia pe
82	41.7	130	14	056095	056095 human immun
83	41.7	130	14	09QL45	09QL45 human immun
84	41.7	130	14	09QL42	09QL42 human immun
85	41.7	130	14	09QL41	09QL41 human immun
86	41.7	130	14	09QL40	09QL40 human immun
87	41.7	130	14	09QL35	09QL35 human immun
88	41.7	130	14	09OKZ5	09OKZ5 human immun
89	41.7	130	14	09OKY6	09OKY6 human immun
90	41.7	130	14	09OKY1	09OKY1 human immun
91	41.7	130	14	09OKY0	09OKY0 human immun
92	41.7	130	14	09OKX8	09OKX8 human immun

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DR InterPro: IPR001245; -.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00069; PKINASE; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR TRANSFERASE: TYROSINE-protein kinase; ATP-binding; SH2 domain;
 KM Phosphorylation.
 FT NON_TER 1 1
 FT DOMAIN <1 70 SH2.
 FT DOMAIN 95 348 PROTEIN KINASE.
 FT NP_BIND 101 109 ATP (BY SIMILARITY).
 FT BINDING 123 123 ATP (BY SIMILARITY).
 FT ACT_SITE 214 214 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40937 MW; D8C549E904EB6D0 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPYA 5
 |||||
 DB 117 STPYA 121

RESULT 50
 RRPO_RECVD STANDARD; PRT; 366 AA.
 ID RRPO_RECVD
 AC P03526;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (SIGMA NS PROTEIN) (CORE
 DE PROTEIN) (RNA-BINDING PROTEIN).
 GN S3.
 OS Reovirus (type 3 / strain Deering).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 OX NCBI_TaxID=10886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84015379; PubMed=6312421;
 RA Richardson M.A., Furuichi Y.;
 RT "Nucleotide sequence of reovirus genome segment S3, encoding non-
 RT structural protein sigma NS.";
 RL Nucleic Acids Res. 11:6399-6408(1983).
 RN [2]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE=83017876; PubMed=6927854;
 RA Antczak J.B., Chmelo R.A., Pickup D.J., Joklik W.K.;
 RT "Sequence at both termini of the 10 genes of reovirus serotype 3
 RT (strain Deering)."
 RL Virology 121:307-319(1982).
 CC -1- FUNCTION: THIS PROTEIN HAS A POLY(C)-DEPENDENT POLY(G) POLYMERASE
 CC ACTIVITY, AND BINDS SINGLE-STRANDED, BUT NOT DOUBLE-STRANDED, RNA.
 CC -1- SIMILARITY: 86.3% SIMILARITY TO REOVIRUS SEROTYPE 2 SIGMA NS
 CC PROTEIN.
 CC -----
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 CC -----
 CC EMBL: X01627; CAA25768.1; -
 CC EMBL: J02330; AAA47280.1; -
 CC PIR: A04126; MNXRSD.
 DR InterPro: IPR002507; -
 DR Pfam: PF01518; PolyG_POL; 1.
 KW Core protein; RNA-binding; Transferase; RNA-directed RNA polymerase.

SQ SEQUENCE 366 AA; 41056 MW; 201A6223C4290D7D CRC64;

Query Match 41.7%; Score 5; DB 1; Length 366;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
 |||||
 DB 189 PVAPT 193

Search completed: August 15, 2001, 12:43:05
 Job time: 495 sec

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DR EMBL: X13464; CAA31824.1; -
DR EMBL: J01804; AAA8616.1; -
DR PIR: J01518; XNEBHC.
DR StyGene; SG10159; hIsc.
DR InterPro; IPR001917; -
DR Pfam; PF00222; aminotran_2.1.
DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
KW Histidine biosynthesis; Transferase; Amino transferase;
KW Pyridoxal phosphate
FT BINDING 217 217 PYRIDOXAL PHOSPHATE (PROBABLE).
FT CONFLICT 148 164 DGTAVFVCSPPNPTGQ -> TAQKMSFVAPILPDN
FT FT 226 226 C -> R (IN REF. 1).
FT CONFLICT 260 260 L -> S (IN REF. 1).
FT CONFLICT 264 265 GI -> ES (IN REF. 1).
FT CONFLICT 349 349 R -> P (IN REF. 1).
SQ SEQUENCE 359 AA: 39715 MW: 6241506A59CBB2A7 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
|||||
DB 249 STPVA 253

RESULT 48
WNT2_CAEEL
ID WNT2_CAEEL STANDARD: PRT: 360 AA.
AC P34889;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE WNT-2 PROTEIN PRECURSOR.
GN WNT-2 OR CMN-2 OR W01B6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=93288400; PubMed=8510930;
RA Shuckleford G.M., Shvachkin S., Shue L., Mason J., Kenyon C.,
RA Varnum H.E.;
RT "Two wnt genes in Caenorhabditis elegans."
RL Oncogene 8:1857-1864 (1993).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Coles L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL, PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- DEVELOPMENTAL STAGE: DETECTED IN ALL LARVAL FORMS AND ADULTS,
CC BUT IS MOST ABUNDANT IN THE EMBRYONIC STAGE.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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DR EMBL: X72943; CAA51448.1; -
DR EMBL: Z68301; CAA92624.1; -
DR PIR: S32695; S32695.
DR MorphPep; W01B6.1; CE03753.
DR InterPro; IPR000970; -
DR Pfam; PF00110; wnt; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 37
FT CHAIN 38 360 WNT-2 PROTEIN.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 73 73 R -> A (IN REF. 2).
FT CONFLICT 186 186 D -> H (IN REF. 2).
FT CONFLICT 221 221 R -> A (IN REF. 2).
FT CONFLICT 229 230 TE -> MQ (IN REF. 2).
FT CONFLICT 333 333 A -> S (IN REF. 2).
SQ SEQUENCE 360 AA: 40551 MW: EA6EAF82A710F46 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TQEVK 11
|||||
DB 328 TQEVK 332

RESULT 49
SRK2_SPOLA
ID SRK2_SPOLA STANDARD: PRT: 362 AA.
AC P42688;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TYROSINE-PROTEIN KINASE SRK2 (EC 2.7.1.112) (FRAGMENT).
GN SRK2.
OS Spongilla lacustris (Freshwater sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haplosclerida; Spongillidae; Spongilla.
OX NCBI_TaxID=6055;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92334872; PubMed=1378585;
RA Otfillie S., Raulf F., Barnekow A., Hannig G., Schartl M.;
RT "Multiple src-related kinase genes, srk1-4, in the fresh water sponge
RT Spongilla lacustris."
RL Oncogene 7:1625-1630 (1992).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -----
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DR EMBL: X61602; CAA43799.1; -
DR HSSP; P00523; 2PK.
DR InterPro; IPR000719; -
DR InterPro; IPR000980; -

OY 3 PVAPT 7
 DB 284 PVAPT 288

RESULT 46
 HIS8_ECOLI
 ID HIS8_ECOLI STANDARD; PRT; 356 AA.
 AC P06986;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-
 DE PHOSPHATE TRANSAMINASE).
 GN HIS8.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-89094829; PubMed-3062174;
 RA Carlomagno M.S., Chiaricelli L., Alfano P., Nappo A.G., Bruni C.B.;
 RT "Structure and function of the Salmonella typhimurium and Escherichia
 coli K-12 histidine operons";
 RL J. Mol. Biol. 203:585-606(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-86059230; PubMed-2999081;
 RA Gisiolla V., Carlomagno M.S., Nappo A.G., Bruni C.B.;
 RT "Cloning, structure, and expression of the Escherichia coli K-12 hisC
 gene";
 RL J. Bacteriol. 164:1317-1323(1985).
 RN [3]
 RP REVISIONS, SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-94260549; PubMed-8201624;
 RA Jovanovic G., Kostic T., Jankovic M., Savic D.J.;
 RT "Nucleotide sequence of the Escherichia coli K12 histidine operon
 revisited";
 RL J. Mol. Biol. 239:433-435(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426517; PubMed-9278503;
 RA Blatner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL Science 277:1233-1238(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-97251358; PubMed-9097040;
 RA Itoh T., Alta H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sempel G., Seki Y., Sivasubraman S., Tagami H.,
 RA Takekida J., Takemoto K., Wada C., Yamamoto Y., Horinouchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 40,150,0 min region on the linkage map";
 RL DNA Res. 3:379-392(1996).
 CC -1- CATALYTIC ACTIVITY: L-HISTIDINOL-PHOSPHATE + 2-OXOGLOUTARATE -
 CC 3-(IMIDAZOL-4-YL)-2-OXOPROPYL PHOSPHATE + GLUTAMATE.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: EIGHTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT

CC AMINOTRANSFERASES.
 CC -----
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 CC -----
 CC EMBL: X03416; CAA27150.1; -;
 CC EMBL: X13462; CAA31813.1; -;
 CC EMBL: U02071; AAA19743.1; -;
 CC EMBL: AE000293; AAC75082.1; -;
 CC EMBL: D90840; CAB21779.1; -;
 CC PIR: A30270; XNECHC.
 CC EcoGene: EG10446; HIS8.
 CC InterPro: IPR001917; -;
 CC Pfam: PF00222; aminotran_2; 1.
 CC PROSITE: PS00599; AA_TRANSF_CLASS_2; 1.
 CC Histidine biosynthesis; Transferase; Aminotransferase;
 CC Pyridoxal phosphate.
 CC BINDING 214 214 PYRIDOXAL PHOSPHATE (PROBABLE).
 CC CONFLICT 130 130 L -> P (IN REF. 1 AND 2).
 CC CONFLICT 149 149 V -> A (IN REF. 1 AND 2).
 CC SEQUENCE 356 AA; 39360 MW; 056CB3C9F894083F CRC64;

Query Match 41.7%; Score 5; DB 1; Length 356;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
 DB 246 STPVA 250

RESULT 47
 HIS8_SALTY
 ID HIS8_SALTY STANDARD; PRT; 359 AA.
 AC P10369;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-
 DE PHOSPHATE TRANSAMINASE).
 GN HIS8.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_Taxid=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LT2;
 RX MEDLINE-89094829; PubMed-3062174;
 RA Carlomagno M.S., Chiaricelli L., Alfano P., Nappo A.G., Bruni C.B.;
 RT "Structure and function of the Salmonella typhimurium and Escherichia
 coli K-12 histidine operons";
 RL J. Mol. Biol. 203:585-606(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LT2;
 RX MEDLINE-97251358; PubMed-9097040;
 RA Itoh T., Alta H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sempel G., Seki Y., Sivasubraman S., Tagami H.,
 RA Takekida J., Takemoto K., Wada C., Yamamoto Y., Horinouchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 40,150,0 min region on the linkage map";
 RL DNA Res. 3:379-392(1996).
 CC -1- CATALYTIC ACTIVITY: L-HISTIDINOL-PHOSPHATE + 2-OXOGLOUTARATE -
 CC 3-(IMIDAZOL-4-YL)-2-OXOPROPYL PHOSPHATE + GLUTAMATE.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: EIGHTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC -----
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CC -1- PATHWAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
-----
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-----
CC DR EMBL; X76713; CAAS4131.1; -.
CC DR HSSP; P00929; TRSY.
CC DR MaizeDB; 102199; -.
CC DR InterPro; IPR002028; -.
CC DR Pfam; PF00290; trp_synA; 1.
CC DR PROSITE; PS00167; TRP-SYNTHASE_ALPHA; 1.
CC DR TRYPTOPHAN BIOSYNTHESIS; Lyase; Chloroplast; Transit peptide.
CC FT TRANSLAT 1 346
CC CHAIN ? 346
CC SO SEQUENCE 346 AA; 36967 MW; 05F8C2635071F3E CRC64;
-----
OY 8 OEVRK 12
DB 278 QEVRK 282
-----
RESULT 45
YMA3_MYCBO
ID YMA3_MYCBO STANDARD; PRT; 354 AA.
DC Q02279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHEETICAL 38.1 KDA PROTEIN IN MAS 3'REGION.
OS Mycobacterium bovis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxId:1765;
[1]
SEQUENCE FROM N.A.
RC STRAIN-BG6;
RC MEDLINE=92406887; PubMed=1527058;
RA Mathur M., Kolattukudy P.E.;
RT "Molecular cloning and sequencing of the gene for mycocerosic acid
RT synthase, a novel fatty acid elongating multifunctional enzyme, from
RT Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guérin.";
RL J. Biol. Chem. 267:19388-19395(1992).
-1- SIMILARITY: SOME, TO M.TUBERCULOSIS RV2285.
-----
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-----
CC DR EMBL; M95808; AAA25370.1; -.
CC DR Hypothetical protein.
CC SO SEQUENCE 354 AA; 37956 MW; 2C77C1259BD3686A CRC64;
-----
Query Match 41.7%; Score 5; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CC MODABCD FOR MOLYBDENUM.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE MODD FAMILY.
CC -----
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CC -----
CC EMBL: X80268; CAA5655.1; -
CC DR EMBL: X99258; CAA67645.1; -
CC DR EMBL: Z83859; CAB06127.1; -
CC DR Tuberculist: RY1860; -
CC KM Molybdenum; Transport; Glycoprotein; Antigen; Signal.
CC FT SIGNAL 1 39
CC FT CHAIN 40 325 MOLYBDATE UPTAKE SECRETED PROTEIN.
CC FT CARBOHYD 49 49 O-LINKED (MAN. . .)
CC FT CARBOHYD 57 57 O-LINKED (MAN. . .)
CC FT CARBOHYD 66 66 O-LINKED (MAN. . .)
CC FT CARBOHYD 316 316 O-LINKED (MAN. . .)
CC SO SEQUENCE 325 AA; 32720 MW; 59E5D0455A97BED CRC64;

Query Match 41.7%; Score 5; DB 1; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
Db 66 TPVAP 70

RESULT 42
ENT2_MOUSE STANDARD; PRT; 327 AA.
ID ENT2_MOUSE
AC 061672;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 2 (EQUILIBRATIVE
DE NITROBENZYLAMERAPTOPURINE RIBOSIDE-INSENSITIVE NUCLEOSIDE TRANSPORTER)
DE (EQUILIBRATIVE NBMPR-INSENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE
DE TRANSPORTER, ET-TYPE) (36 KDA NUCLEOLAR PROTEIN HNP36) (HYDROPHOBIC
DE NUCLEOLAR PROTEIN, 36 KDA) (DELAYED-EARLY RESPONSE PROTEIN 12).
GN SLIC29A2 OR ENT2 OR HNP36 OR DER12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10950;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Fibroblast;
RX MEDLINE=95367016; PubMed=7639753;
RA Williams J.B., Lanahan A.A.;
RT "A mammalian delayed-early response gene encodes HNP36, a novel,
RT conserved nucleolar protein."
RL Biochem. Biophys. Res. Commun. 213:325-333(1995).
CC -1- FUNCTION: MEDIATES EQUILIBRATIVE TRANSPORT OF PURINE AND
CC PYRIMIDINE NUCLEOSIDES, AND THE PURINE BASE HYPOXANTHINE.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR. INTEGRAL MEMBRANE
CC PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM AND A SHORT
CC FORM/HNP36 (SHOWN HERE); SEEMS TO BE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- INDUCTION: BY PLATELET DERIVED GROWTH FACTOR (PDGF) AND FIBROBLAST
CC GROWTH FACTOR (FGF).
CC -1- SIMILARITY: BELONGS TO THE SLIC29A FAMILY OF TRANSPORTERS.
CC -----
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CC -----
CC EMBL: X86682; CAA60381.1; -
CC DR MGD: MG1:1345278; SLIC29a2.
CC DR InterPro: IPR002259; -
CC DR Pfam: PF01733; Nucleoside_tran; 1.
CC DR PRINTS: PR01130; DERENTRNSPT.
CC KM Nuclear protein; Transmembrane; Transport; Alternative splicing.
CC FT TRANSMEM 2 22 POTENTIAL.
CC FT TRANSMEM 32 52 POTENTIAL.
CC FT TRANSMEM 63 83 POTENTIAL.
CC FT TRANSMEM 159 179 POTENTIAL.
CC FT TRANSMEM 194 214 POTENTIAL.
CC FT TRANSMEM 231 251 POTENTIAL.
CC FT TRANSMEM 267 287 POTENTIAL.
CC FT TRANSMEM 303 323 POTENTIAL.
CC SO SEQUENCE 327 AA; 36113 MW; 5D2D3FF4BBD592B6 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTOE 9
Db 100 APTOE 104

RESULT 43
YB56_XENLA STANDARD; PRT; 336 AA.
ID YB56_XENLA
AC P21574;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CYTOPLASMIC RNA-BINDING PROTEIN P56 (Y BOX BINDING PROTEIN-2) (Y-BOX
DE TRANSCRIPTION FACTOR) (MRNP4).
GN FRG2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91062413; PubMed=2247479;
RA Tafuri S.R., Wolfe A.P.;
RT "Xenopus Y-box transcription factors: molecular cloning, functional
RT analysis and developmental regulation."
RL Proc. Natl. Acad. Sci. U.S.A. 87:9028-9032(1990).
RN [2]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=92107999; PubMed=1729676;
RA Murray M.T., Schiller D.L., Franke W.W.;
RT "Sequence analysis of cytoplasmic mRNA-binding proteins of Xenopus
RT oocytes identifies a family of RNA-binding proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 89:11-15(1992).
RN [3]
RP PARTIAL SEQUENCE.
RC TISSUE-Ovary;
RX MEDLINE=92332467; PubMed=1629179;
RA Deschamps S., Viel A., Garrigos M., Denis H., le Maire M.;
RT "MRNP4, a major mRNA-binding protein from Xenopus oocytes is
RT identical to transcription factor FRG Y2."
RL J. Biol. Chem. 267:13799-13802(1992).
RN [4]
RP PARTIAL SEQUENCE.
RC TISSUE-Ovary;
RX MEDLINE=91224309; PubMed=1902800;

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DR MGD; MGI:894407; Tparl.
 DR InterPro: IPR001727; .
 DR Pfam: PF01169; UPE0016; 1.
 DR PROSITE: PS01214; UPE0016; 1.
 KM TRANSMEMBRANE.
 FT TRANSMEM 16 36 POTENTIAL.
 FT TRANSMEM 90 110 POTENTIAL.
 FT TRANSMEM 127 147 POTENTIAL.
 FT TRANSMEM 152 172 POTENTIAL.
 FT TRANSMEM 228 248 POTENTIAL.
 FT TRANSMEM 267 287 POTENTIAL.
 FT TRANSMEM 299 319 POTENTIAL.
 SO SEQUENCE 323 AA; 34683 MM; 4CID1201ADEFL333 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
 |||||
 DB 73 TPVAP 77

RESULT 40
 MODD_MYCBO STANDARD; PRT: 325 AA.
 AC 030620; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MOLYBDATE UPTAKE SECRETED PROTEIN PRECURSOR (ALA-PRO RICH 45/47 KDA
 DE SECRETED PROTEIN) (IMMUNOGENIC PROTEIN MPT3?) (ANTIGEN MPT-32) (45-KDA
 DE GLYCOPROTEIN) (FIBRONECTIN ATTACHMENT PROTEIN) (FAP-B).
 GN MODD OR APA.
 OS Mycobacterium bovis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BG3;
 RA Zhao W., Schorey J.S., Bong-Mastek M., Brown E.J., Ratliff T.L.;
 RT "Identification, sequence and characterization of the M. bovis BCG
 RT fibronectin attachment protein."
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC MODABD FOR MOLYBDENUM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE MODD FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF013569; AAB71842.1;
 KW MolYbdenuM; Transport; Glycoprotein; Antigen; signal.
 FT SIGNAL 1 39 BY SIMILARITY.
 FT CHAIN 40 325 MOLYBDATE UPTAKE SECRETED PROTEIN.
 FT CARBOHYD 49 49 O-LINKED (MAN. . .) (BY SIMILARITY).
 FT CARBOHYD 57 57 O-LINKED (MAN. . .) (BY SIMILARITY).
 FT CARBOHYD 66 66 O-LINKED (MAN. . .) (BY SIMILARITY).
 FT CARBOHYD 316 316 O-LINKED (MAN. . .) (BY SIMILARITY).
 SO SEQUENCE 325 AA; 32686 MM; D3419CA5547D91E9 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
 |||||
 DB 66 TPVAP 70

RESULT 41
 MODD_MYCTU STANDARD; PRT: 325 AA.
 AC 050906; 008062; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MOLYBDATE UPTAKE SECRETED PROTEIN PRECURSOR (ALA-PRO RICH 45/47 KDA
 DE SECRETED PROTEIN) (IMMUNOGENIC PROTEIN MPT3?) (ANTIGEN MPT-32) (45-KDA
 DE GLYCOPROTEIN) (FIBRONECTIN ATTACHMENT PROTEIN) (FAP-B).
 GN MODD OR APA OR RV1860 OR MTCY359.13.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=96009758; PubMed=7558311;
 RA Laqueyrie A., Miltzer P., Romain F., Elgmeler K., Cole S.,
 RA Marchal G.;
 RT "Cloning, sequencing, and expression of the apa gene coding for the
 RT Mycobacterium tuberculosis 45/47-kilodalton secreted antigen
 RT complex."
 RL Infect. Immun. 63:4003-4010(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA Laqueyrie A.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98293987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Pettwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [4]
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RX MEDLINE=9109989; PubMed=1898899;
 RA Nagai S., Wiker H.G., Harboe M., Kinomoto M.;
 RT "Isolation and partial characterization of major protein antigens in
 RT the culture fluid of Mycobacterium tuberculosis."
 RL Infect. Immun. 59:372-382(1991).
 RN [5]
 RP PARTIAL SEQUENCE, AND GLYCOSYLATION.
 RX MEDLINE=96547792; PubMed=7622204;
 RA Dobos K.M., Swiderex K., Khoo K.-H., Brennan P.J., Bellisle J.T.;
 RT "Evidence for glycosylation sites on the 45-kilodalton glycoprotein of
 RT Mycobacterium tuberculosis."
 RL Infect. Immun. 63:2846-2853(1995).
 RN [6]
 RP PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=96196153; PubMed=8626314;
 RA Dobos K.M., Khoo K.-H., Swiderex K.M., Brennan P.J., Bellisle J.T.;
 RT "Definition of the full extent of glycosylation of the 45-kilodalton
 RT glycoprotein of Mycobacterium tuberculosis."
 RL J. Bacteriol. 178:2498-2506(1996).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM


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RX MEDLINE-93250487; PubMed-7763615;
RA Dupille E., Rombaldi C., Lelievre J.M., Cleyet-Marel J.C., Pech J.C.,
RA Latche A.;
RT "Purification, properties and partial amino-acid sequence of 1-
RT aminocyclopropane-1-carboxylic acid oxidase from apple fruits.";
RL Planta 190:65-70(1993).
CC -1- CATALYTIC ACTIVITY: 1-AMINOCYCLOPROPANE-1-CARBOXYLATE + O2 =
CC ETHYLENE + HCN + CO(2) + 2 H(2)O.
CC -1- COFACTOR: IRON AND ASCORBATE.
CC -1- PATHWAY: LAST STEP IN THE BIOSYNTHESIS OF ETHYLENE.
CC -1- SUBUNIT: MONOMER.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING FRUIT RIPENING.
CC -1- INDUCTION: BY ETHYLENE AND BY WOUNDING.
CC -1- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
CC OXIDOREDUCTASES.
CC -----
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CC -----
CC EMBL: X61390; CAA33662.1; -.
CC EMBL: M61794; AAA33412.1; -.
CC EMBL: Y14005; CAA74328.1; -.
CC PIR: S22513; S22513.
CC Interpro: IPR002419; -.
CC DR Pfam: PF00671; Fe_AscOxidored; 1.
CC KW Fruit ripening; Ethylene biosynthesis; Oxidoreductase; Iron;
CC Vitamin C; Multigene family.
SQ SEQUENCE 314 AA; 35410 MW; BEADA64C7AD10E1E CRC64;

Query Match 41.7%; Score 5; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPYA 5
DB 308 STPYA 312

RESULT 38
SPUR NPVOP STANDARD; PRT; 321 AA.
AC 065328; 012842; 012553;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SPHEROIDIN-LIKE PROTEIN PRECURSOR (SPINDOLIN-LIKE PROTEIN) (37 KDA
DE GLYCOPROTEIN).
GN SLP OR GP37.
OS Orgyia pseudotsugata multicausid polyhedrosis virus (OpNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10450;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93100831; PubMed-8380088;
RA Gross C.H., Wolganot G.M., Russell R.L., Pearson M.N., Rohrmann G.F.;
RT "A 37-kilodalton glycoprotein from a baculovirus of Orgyia
RT pseudotsugata is localized to cytoplasmic inclusion bodies.";
RL J. Virol. 67:469-475(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97271300; PubMed-9126251;
RA Atkins C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA Rohrmann G.F.;
RT "The sequence of the Orgyia pseudotsugata multicausid nuclear
RT polyhedrosis virus genome.";
RL Virology 229:381-399(1997).

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CC -1- FUNCTION: COMPONENT OF THE VIRUS OCCLUSION BODIES, WHICH ARE LARGE
CC PROTEINACEOUS STRUCTURES (POLYHEDRA), THAT PROTECT THE VIRUS FROM
CC THE OUTSIDE ENVIRONMENT FOR EXTENDED PERIODS UNTIL THEY ARE
CC INGESTED BY INSECT LARVAE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE PERIPHERY OF OCCLUSION
CC BODIES AND WITH THE INTERNAL MEMBRANES OF INFECTED CELLS.
CC -1- DEVELOPMENTAL STAGE: VERY LATE PHASE OF INFECTION.
CC -1- SIMILARITY: TO CBEPV AND HABPV SPINDOLINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D13306; BAA02566.1; -.
CC EMBL: U75930; AAC59068.1; -.
CC KW Viral occlusion body; Signal; Glycoprotein; Late protein.
CC FT SIGNAL 1 18 POTENTIAL.
CC FT CHAIN 19 321 SPHEROIDIN-LIKE PROTEIN.
CC FT CARBOHYD 192 192 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 321 AA; 36136 MW; B935809F06B56CA9 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPYA 5
DB 23 STPYA 27

RESULT 39
PF27_MOUSE STANDARD; PRT; 323 AA.
ID PF27_MOUSE
AC P52875;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRANSMEMBRANE PROTEIN PF27 (TPA REGULATED LOCUS PROTEIN).
GN TPRL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE:teratocarcinoma;
RX MEDLINE-89076283; PubMed-3202867;
RA Akagi J., Nomiyama H., Setoyama C., Shimada K., Akagi M.;
RT "Messenger RNA expressed in mouse teratocarcinoma stem cells and
RT down-regulated by a tumor-promoting phorbol ester codes for a novel
RT transmembrane protein.";
RL Biochem. Biophys. Res. Commun. 157:548-557(1988).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN UNDIFFERENTIATED MOUSE F9
CC TERATOCARCINOMA STEM CELLS BUT DISAPPEARING RAPIDLY AFTER
CC TREATMENT WITH A TUMOR-PROMOTING PHORBOL ESTER.
CC -1- SIMILARITY: BELONGS TO THE UPF0016 FAMILY.
CC -----
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CC -----
CC EMBL: M23568; AAA40456.1; -.

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DR EMBL: M63743; AAA33997.1; -
DR EMBL: M95400; AAA34019.1; -
DR EMBL: M00353; AAA33995.1; -
DR EMBL: D86929; BAA13184.1; -
DR EMBL: D86930; BAA13185.1; -
DR EMBL: AB002810; BAA19673.1; -
DR PIR: A25776; A25776.
DR Mendel: 13686; GLYMA:1087.1.
DR Mendel: 16777; GLYMA:1087.mm16777.
DR InterPro: IPR002042; -
DR Pfam: PF01014; URICASE; 1.
DR PRINTS: PR00093; URICASE.
DR PROSITE: PS00366; URICASE; 1.
DR PROSITE: PS00342; MICROBODIES_CTER; 1.
KM Modulation: oxidoreductase; Peroxisome; Purine metabolism.
FT SITE 307 309 MICROBODY TARGETING SIGNAL (POTENTIAL).
FT VARIANT 3 3 Q -> K (IN CV. AKISENGOKU).
FT VARIANT 235 235 S -> T.
FT CONFLICT 60 60 D -> E (IN REF. 2).
FT CONFLICT 195 195 Y -> C (IN REF. 4).
SQ SEQUENCE 309 AA: 35138 MW: 6FBC2A758FBA982 CRC64:

Query Match 41.7%; Score 5; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYK 12
11111
DB 215 OEYK 219

RESULT 36
ID URID_SOYBN STANDARD: PRT; 309 AA.
AC 004104;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE URICASE II ISOZYME 2 (EC 1.7.3.3) (URATE OXIDASE) (NODULIN 35) (N-35)
DE (NON-SYMBIOTIC URICASE).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 245-262.
RC STRAIN-CV. DARE;
RA Nguyen T., Zelechowska M., Foster V., Bergmann H., Verma D.P.S.;
RT "Primary structure of the soybean nodulin-35 gene encoding uricase II
RT localized in the peroxisome of uninfected cells of nodules";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5040-5044(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. AKISENGOKU; TISSUE=Root nodules;
RA Takane K., Tajima S., Kouchi H.;
RT "Two distinct uricase II (nodulin 35) genes are differentially
RT expressed in soybean plants";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXYISOURATE +
CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PEROXISOMAL.
CC -1- SIMILARITY: BELONGS TO THE URICASE FAMILY.
CC -----

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DR EMBL: M10594; AAA33994.1; -
DR EMBL: AB002807; BAA19670.1; -
DR EMBL: AB002809; BAA19672.1; -
DR Mendel: 16776; GLYMA:1087.mm16776.
DR InterPro: IPR002042; -
DR Pfam: PF01014; URICASE; 1.
DR PRINTS: PR00093; URICASE.
DR PROSITE: PS00366; URICASE; 1.
DR PROSITE: PS00342; MICROBODIES_CTER; 1.
KM Oxidoreductase; Peroxisome; Purine metabolism.
FT CONFLICT 208 208 L -> F (IN REF. 1).
SQ SEQUENCE 309 AA: 35137 MW: 81B8F87ACAA00A9 CRC64:

Query Match 41.7%; Score 5; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYK 12
11111
DB 215 OEYK 219

RESULT 37
ID ACCO_MALDO STANDARD: PRT; 314 AA.
AC 000985; 024063;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (EC 1.-.-.) (ACC OXIDASE)

DE (ETHYLENE-FORMING ENZYME) (EFE) (PROTEIN AP4 OR PHE12).
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Rosales; Rosaceae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. GOLDEN DELICIOUS; TISSUE=Fruit;
RX MEDLINE=92322950; PubMed=137761;
RA Ross G.S., Knighton M.L., Lay-Yee M.;
RT "An ethylene-related cDNA from ripening apples";
RL Plant Mol. Biol. 19:231-238(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Dong J.G., Olsen D.B., Silverstone A., Yang S.F.;
RT "Sequence of a cDNA coding for a 1-aminocyclopropane-1-carboxylate
RT oxidase homolog from apple fruit";
RL Plant Physiol. 98:1530-1531(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. GOLDEN DELICIOUS;
RA Castiglione S., Malerba M., Pirolo B., Blanchetti R., Sala F.,
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION, AND SEQUENCE OF 115-134.
RX MEDLINE=93028548; PubMed=1409700;
RA Dong J.G., Fernandez-Maculet J.C., Yang S.F.;
RT "Purification and characterization of
RT 1-aminocyclopropane-1-carboxylate oxidase from apple fruit";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9789-9793(1992).
RN [5]
RP CHARACTERIZATION, AND PARTIAL SEQUENCE.
CC -----

CC -1- PATHWAY: FIRST STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
 CC COMPLEX.
 CC -----
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 CC -----
 CC EMBL: X65612; CAA46563.1; -
 CC PIR: JN0518; JN0518.
 CC HSSP: P05521; 1TH7.
 CC Luminescence: Transferase: Acyltransferase.
 CC KM
 CC SSEQUENCE 305 AA; 34384 MW; 0BDAA76D08913164 CRC64;
 SO

Query Match 41.7%; Score 5; DB 1; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVAK 12
 Db 219 QEVAK 223

RESULT 34
 POLG_HCVH7 STANDARD: PRT; 309 AA.
 ID POLG_HCVH7
 AC P27955;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GENOME POLYPROTEIN (CONTAINS: MATRIX PROTEIN (ENVELOPE PROTEIN M);
 DE MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN NS1 (FRAGMENT).
 OS Hepatitis C virus (isolate HCT27) (HCV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11109;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91112009; PubMed=1846505;
 RA Weiner A.J., Brauer M.J., Rosenblatt J., Richman K.H., Tung J.,
 RA Crawford K., Bonino F., Saracco G., Choo Q.-L., Houghton M.,
 RA Han J.H.;
 RT "Variable and hypervariable domains are found in the regions of HCV
 RT pestivirus envelope glycoproteins";
 RT Virology 180:842-848(1991).
 RL

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 CC -----
 CC EMBL: X53133; CAA37293.1; -
 CC InterPro: IPR002519; -
 CC InterPro: IPR002521; -
 CC InterPro: IPR002531; -
 CC Pfam: PF01560; HCV_NSI; 1.
 CC Pfam: PF01542; HCV_core; 1.
 CC Pfam: PF01539; HCV_env; 1.
 CC Transmembrane: Nonstructural protein.
 CC KM
 CC Transmembrane: Nonstructural protein.
 CC

FT CHAIN <1 63 MATRIX PROTEIN (POTENTIAL).
 FT CHAIN 64 255 MAJOR ENVELOPE PROTEIN E (POTENTIAL).
 FT CHAIN 256 >309 NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 309 309
 SO SEQUENCE 309 AA; 32922 MW; 6E858E9C3D0B9EA9 CRC64;
 S

Query Match 41.7%; Score 5; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
 Db 113 PVAPT 117

RESULT 35
 URIC_SOYBN STANDARD: PRT; 309 AA.
 ID URIC_SOYBN
 AC P04670; P34805; P93160; P93161; O04105;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUL-1999 (Rel. 38, Last annotation update)
 DE URICASE II ISOZYME 1 (EC 1.7.3.3) (URATE OXIDASE) (MODULIN 35) (N-35)
 DE (MODULE SPECIFIC URICASE).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. PRIZE;
 RC Suzuki H., Verma D.P.S.;
 RT "Soybean nodule-specific uricase (modulin-35) is expressed and
 RT assembled into a functional tetrameric holoenzyme in Escherichia
 RT coli";
 RL Plant Physiol. 95:384-389(1991).
 RL

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 CC -----
 CC SEQUENCE FROM N.A.
 RC STRAIN-CV. AKISENGOKU; TISSUE=Root nodules;
 RA Takane K., Tanaka K., Tajima S., Okazaki K., Kouchi H.;
 RT Expression of uricase II gene (modulin-35) in cotyledons of soybean
 RT plants";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. AKISENGOKU; TISSUE=Root nodules;
 RA Takane K., Tajima S., Kouchi H.;
 RT "Two distinct uricase II (modulin 35) genes are differentially
 RT expressed in soybean plants";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS A SUBUNIT OF THE MODULE SPECIFIC URICASE.
 CC -1- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O -> 5-HYDROXYISOURATE +
 CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: PEROXISOMAL.
 CC -1- INDUCTION: DURING NODULATION IN LEGUME ROOTS AFTER RHIZOBIUM
 CC INFECTION.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO THE URICASE FAMILY.
 CC -----
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FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 268 AA; 30386 MW; 2746ED6CC5D44AF2 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVA 5
   |||||
Db 26 STPVA 30

RESULT 31
URED_SYNY3
ID URED_SYNY3 STANDARD: PRT: 270 AA.
AC P73047;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UREASE ACCESSORY PROTEIN URED.
GN URED OR SLI1639.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Horouchi T., Matsuno A., Muraaki A., Nakazaki N., Nario K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.
CC -1- SIMILARITY: BELONGS TO THE URED FAMILY.
CC -----
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CC -----
CC EMBL; D90903; BAA17068.1; ALT_INIT.
CC DR InterPro: IPR002669; -
CC DR Pfam: PF01774; Ured; 1.
CC KW Nickel.
SQ SEQUENCE 270 AA; 30522 MW; FAA820E257B69286 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TOEVK 11
   |||||
Db 254 TOEVK 258

RESULT 32
YBZ7_YEAST
ID YBZ7_YEAST STANDARD: PRT: 296 AA.
AC P38279;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHEETICAL 33.5 KDA PROTEIN IN MRPS9-YSW1 INTERGENIC REGION.
GN YBR147W OR YBR1124.

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OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RA Enlian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
RA Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,
RA Wolter R., Brendel M., Bauer J., Braun H., Derr K., Duesterhus S.,
RA Gruenbein R., Hedges D., Klesau P., Korol S., Krems B., Proft M.,
RA Siegers K., Baur A., Boles E., Miosga T.,
RA Schaeft-Gerstenschlaeger I., Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: SOME, TO S.POMBE SPAC2E12.03C AND SPAC17C9.10.
CC -----
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CC -----
CC EMBL; Z36016; CAAB5105.1; -
CC DR PIR: S46018;
CC DR SGD: S0000351; YBR147W.
CC KW Hypothetical protein; Transmembrane.
FT TRANSSEM 13 33 POTENTIAL.
FT TRANSSEM 45 65 POTENTIAL.
FT TRANSSEM 69 89 POTENTIAL.
FT TRANSSEM 164 184 POTENTIAL.
FT TRANSSEM 200 220 POTENTIAL.
FT TRANSSEM 239 259 POTENTIAL.
FT TRANSSEM 263 283 POTENTIAL.
SQ SEQUENCE 296 AA; 33496 MW; 50D65896A1BAFB43 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QEVK 12
   |||||
Db 103 QEVK 107

RESULT 33
LXD2_PHOE
ID LXD2_PHOE STANDARD: PRT: 305 AA.
AC Q06878;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ACYL TRANSFERASE (EC 2.3.1.-) (ACT) (MYRISTOYL-ACP-SPECIFIC
DE THIOESTERASE).
GN LUXD.
OS Photobacterium leiognathi.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC Photobacterium.
OX NCBI_TaxID=658;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN=741;
RX MEDLINE=93231531; PubMed=8472957;
RA Chao Y.-F., Weng S.-F., Lin J.-W.;
RT "Sequence of the luxD gene encoding acyltransferase of the lux operon
RT from Photobacterium leiognathi.";
RL Gene 126:155-156(1993).
CC -1- FUNCTION: ACYL TRANSFERASE IS PART OF THE FATTY ACID REDUCTASE
CC SYSTEM REQUIRED FOR ALDEHYDE BIOSYNTHESIS; IT PRODUCES FATTY
CC ACIDS FOR THE LUMINESCENT REACTION.

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-L2/434/BU: PLASMID-PLGV440;
RX MEDLINE-89013895; PubMed-2845228;
RA Comanducci M., Ricci S., Ratti G.;
RT "The structure of a plasmid of Chlamydia trachomatis believed to be
RL required for growth within mammalian cells.";
RN MOL. Microbiol. 2:531-538(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-L1/440/LN: PLASMID-PLGV440;
RX MEDLINE-88233998; PubMed-2836808;
RA Hatt C., Ward M.E., Clarke I.N.;
RT "Analysis of the entire nucleotide sequence of the cryptic plasmid of
RL Chlamydia trachomatis serovar L1. Evidence for involvement in DNA
RN replication.";
RN Nucleic Acids Res. 16:4053-4067(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-G0/86 / SEROTYPE D: PLASMID-PCHL1;
RX MEDLINE-90301796; PubMed-2194229;
RA Comanducci M., Ricci S., Cevenini R., Ratti G.;
RT "Diversity of the Chlamydia trachomatis common plasmid in biovars
RL with different pathogenicity.";
RN Plasmid 23:149-154(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE B: PLASMID-PCTT1;
RX MEDLINE-88177106; PubMed-3444859;
RA Stiprakash K.S., Macavoy E.S.;
RT "Characterization and sequence of a plasmid from the trachoma biovar
RL Plasmid 18:205-214(1987).
RN [5]
RP SEQUENCE OF 1-10.
RC STRAIN-L2/434/BU;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RT Submitted (SEP-1994) to the SWISS-PROT data bank.
RN [6]
RP MISCELLANEOUS: PCR3-D IS REQUIRED FOR GROWTH WITHIN MAMMALIAN
RN CELLS.
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF PLASMID PLGV440.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 126.
CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 38.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X07547; CAA30423.1; -
DR EMBL: X06707; CAA39894.1; -
DR EMBL: J03321; AAA91571.1; -
DR EMBL: M19487; AAB02589.1; ALT_FRAME.
DR PIR: S01922; S01922.
DR PIR: S00790; S00790.
DR PIR: S00791; S00791.
RN Plasmid.
KM
FT INITMET 0 0
FT VARIANT 11 11 Q -> E (IN PLASMIDS PCHL1 AND PCTT1).
FT VARIANT 60 60 P -> S (IN PLASMIDS PCHL1 AND PCTT1).
FT VARIANT 85 85 D -> N (IN PLASMID PCTT1).
FT VARIANT 89 89 G -> D (IN PLASMIDS PCHL1 AND PCTT1).
FT VARIANT 108 108 T -> K (IN PLASMID PCHL1).
FT VARIANT 137 137 R -> S (IN PLASMIDS PCHL1 AND PCTT1).
FT VARIANT 188 188 K -> N (IN PLASMID PCTT1).
FT VARIANT 190 190 Y -> C (IN PLASMIDS PCHL1 AND PCTT1).

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FT VARIANT 200 200 V -> I (IN PLASMID PCHL1).
FT VARIANT 209 209 R -> S (IN PLASMIDS PCHL1 AND PCTT1).
FT VARIANT 211 211 I -> T (IN PLASMIDS PCHL1 AND PCTT1).
SQ SEQUENCE 263 AA, 27791 MW, A3FF2469B1C89703 CRC64;

Query Match
Best Local Similarity 100.0%, Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STRVA 5
Db 39 STRVA 43

RESULT 30
HB2X_HUMAN STANDARD; PRT; 268 AA.
ID HB2X_HUMAN
AC P05538;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DX BETA CHAIN PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87250501; PubMed-3036828;
RA Jonsson A.K., Hyldig-Nielsen J.J., Serenius B., Larhammar D.,
RA Andersson G., Joergensen F., Peterson P.A., Rask L.;
RT "Class II genes of the human major histocompatibility complex.
RL Comparisons of the DQ and DX alpha and beta genes.";
RN J. Biol. Chem. 262:8767-8777(1987).
RN [2]
RP SEQUENCE OF 38-125 FROM N.A.
RX MEDLINE-85216510; PubMed-3858830;
RA Okada K., Boss J.M., Prentice H., Spies T., Mengler R., Auftray C.,
RA Lillie J.W., Grossberger D., Strominger J.L.;
RT "Gene organization of DC and DX subregions of the human major
RL histocompatibility complex.";
RN Proc. Natl. Acad. Sci. U.S.A. 82:3410-3414(1985).
RN [3]
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RN -----
DR EMBL: M29614; -; NOT_ANNOTATED_CDS.
DR EMBL: M29615; -; NOT_ANNOTATED_CDS.
DR EMBL: M1136; -; NOT_ANNOTATED_CDS.
DR PIR: D29312; D29312.
DR HSSP: P13760; 2SEB.
DR InterPro: IPR000353; -
DR InterPro: IPR000495; -
DR InterPro: IPR003006; -
DR Pfam: PF00969; MHC_II_beta; 1.
DR Pfam: PF00047; Iy; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KM MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 32
FT CHAIN 33 268 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 33 126 DX BETA CHAIN.
FT DOMAIN 127 229 EXTRACELLULAR BETA-1.
FT TRANSMEM 230 250 EXTRACELLULAR BETA-2.
FT DOMAIN 251 268 CYTOPLASMIC TAIL.
FT DISULFID 47 110 BY SIMILARITY.
FT DISULFID 148 204 BY SIMILARITY.

```

RT "Complete amino acid sequence of an HLA-DR antigen-like beta chain as
 RT predicted from the nucleotide sequence: similarities with
 RT immunoglobulin and HLA-A, -B, and -C antigens."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3687-3691(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97419171; PubMed-9271631;
 RA Ellis M.C., Heltimer A.H., Ruddy D.A., Hansen S.L., Kronmal G.S.,
 RA McClelland E., Quintana L., Drayna D.T., Aldrich M.S., Mlynar E.;
 RT "HLA class II haplotype and sequence analysis support a role for DQ in
 RT narcolepsy." 46:410-417(1997).
 RL Immunogenetics 46:410-417(1997).
 CC -I- MISCELLANEOUS: THE SEQUENCE SHOWN WAS PREVIOUSLY CALLED AN HLA-DR
 CC BETA CHAIN BY REF.3 AUTHORS.
 CC -----
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 CC -----
 DR EMBL: K02405; AAA75521.1; -;
 DR EMBL: U92032; AAB9191.1; -;
 DR PIR: A02231; HLHDB.
 DR HSSP: P13760; 2SEB.
 DR InterPro: IPR000353; -;
 DR InterPro: IPR000495; -;
 DR InterPro: IPR003006; -;
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR Pfam: PF00047; Ig; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 32
 FT CHAIN 33 261
 FT DOMAIN 33 126
 FT DOMAIN 127 220
 FT DOMAIN 221 230
 FT TRANSMEM 231 251
 FT DOMAIN 252 261
 FT DISULFID 47 111
 FT DISULFID 149 205
 FT CARBOHYD 51 51
 FT VARIANT 167 167
 FT CONFLICT 69 69
 FT SEQUENCE 261 AA; 29733 MW; 8957ACD3E93DD105 CRC64;
 SQ
 Query Match 41.7%; Score 5; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.le+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STPVA 5
 DB 26 STPVA 30
 RESULT 28
 ID HB24_HUMAN STANDARD: PRT; 261 AA.
 AC P01920;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(3) BETA CHAIN PRECURSOR
 DE (CLONE II-102).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84070816; PubMed-6316358;
 RA Larhammar D., Hyldig-Nielsen J.J., Servenius B., Andersson G.,
 RA Rask L., Peterson P.A.;
 RT "Exon-intron organization and complete nucleotide sequence of a human
 RT major histocompatibility antigen DC beta gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7313-7317(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87250501; PubMed-3036828;
 RA Jonsson A.K., Hyldig-Nielsen J.J., Servenius B., Larhammar D.,
 RA Andersson G., Joergensen F., Peterson P.A., Rask L.;
 RT "Class II genes of the human major histocompatibility complex.
 RT Comparisons of the DQ and DX alpha and beta genes." J.
 RL J. Biol. Chem. 262:8767-8777(1987).
 CC -----
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 CC -----
 DR EMBL: K01499; AAA98746.1; -;
 DR EMBL: M29613; -; NOT_ANNOTATED_CDS.
 DR EMBL: M29616; -; NOT_ANNOTATED_CDS.
 DR PIR: A02234; HLH01C.
 DR PIR: C29312; C29312.
 DR HSSP: P13760; 2SEB.
 DR InterPro: IPR000353; -;
 DR InterPro: IPR000495; -;
 DR InterPro: IPR003006; -;
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR Pfam: PF00047; Ig; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 32
 FT CHAIN 33 261
 FT DOMAIN 33 126
 FT DOMAIN 127 220
 FT DOMAIN 221 230
 FT TRANSMEM 231 251
 FT DOMAIN 252 261
 FT DISULFID 47 111
 FT DISULFID 149 205
 FT CARBOHYD 51 51
 FT SEQUENCE 261 AA; 29870 MW; 8C2CFE6C080D4AF1 CRC64;
 SQ
 Query Match 41.7%; Score 5; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.le+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STPVA 5
 DB 26 STPVA 30
 RESULT 29
 ID GP3D_CHLTR STANDARD: PRT; 263 AA.
 AC P10557; P08783; P08784; Q46431;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VIRULENCE PLASMID PROTEIN GP3-D (PROTEINS P-6/P-7).
 DE Chlamydia trachomatis.
 OS Plasmid pG6V440, Plasmid pCHL1, and Plasmid pCTT1.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OC NCBI_TaxID=813;

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE-96177552; PubMed-604303;
 RA Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
 RT "Sequence analysis of 56 kb from the genome of the bacterium
 MYCOPLASMA PNEUMONIAE comprising the dnaa region, the atp operon and a
 RT cluster of ribosomal protein genes.";
 RL Nucleic Acids Res. 24:628-639(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE-97105885; PubMed-8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
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 CC -----
 DR EMBL: U34816; AAC43647.1; -;
 DR EMBL: AE000017; AAP95803.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 250 AA; 28662 MW; 4378A2834BBB7877 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYVK 12
 Db 24 OEYVK 28

RESULT 26
 CB24_ARATH STANDARD; PRT; 251 AA.
 ID CB24_ARATH
 AC P27521;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR (LHCII TYPE III CAB-4)
 DE (LHCP).
 GN CAB4 OR P1P2.20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang H., Hanley S., Goodman H.M.;
 RT "Isolation, characterization and chromosomal location of a new cab
 RT gene from Arabidopsis thaliana.";
 RL Plant Physiol. 96:1387-1388(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Choise N., Robert C., Brotier P., Wincker P., Catolico L.,
 RA Attiguenave F., Saurin W., Weissenbach J., Mewes H.-W., Lemcke K.,
 RA Mayer K.F.X., Queller F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT
 CC RECEPTOR. IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS
 CC WITH WHICH IT IS CLOSELY ASSOCIATED. THE N-TERMINUS OF THE PROTEIN
 CC EXTENDS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF

CC GRANAL MEMBRANES AND PHOTOREGULATED BY REVERSIBLE PHOSPHORYLATION
 CC OF ITS THREONINE RESIDUES; BOTH ARE BELIEVED TO MEDIATE THE
 CC DISTRIBUTION OF EXCITATION ENERGY BETWEEN PHOTOSYSTEMS I AND II.
 CC -1- SUBUNIT: THE LHC COMPLEX CONSISTS OF CHLOROPHYLLS (A & B) AND
 CC CHLOROPHYLL A-B BINDING PROTEINS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
 CC -----
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 CC -----
 DR EMBL: M63931; AAA32760.1; -;
 DR EMBL: AL132955; CAB61973.1; -;
 DR InterPro: IPR001344; -;
 DR Pfam: PF00504; chloroa_b-bind; 1.
 KW Chlorophyll; Photosynthesis; Photosystem I; Photosystem II;
 KW Thylakoid membrane; Chloroplast; Transit peptide; Multigene family;
 KW Transmembrane; Phosphorylation.
 FT TRANSIT 1
 FT CHAIN 1 251 CHLOROPHYLL A-B BINDING PROTEIN 4.
 FT TRANSMEM 211 227 POTENTIAL.
 SQ SEQUENCE 251 AA; 27733 MW; DCB8390C2AED9D22 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APDPE 9
 Db 196 APDPE 200

RESULT 27
 HB21_HUMAN STANDARD; PRT; 261 AA.
 ID HB21_HUMAN
 AC P01918; P01917;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(1) BETA CHAIN PRECURSOR
 DE (DC-3 BETA CHAIN).
 GN HLA-DQB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84298108; PubMed-6206493;
 RA Boss J.M., Strominger J.L.;
 RT "Cloning and sequence analysis of the human major histocompatibility
 RT complex gene DC-3 beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5199-5203(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84031733; PubMed-6415003;
 RA Larhammar D., Andersson G., Andersson M., Bill P., Boehme J.,
 RA Claesson L., Denaro M., Emmoth E., Gustafsson K., Hammarling U.,
 RA Heldin E., Hyldig-Nielsen J.J., Lind P., Schenning L., Servenius B.,
 RA Widmark E., Rask L., Peterson P.A.;
 RT "Molecular analysis of human class II transplantation antigens and
 RT their genes.";
 RL Hum. Immunol. 8:95-103(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-82247917; PubMed-6954511;
 RA Larhammar D., Schenning L., Gustafsson K., Wiman K., Claesson L.,
 RA Rask L., Peterson P.A.;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PROEV 10
|||||

DB 118 PROEV 122

RESULT 23
SOD3_PLEBO STANDARD: PRT: 239 AA.

AC P50060:
01-OCT-1996 (rel. 34, Created)
01-OCT-1996 (rel. 34, Last sequence update)
30-MAY-2000 (rel. 39, Last annotation update)
DE SUPEROXIDE DISMUTASE [MN] 3 PRECURSOR (EC 1.15.1.1) (FRAGMENT).
GN SOD3.
OS Plectonema boryanum.
OC Bacteria; Cyanobacteria; Oscillatoriales; Plectonema.
OX NCBI_TaxID=1184;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-UTEX 485;
RX MEDLINE=95164530; PubMed=7860607;
RA Campbell W.S., Laudenbach D.E.;
RT "Characterization of four superoxide dismutase genes from a filamentous cyanobacterium."
RL J. Bacteriol. 177:964-972(1995).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
CC -----
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CC -----
CC EMBL: 017611; AAA69953.1; -.
CC DR HSSP: P09214; IMAAG.
CC DR InterPro: IPR001189; -.
CC DR Pfam: PF00081; sodef; 1.
CC DR PROSITE: PS00088; SOD_MN; 1.
CC KM Oxidoreductase; Manganese; Multigene family; Signal.
CC FT NON_TER 1
CC FT SIGNAL <1 30
CC FT CHAIN 31 239
CC FT METAL 57
CC FT METAL 112 112
CC FT METAL 195 195
CC FT METAL 199 199
CC FT METAL 239 AA; 26854 MW; 242CB3C9C61D100 CRC64;
CC SQ SEQUENCE

Query Match 41.7%; Score 5; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
|||||

DB 18 STPVA 22

RESULT 24
Y984_CAMJE STANDARD: PRT: 246 AA.
AC P43491; Q9PNV5;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-OCT-2000 (rel. 40, Last sequence update)

DT 01-OCT-2000 (rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN CJ0984.
GN CJ0984.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 43431;
RX MEDLINE=95247673; PubMed=7730270;
RA Hani E.K., Chan V.L.;
RT "Expression and characterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hppuricase) gene in Escherichia coli."
RL J. Bacteriol. 177:2396-2402(1995).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-NCIT 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S., Jagsis K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vleet A.H.M., Whitehead S., Barrrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences."
RL Nature 403:665-668(2000).
CC -----
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CC -----
CC EMBL: 236940; CAA85397.1; -.
CC DR EMBL: AL139076; CAB73240.1; -.
CC KM Hypothetical protein.
CC FT CONFLICT 16 16
CC FT CONFLICT 21 21
CC FT CONFLICT 42 42
CC FT CONFLICT 51 51
CC FT CONFLICT 118 118
CC FT CONFLICT 160 160
CC FT CONFLICT 212 212
CC SQ SEQUENCE 246 AA; 28820 MW; 378876C1703D70CF CRC64;
CC -----

Query Match 41.7%; Score 5; DB 1; Length 246;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTOE 9
|||||

DB 75 APTOE 79

RESULT 25
Y687_MYCPN STANDARD: PRT: 250 AA.
AC Q50315;
DT 01-OCT-2000 (rel. 40, Created)
DT 01-OCT-2000 (rel. 40, Last sequence update)
DT 01-OCT-2000 (rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MPN687 (K05_ORF250).
GN MPN687 OR MP155.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN (1)

Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
 McDonald L., Atriach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 Venter J.C.;
 RT Complete genome sequence of *Treponema pallidum*, the syphilis
 agent.
 RT *aplocheate*.*;
 RT Science 281:375-388(1998).
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 5-PHOSPHATE - D-XYLULOSE 5-
 PHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE RIBULOSE-PHOSPHATE 3-EPIMERASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U97573; AAC08057.1; .
 DR EMBL: AE001263; AAC65902.1; .
 DR TIGR: TP0945; .
 DR InterPro: IPR000056; .
 DR Pfam: PF00834; Ribul_P_3.epim: 1.
 DR PROSITE: PS01065; RIBUL_P_3-EPIMER_1; 1.
 DR PROSITE: PS01066; RIBUL_P_3-EPIMER_2; 1.
 KW Isomerase: Carbohydrate metabolism.
 SQ SEQUENCE 218 AA; 23514 MW; 0066263301FA2FCA CRC64;

Query Match 41.7%; Score 5; DB 1; Length 218;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
 |||||
 DB 120 STPVA 124

RESULT 21
 TRKA_PYRHO STANDARD; PRT; 228 AA.
 ID TRKA_PYRHO
 AC 057719;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKA HOMOLOG.
 GN TRKA OR PH1884.
 OS *Pyrococcus horikoshii*.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; *Pyrococcus*.
 OX NCBI_TaxID=53935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Hatake Y., Hino Y.,
 Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 Masuchi Y., Shizuya H., Kikuchi H.;
 RT Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.*;
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: PART OF A POTASSIUM TRANSPORT SYSTEM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TRKA FAMILY.
 CC -----
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 CC -----
 DR EMBL: AP000007; BAA3111.1; .
 KW Transport; Potassium transport; NAD.
 FT NP_BIND 2. 31 NAD (POTENTIAL).
 SQ SEQUENCE 228 AA; 25323 MW; F64E2D14FE3FFD6 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 228;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVK 12
 |||||
 DB 215 QEVK 219

RESULT 22
 KLR2_CAVPO STANDARD; PRT; 239 AA.
 ID KLR2_CAVPO
 AC P12323;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GLANDULAR KALLIKREIN, PROSTATIC (EC 3.4.21.35) (TISSUE KALLIKREIN)
 DE (PROSTATE ESTERASE).
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; *Cavia*.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=8800549; PubMed=3307909;
 RX Dunbar J.C., Bradshaw R.A.;
 RT Amino acid sequence of guinea pig prostate kallikrein.*;
 RL Biochemistry 26:3471-3478(1987).
 CC -1- FUNCTION: GLANDULAR KALLIKREIN CLEAVE MET-LYS AND ARG-SER BONDS
 IN KININOGEN TO RELEASE LYS-BRADYKININ.
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-1-XAA BONDS IN
 SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE
 KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS OF
 MET-1-XAA OR LEU-1-XAA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY. KALLIKREIN SUBFAMILY.
 CC -----
 DR PIR: A27207; A27207.
 DR HSP: P00757; 1SGF.
 DR MEROPS: S01.160; .
 DR InterPro: IPR001254; .
 DR InterPro: IPR001314; .
 DR Pfam: PF00089; TRYPSIN_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Kininogenase; Glycoprotein.
 FT ACT_SITE 41
 FT ACT_SITE 96
 FT ACT_SITE 191
 FT ACT_SITE 191
 FT CARBOHYD 78
 FT CARBOHYD 169
 FT CARBOHYD 169
 FT DISULFID 7
 FT DISULFID 151
 FT DISULFID 26
 FT DISULFID 42
 FT DISULFID 128
 FT DISULFID 197
 FT DISULFID 162
 FT DISULFID 176
 FT DISULFID 187
 FT DISULFID 212
 FT VARIANT 50
 FT VARIANT 50
 SQ SEQUENCE 239 AA; 25989 MW; 56DC81BC10D49A64 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 99;

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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

DR EMBL: X13065; CAA31470.1; -
DR EMBL: X13065; CAA31469.1; -
DR PIR: S04827; S04827.
DR PIR: S04826; S04826.
KM Early Protein.
FT CHAIN 1 209 PROTEIN 40A.
FT CHAIN 115 209 PROTEIN 40B.
SQ SEQUENCE 209 AA; 22974 MW; DD399BAA02E7643D CRC64;

Query Match 41.7%; Score 5; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 QEVK 11
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|
|
DB 59 QEVK 63

RESULT 18
V3P_ADEA1
ID V3P_ADEA1 STANDARD: PRT: 217 AA.
AC P19416; Q64818; (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-MAR-1992 (Rel. 21, Last annotation update)
DE 33 KDA PHOSPHOPROTEIN.
OS Human adenovirus type 41.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10524;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TAK:
RX MEDLINE=90272433; PubMed=2349115;
RA Slemenda S.B., Plenzak N.J., Velarde J. Jr., Plenzak D.,
RA Luftig R.B.;
RT "Nucleotide sequence of the region coding for 100K and 33K proteins
RT of human enteric adenovirus type 41 (Tak).";
RL Nucleic Acids Res. 18:3069-3069(1990).
RN [2]
RP SEQUENCE OF 203-217 FROM N.A.
RC STRAIN-TAK:
RX MEDLINE=89345113; PubMed=2762136;
RA Plenzak N.J., Velarde J. Jr., Plenzak D., Luftig R.B.;
RT "Nucleotide sequence of human enteric adenovirus type 41 hexon-
RT associated protein VIII precursor (pVIII) including the early region
RT E3 promoter.";
RL Nucleic Acids Res. 17:5398-5398(1989).
CC -----
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DR EMBL: X52532; CAB38632.1; -
DR EMBL: X15137; CAA33236.1; -
DR PIR: S04851; S04851.
DR PIR: S10212; S10212.
KW Late protein: Phosphorylation.
SQ SEQUENCE 217 AA; 24740 MW; B6ECDA6B3C24EC3E CRC64;

Query Match 41.7%; Score 5; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 91;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 PVAPT 7
|
|
|
|
DB 118 PVAPT 122

RESULT 19
Y067_SCHPO
ID Y067_SCHPO STANDARD: PRT: 217 AA.
AC Q10319;
DT 01-OCT-1996 (Rel. 34, Created)
DR 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHEICAL 24.9 KDA PROTEIN C1768.07 IN CHROMOSOME I.
GN SPAC1768.07.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO HUMAN AFG AND ENL AND YEAST TRANSCRIPTION
CC INITIATION FACTOR TFIIF SMALL SUBUNIT (TFIIF/ANCI1).
CC -1- SIMILARITY: STRONG, TO YEAST YNL107W.
CC -----
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DR EMBL: Z69795; CAA93690.1; -
KW Hypothetical protein.
SQ SEQUENCE 217 AA; 24946 MW; A274C2AFB0620D7F CRC64;

Query Match 41.7%; Score 5; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVK 12
|
|
|
|
DB 191 QEVK 195

RESULT 20
RPE_TREPA
ID RPE_TREPA STANDARD: PRT: 218 AA.
AC Q66107;
DT 30-MAY-2000 (Rel. 39, Created)
DR 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RIBULOSE-5-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1) (PENTOSE-5-PHOSPHATE 3-
DE EPIMERASE) (PPE) (RSP3E).
GN RPE OR TP0945.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RA Shevchenko D.V., Atkins D.R., Radolf J.D.;
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;

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 CC -----
 DR EMBL: U39696; AAC71377.1; -.
 DR TIGR: MG159; -.
 DR InterPro: IPR001854; -.
 DR Pfam: PF00831; RIBOSOMAL_L29; 1.
 DR PROSITE: PS00579; RIBOSOMAL_L29; 1.
 KW Ribosomal protein.
 SO SEQUENCE 200 AA; 23258 MW; 5BC115E52AA5EA92 CRC64;
 OY 8 OEYK 12
 DB 170 OEYK 174
 Query Match 41.7%; Score 5; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 OEYK 12
 DB 170 OEYK 174
 RESULT 15
 ID IMMU_BPSPB STANDARD; PRT; 201 AA.
 AC P06650;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE IMMUNITY PROTEIN.
 GN D.
 OS Bacteriophage SP-beta.
 OC Viruses: dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
 OC Lambda phage group.
 NC NCBL_TaxID=10722;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C2;
 RX MEDLINE=86304188; PubMed=3091583;
 RA McLaughlin J.R., Wong H.C., Ting Y.E., van Arsdell J.N., Chang S.;
 RT "Control of lysogeny and immunity of Bacillus subtilis temperate
 RT bacteriophage SP beta by its d gene.";
 RL J. Bacteriol. 167:952-959(1986).
 CC -----
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 CC -----
 CC EMBL: M13821; AAA8544.1; -.
 DR PIR: A24499; IMBPSB.
 SO SEQUENCE 201 AA; 22087 MW; 25C0694D288FDAB CRC64;
 OY 6 PROEV 10
 DB 156 PROEV 160
 Query Match 41.7%; Score 5; DB 1; Length 201;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 PROEV 10
 DB 156 PROEV 160
 RESULT 16
 ID VAD1_TREPA STANDARD; PRT; 206 AA.
 AC O83443;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE V-TYPE ATP SYNTHASE SUBUNIT D 1 (EC 3.6.1.34) (V-TYPE ATPASE SUBUNIT D
 DE 1).
 GN ATPD1 OR TP0428.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBL_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NICHOLS;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artinsh P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998).
 CC -I- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE.
 CC -I- SIMILARITY: BELONGS TO THE V-ATPASE D SUBUNIT FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE001220; AAC65414.1; -.
 DR TIGR: TP0428; -.
 DR InterPro: IPR002699; -.
 DR Pfam: PF01813; ATP-synt_D; 1.
 KW Hydrolase; ATP synthesis; Hydrogen ion transport.
 SO SEQUENCE 206 AA; 23803 MW; BC33C36FC5795483 CRC64;
 OY 8 OEYK 12
 DB 80 OEYK 84
 Query Match 41.7%; Score 5; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 OEYK 12
 DB 80 OEYK 84
 RESULT 17
 ID VG40_BPPH8 STANDARD; PRT; 209 AA.
 AC P14817; P14818;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PROTEINS 40A/40B.
 GN 40.
 OS Bacteriophage phi-80.
 OC Viruses: dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
 OC Lambda phage group.
 NC NCBL_TaxID=10713;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89011978; PubMed=3172225;
 RA Ogawa T., Ogawa H., Tomizawa J.;
 RT "Organization of the early region of bacteriophage phi 80. Genes and
 RT proteins.";
 RL J. Mol. Biol. 202:537-550(1988).
 CC -----
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RA Eki T., Naitou M., Hagihara H., Ozawa M., Sasaguma S.-I.,
 RA Sasaguma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.,
 RT "Analysis of a 36.2 kb DNA sequence including the right telomere of
 RT chromosome VI from *Saccharomyces cerevisiae*.";
 RL Yeast 12:149-167(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
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 CC -----
 CC EMBL: D50617; BAA09284.1; -;
 DR EMBL: D44597; BAA08011.1; -;
 DR SGD: S0001941; YFR045W.
 DR InterPro: IPR001993; -;
 DR Pfam: PF00153; MITO_CARR; 1.
 DR PROSITE: PS00215; MITOCH_CARRIER; 1.
 DR Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
 KW Transmembrane; Transport.
 SQ SEQUENCE 178 AA; 19901 MW; D57433A7D1AA4FE5 CRC64;

Query Match 41.7%; Score 5; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STPVA 5
 Db 27 STPVA 31

RESULT 13
 ID EFPL_CHLPN STANDARD: PRT: 185 AA.
 AC Q92900; Q929076;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ELONGATION FACTOR P.1 (EF-P 1).
 GN EFPI OR CPO0184 OR CPO584.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHL029;
 RX MEDLINE=9920606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammell C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
 RA Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
 RA Bowman C., Dodson R., Gwinn M., Nelson W., Deboy R., Kolonel J.,
 RA McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;

RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CHL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 CC -1- FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATE EFFICIENT
 CC TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED
 CC 70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING
 CC THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING
 CC THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE
 CC (BY SIMILARITY).
 CC -1- PATHWAY: PROTEIN BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE ELONGATION FACTOR P FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE001604; AAD18337.1; -;
 DR EMBL: AE002217; AAF38402.1; -;
 DR EMBL: AP002545; BAA98394.1; -;
 DR TIGR: CP0584; -;
 DR InterPro: IPR001059; -;
 DR Pfam: PF01132; EFP; 1.
 DR PROSITE: PS01275; EFP; 1.
 KW Protein biosynthesis; Elongation factor.
 SQ SEQUENCE 185 AA; 20673 MW; 6C6432CFEB70354A CRC64;

Query Match 41.7%; Score 5; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 TOEVR 11
 Db 57 TOEVR 61

RESULT 14
 ID RL29_MYCGE STANDARD: PRT: 200 AA.
 AC P47405;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L29.
 GN RPL29 OR RPL29 OR MG159.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=96026346; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
 RA Nguyen D.T., Utterback T.R., Sausck D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bolt K.F., Hu P.-C., Lucier T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RL Science 270:397-403(1995).
 CC -1- SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN
  [1]
  SEQUENCE FROM N.A.
  MEDLINE=83300036; PubMed=6412231;
  RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
  RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
  RT allele J-C locus and evidence for several b4-related sequences in
  RT the rabbit genome.";
  RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
  [2]
  SEQUENCE FROM N.A.
  MEDLINE=82060334; PubMed=6795636;
  RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
  RT "Nucleotide sequence of constant and 3' untranslated regions of a
  RT kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
  RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
  [3]
  SEQUENCE:
  RA MEDLINE=75133568; PubMed=1091650;
  RA Chen K.C.S., Kindt T.J., Krause R.M.;
  RT "Primary structure of the L chain from a rabbit homogeneous antibody
  RT to streptococcal carbohydrate. II. Sequence determination of peptides
  RT from tryptic and peptic digests.";
  RL J. Biol. Chem. 250:3289-3296(1975).
  CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE
  CC SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI & WAS ISOLATED FROM
  CC THE SERUM OF A SINGLE RABBIT.
  -----
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  -----
  CC EMBL: X00231; CAA25051.1; -.
  DR PIR: A02122; K4RB.
  DR InterPro: IPR000495; -.
  DR InterPro: IPR003006; -.
  DR Pfam: PF00047; 19; 1.
  DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
  KW Immunoglobulin domain; Immunoglobulin C region.
  FT NON_TER 1 1
  FT DISULFID 26 85 INTERCHAIN (WITH A HEAVY CHAIN).
  FT DISULFID 103 103 N -> D (IN REF. 3).
  FT CONFLICT 58 58
  FT SEQUENCE 103 AA; 11043 MW; 5FC5ACCB8B60E68DB CRC64;
  -----
  Query Match 41.7%; Score 5; DB 1; Length 103;
  Best Local Similarity 100.0%; Pred. No. 48;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  OY 3 PVAPT 7
  Db 2 PVAPT 6
  -----
  RESULT 11
  RPL1_BPMU STANDARD; PRT; 174 AA.
  AC P06019;
  DT 13-AUG-1987 (Rel. 05, Created)
  DT 13-AUG-1987 (Rel. 05, Last sequence update)
  DT 01-OCT-2000 (Rel. 40, Last annotation update)
  DE REPRESSOR PROTEIN CI.
  GN CI OR 1.
  OS Bacteriophage Mu.
  OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
  OX NCBI_TaxID=10677;

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RN
  [1]
  SEQUENCE FROM N.A.
  MEDLINE=83012203; PubMed=6214696;
  RX Pries H., Kamp D., Kahmann R., Breuer B., Dellus H.;
  RA "Nucleotide sequence of the immunity region of Bacteriophage Mu.";
  RL Mol. Gen. Genet. 186:315-321(1982).
  [2]
  SEQUENCE FROM N.A.
  RA Pries H., Brauer B., Schmidt C., Kamp D.;
  RT "Sequence of the left end of Mu.";
  RL (in) Symonds N., Tousseint A., van de Putte P., Howe M.M. (eds.);
  RL Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press,
  RL New York (1987).
  [3]
  SEQUENCE FROM N.A.
  RA Morgan G., Hatfull G., Hendrix R.;
  RT "Genome of bacteriophage Mu and comparison with the Haemophilus
  RT influenzae Mu-like prophage PluMu.";
  RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
  -----
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  CC or send an email to license@isb-sib.ch).
  -----
  CC EMBL: V01464; CAA24711.1; -.
  DR EMBL: M64097; AAA32376.1; -.
  DR EMBL: AF083977; AAF01132.1; -.
  DR PIR: S07291; S07291.
  DR HSSP: P07636; ITNS.
  KW Transcription regulation; Repressor; DNA-binding.
  SQ SEQUENCE 174 AA; 19213 MW; 11A4B3F5B85E49C5 CRC64;
  -----
  Query Match 41.7%; Score 5; DB 1; Length 174;
  Best Local Similarity 100.0%; Pred. No. 75;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  OY 8 OEYVK 12
  Db 168 OEYVK 172
  -----
  RESULT 12
  YFL5_YEAST STANDARD; PRT; 178 AA.
  AC P43617;
  DT 01-NOV-1995 (Rel. 32, Created)
  DT 01-NOV-1995 (Rel. 32, Last sequence update)
  DT 01-FEB-1996 (Rel. 33, Last annotation update)
  DE PUTATIVE MITOCHONDRIAL CARRIER YFR045W.
  GN YFR045W.
  OS Saccharomyces cerevisiae (Baker's yeast).
  OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
  OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
  OX NCBI_TaxID=4932;
  [1]
  SEQUENCE FROM N.A.
  RC STRAIN=S288C / AB972;
  RX MEDLINE=95400292; PubMed=7670463;
  RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
  RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
  RA Yamazaki M., Tashiro H., Eki T.;
  RT "Analysis of the nucleotide sequence of chromosome VI from
  RT Saccharomyces cerevisiae.";
  RL Nat. Genet. 10:261-268(1995).
  [2]
  SEQUENCE FROM N.A.
  RC STRAIN=S288C / AB972;
  RX MEDLINE=96287652; PubMed=8686379;

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CC -----
 CC EMBL: A6000594; AAD07880.1; -
 CC TIGR: HP0830; -
 DR InterPro: IPR000120; -
 DR Pfam: PF01425; Amidase; 1.
 DR PROSITE: PS00571; AMIDASES; 1.
 KW Protein biosynthesis; Ligase.
 SO SEQUENCE 453 AA; 49652 MW; A35814B32F1AE13A CRC64;

Query Match 50.0%; Score 6; DB 1; Length 453;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
 Db 373 TPVAPT 378

RESULT 6
 ABPL_SACEX STANDARD; PRT; 617 AA.
 ID ABPL_SACEX
 AC p38479;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE ACTIN BINDING PROTEIN.
 GN ABPL
 OS Saccharomyces exiguus (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces;
 OX NCBI_TaxID=34358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 379;
 RX MEDLINE=94154001; PubMed=8110838;
 RA Lange U., Steiner S., Grollig F., Wagner G., Philippsen P.;
 RT Cloning and sequencing of a gene coding for an actin binding protein
 RT of Saccharomyces exiguus.";
 RL Blochum, Biophys. Acta 1217:214-218(1994).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE SPATIAL ORGANIZATION OF CELL.
 CC SURFACE GROWTH. AN OVERPRODUCTION OF ABPL CAUSES THE ASSEMBLY OF
 CC THE CORTICAL ACTIN SKELETON AT INAPPROPRIATE SITES ON THE CELL
 CC SURFACE, RESULTING IN DELocalIZED SURFACE GROWTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CORTICAL CYTOSKELETON.
 CC -1- SIMILARITY: TO SIGNAL TRANSDUCTION PROTEINS AND MYOSIN I.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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CC -----
 CC EMBL: X73977; CAA52156.1; -
 CC PIR: S42719; S42719.
 DR HSP: P19174; 1HSO.
 DR InterPro: IPR001452; -
 DR InterPro: IPR002108; -
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00241; cofilin.ADF; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PSS0002; SH3; 1.
 KW Cytoskeleton; Actin-binding; SH3 domain; Repeat.
 FT DOMAIN 86 97 ACTIN-BINDING (POTENTIAL).

FT DOMAIN 557 617 SH3.
 FT DOMAIN 486 501 POLY-GLU.
 FT DOMAIN 523 529 POLY-GLU.
 FT DOMAIN 202 600 3 X 10 AA APPROXIMATE REPEATS.
 FT REPEAT 202 211 1-1.
 FT REPEAT 444 453 1-2.
 FT REPEAT 591 600 1-3.
 FT DOMAIN 495 538 2 X 16 AA REPEATS OF E(7)-A-D-A-P-S-L-P-S-R.
 FT REPEAT 495 510 2-1.
 FT REPEAT 523 538 2-2.
 SO SEQUENCE 617 AA; 68420 MW; 540A785191B65F85 CRC64;

Query Match 50.0%; Score 6; DB 1; Length 617;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
 Db 412 TOEVKK 417

RESULT 7
 ENV_FOAMV STANDARD; PRT; 985 AA.
 ID ENV_FOAMV
 AC P14351;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ENV POLYPROTEIN (COAT POLYPROTEIN).
 GN ENV.
 OS Human spumaretrovirus (Foamy virus).
 OC Viruses; Retrovid viruses; Retroviridae; Spumavirus.
 OX NCBI_TaxID=11963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88004420; PubMed=2820721;
 RA Fluegel R.M., Retzlaff A., Maurer B., Darai G.;
 RT Nucleotide sequence analysis of the env gene and its flanking
 RT regions of the human spumaretrovirus reveals two novel genes.";
 RL EMBO J. 6:2077-2084(1987).
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CC -----
 CC EMBL: X05591; CAA29086.1; -
 CC DR EMBL: M54978; AAA46123.1; -
 DR PIR: C29685; VCLJSP.
 KW Coat protein; Transmembrane; Polyprotein; Glycoprotein.
 FT TRANSMEM 64 84 I (POTENTIAL).
 FT TRANSMEM 958 978 II (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 121 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 524 524 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 779 779 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 805 805 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 830 830 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 985 AA; 113494 MW; 60F5888EA931BEOAF CRC64;

```
RESULT 3
VGG_BPCHK STANDARD: PRT: 187 AA.
ID VGG_BPCHK
AC 038042:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MAJOR SPIKE PROTEIN (G PROTEIN) (GPC).
GN G.
OS Bacteriophage phi-K.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
ON NCI_TaxID=10848;
RN [1]
RP SEQUENCE FROM N.A.
RA Kodaira K.-I., Tadokoro H., Suzuki K., Oki M., Manto S., Taketo A.;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAJOR SPIKE COMPONENT. INVOLVED IN THE ATTACHMENT TO
CC THE BACTERIAL HOST.
CC -1- SUBUNIT: THE VIRION IS COMPOSED OF 60 COPIES EACH OF THE F, G, AND
CC J PROTEINS, AND 12 COPIES OF THE H PROTEIN. THERE ARE 12 SPIKES
CC WHICH ARE EACH COMPOSED OF 5 G AND ONE H PROTEINS.
CC -----
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CC -----
DR EMBL; X60323; CAA42892.1; -.
DR HSSP; P03643; IAL0.
KW Coat protein.
SQ SEQUENCE 187 AA: 19569 MW: C5C5CEC891241701 CRC64:

Query Match
Best Local Similarity 50.0%; Score 6; DB 1; Length 187;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
Db 25 TPVAPT 30

RESULT 4
GATA_HELPJ STANDARD: PRT: 453 AA.
ID GATA_HELPJ
AC 092L13:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADT
DE SUBUNIT A).
GN GATA OR JHP0769.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carnel G.,
RA Tumilino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang O., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC GLN-TRNA(GLN) THROUGH THE TRANSAMIDATION OF MISACYLATED GLU-
CC TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
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CC REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
CC AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE - ADP
CC + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMATE.
CC -1- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
CC -----
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CC -----
DR EMBL; AE001507; AAD06348.1; -.
DR InterPro; IPR000120; -.
DR Pfam; PF01425; Amidase; 1.
DR PROSITE; PS00571; AMIDASES; 1.
KW Protein biosynthesis; Ligase.
SQ SEQUENCE 453 AA: 49749 MW: FD97731532E77397 CRC64:

Query Match
Best Local Similarity 50.0%; Score 6; DB 1; Length 453;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
Db 373 TPVAPT 378

RESULT 5
GATA_HELPY STANDARD: PRT: 453 AA.
ID GATA_HELPY
AC P56114:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADT
DE SUBUNIT A).
GN GATA OR HP0830.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervilange A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khaliq H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watney L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC GLN-TRNA(GLN) THROUGH THE TRANSAMIDATION OF MISACYLATED GLU-
CC TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
CC REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
CC AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE - ADP
CC + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMATE.
CC -1- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
CC -----
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FT	DOMAIN	311	355	19 X 2 AA TANDEM REPEATS OF T-N.
SO	SEQUENCE	484 AA:	50587 MW:	3CC0F90591E14E0F CRC64;

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 484;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	STPVAPRQVEKK	12
Db	146	STPVAPRQVEKK	157

ALIGNMENTS

RESULT 1
P60_LISMO STANDARD; PRT; 484 AA.

AC P21171;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria: Firmicutes: Bacillus/Clostridium group:
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-49.
RC STRAIN-SV1/2A EGD(KAUFMANN);
RA MEDLINE=90256283; PubMed=2111287;
RA Koehler S., Leimeister-Waechter M., Chakraborty T., Lottspeich F.,
RA Goebel W.;
RT "The gene coding for protein p60 of Listeria monocytogenes and its
RT use as a specific probe for Listeria monocytogenes.";
RL Infect. Immun. 58:1943-1950(1990).
RN [2]
RP DISCUSSION OF SEQUENCE.
RA MEDLINE=93094153; PubMed=1459966;
RA Bubert A., Kuhn M., Goebel W., Koehler S.;
RT "Structural and functional properties of the p60 proteins from
RT different Listeria species.";
RL J. Bacteriol. 174:8166-8171(1992).
CC -1- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE
CC INVASION OF NONPROFESSIONAL PHAGOCYTTIC CELLS BY LISTERIA.
CC -1- SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA P60 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X52268; CAA36509.1; -
CC PIR: A41487; A41487.
CC InterPro: IPR000064; -
CC InterPro: IPR002482; -
CC Pfam: PF00877; NLPC_P60; 1.
CC Pfam: PF01476; PG_binding_2; 2.
CC Signal: Repeat. 1 27
CC STGNL 28 484 PROTEIN P60.
FT CHAIN

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 484;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 155;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPVAPT 7
Db 12 TPVAPT 17

837	4	33.3	254	1	FRI_PHAVU	P25699 phaseolus v	910	4	33.3	264	1	PUL_HUMAN	P17947 homo sapien
838	4	33.3	254	1	GLTF_ECOLI	P28721 escherichia	911	4	33.3	264	1	RCII_BPP4	P13055 bacterioph
839	4	33.3	254	1	KDSB_CHLPP	O9809 chlamydia p	912	4	33.3	264	1	RSP4_STRPU	P46771 strongyloce
840	4	33.3	254	1	TPIS_ARATH	P46491 arabidopsis	913	4	33.3	264	1	TRPA_SYNN3	P77996 synechocyst
841	4	33.3	254	1	TPIS_PETHY	P46495 petunia hyb	914	4	33.3	264	1	TRPC_LACIA	Q01999 lactococcus
842	4	33.3	254	1	YN08_YEAST	P53904 saccharomyc	915	4	33.3	265	1	APAI_PIG	P18648 sus scrofa
843	4	33.3	255	1	FLA5_PYRHO	O58286 pyrococcus	916	4	33.3	265	1	DH47_ARATH	P15168 arabidopsis
844	4	33.3	255	1	GRPS_MYXXA	P59333 pyrococcus	917	4	33.3	265	1	IOD2_HUMAN	Q02813 homo sapien
845	4	33.3	255	1	RL8B_YEAST	P17076 saccharomyc	918	4	33.3	265	1	LECN_PEA	P16270 pisum sativ
846	4	33.3	255	1	RL8B_YEAST	P29453 saccharomyc	919	4	33.3	265	1	PSBP_MARPS	Q40407 narciassus p
847	4	33.3	255	1	RNH2_BACSU	O31744 bacillus su	920	4	33.3	265	1	RRAP_ECOLI	P25741 escherichia
848	4	33.3	255	1	RPSF_BACLI	P26764 bacillus li	921	4	33.3	265	1	TRPA_METTM	P26920 methanobact
849	4	33.3	255	1	RPSF_BACSU	P07860 bacillus su	922	4	33.3	265	1	YM12_PARTE	P15613 paramecium
850	4	33.3	255	1	TONB_YEREN	O05740 yeastinia su	923	4	33.3	266	1	ELH2_ACICA	P00633 actinobact
851	4	33.3	255	1	TRPC_BACME	P70937 bacillus me	924	4	33.3	266	1	HMUV_YERPE	O06993 yeastinia pe
852	4	33.3	255	1	YORE_PSECT	Q03003 pseudomonas	925	4	33.3	266	1	PUL_MOUSE	P17433 mus musculu
853	4	33.3	256	1	GL02_RHOCA	P96981 rhododactet	926	4	33.3	266	1	SURE_METTA	Q57979 methanococc
854	4	33.3	256	1	GSC_MOUSE	Q02591 mus musculu	927	4	33.3	266	1	UXUR_HAETN	P4487 haemophilus
855	4	33.3	256	1	YI65_METYA	O57629 methanococc	928	4	33.3	267	1	PSBP_SPIOL	P12302 spinacia ol
856	4	33.3	257	1	CHIF_SALTU	O05630 salmoneilla	929	4	33.3	267	1	STO3_CAEBL	Q20657 caenorhabdi
857	4	33.3	257	1	CG1C_ORYSA	P93411 oryza sativ	930	4	33.3	267	1	TRPA_BACSU	P07601 bacillus su
858	4	33.3	257	1	COAT_TYLCM	P27257 tomato yell	931	4	33.3	267	1	Y412_METTA	Q57855 methanococc
859	4	33.3	257	1	COAT_TYLCU	P36608 tomato yell	932	4	33.3	268	1	ENGA_SALTU	Q5X818 salmoneilla
860	4	33.3	257	1	HS70_LUPPO	P16121 lupinus pol	933	4	33.3	268	1	INHA_MYCAV	O07400 mycobacteri
861	4	33.3	257	1	KLK1_MACPA	Q07276 macaca fasc	934	4	33.3	268	1	KSGA_RICPR	O05952 r dimethyla
862	4	33.3	257	1	TRPC_AQUAE	O67657 aquilex aeo	935	4	33.3	268	1	YH66_YEAST	P38740 saccharomyc
863	4	33.3	257	1	YVGI_CAEBL	P55326 caenorhabdi	936	4	33.3	269	1	INHA_MYCSM	P28829 mycobacteri
864	4	33.3	258	1	H1_YEAST	P53551 saccharomyc	937	4	33.3	269	1	INHA_MYCTU	P46533 mycobacteri
865	4	33.3	258	1	HB21_SPAEH	P15464 spialax leuc	938	4	33.3	269	1	NODC_VIBCH	Q65521 vibrio chol
866	4	33.3	258	1	KLK1_PAPHA	Q28773 papio hamad	939	4	33.3	269	1	TRPA_BACST	P19867 bacillus st
867	4	33.3	258	1	YH33_THEMA	O9X255 thermotoga	940	4	33.3	270	1	HCE1_ORYLA	P01580 oryza lat
868	4	33.3	259	1	GATR_ECOLI	P36930 escherichia	941	4	33.3	270	1	ILIA_MOUSE	P01582 mus musculu
869	4	33.3	259	1	MOTA_TREPA	O07886 treponema p	942	4	33.3	270	1	MOTA_BACSU	P28611 bacillus su
870	4	33.3	259	1	MSP8_EIMAC	P09125 elmeria ace	943	4	33.3	270	1	PANB_THEMA	O9X251 thermotoga
871	4	33.3	259	1	NAD6_METTA	Q58747 methanococc	944	4	33.3	270	1	PYRD_THEMA	Q59Y98 thermotoga
872	4	33.3	259	1	RNS2_ARATH	P42814 arabidopsis	945	4	33.3	270	1	TRPA_METTH	P28797 methanobact
873	4	33.3	260	1	1433_LYCSES	P93209 lycopersico	946	4	33.3	270	1	YIDA_ECOLI	O09997 escherichia
874	4	33.3	260	1	143C_TOBAC	P93343 nicotiana t	947	4	33.3	271	1	RL7A_ANOFA	O76732 anopheles g
875	4	33.3	260	1	COAT_TYLCV	P27256 tomato yell	948	4	33.3	271	1	VDLC_HELPU	O9XKWI heliobacte
876	4	33.3	260	1	PSMA_THEK1	O24733 thermococcu	949	4	33.3	271	1	Y228_TREPA	O83256 treponema p
877	4	33.3	260	1	SHF_MOUSE	Q62227 mus musculu	950	4	33.3	271	1	YSM4_CAEBL	Q10124 caenorhabdi
878	4	33.3	260	1	TRPC_LACCA	P17217 lactobacilli	951	4	33.3	271	1	YW34_MYCTU	O05879 mycobacteri
879	4	33.3	260	1	VG38_BPK3	P07876 bacterioph	952	4	33.3	272	1	RSR1_YEAST	P13856 saccharomyc
880	4	33.3	261	1	DHG2_BACME	P39483 bacillus me	953	4	33.3	272	1	VG67_HSVB	P28984 equine herp
881	4	33.3	261	1	KLK2_HUMAN	P20151 homo sapien	954	4	33.3	272	1	YIS2_SHISO	P16940 shigella so
882	4	33.3	261	1	KIK3_HUMAN	P07288 homo sapien	955	4	33.3	273	1	GIAB_GIALA	P15518 giardia lam
883	4	33.3	261	1	MOTB_BACSU	P28612 bacillus su	956	4	33.3	273	1	TRPC_BRATA	P94327 bradyrhizob
884	4	33.3	261	1	RNG6_MOUSE	P28078 mus musculu	957	4	33.3	274	1	BRP1_STRAU	P33912 streptomyc
885	4	33.3	261	1	TNPF5_BOVIN	P51749 bos taurus	958	4	33.3	274	1	PRCE_ARATH	O23717 arabidopsis
886	4	33.3	261	1	Y497_MYCLE	P54580 mycobacteri	959	4	33.3	274	1	SAC7_YEAST	P17121 saccharomyc
887	4	33.3	261	1	YOB4_CAEBL	O09257 caenorhabdi	960	4	33.3	274	1	VGLE_HSV2	P13289 herpes slmp
888	4	33.3	262	1	APAI_BRARE	Q43363 brachydanto	961	4	33.3	274	1	Y026_METTA	O60343 methanococc
889	4	33.3	262	1	COR4_WHEAT	P46524 tritlicum ae	962	4	33.3	274	1	YBLC_SCHPO	O691V0 schizosacch
890	4	33.3	262	1	IOD2_MOUSE	Q92419 mus musculu	963	4	33.3	274	1	YDDG_ECOLI	P46136 escherichia
891	4	33.3	262	1	IOD2_RAT	P07051 rattus norv	964	4	33.3	275	1	FLA5_PYRKO	O9V247 pyrococcus
892	4	33.3	262	1	KLK1_HUMAN	P06870 homo sapien	965	4	33.3	275	1	RK2_CYAPA	P15764 cyanophora
893	4	33.3	262	1	RS4Y_HUMAN	P22090 homo sapien	966	4	33.3	275	1	VE39_NPVAC	P11042 autographa
894	4	33.3	262	1	RS4_CHICK	P47836 gallus gall	967	4	33.3	275	1	VGIM_PUUMB	P41264 pumulia vir
895	4	33.3	262	1	RS4_CHICK	P47836 gallus gall	968	4	33.3	276	1	COAT_TNVA	P22959 tobacco nec
896	4	33.3	262	1	RS4_CHICK	P47836 gallus gall	969	4	33.3	276	1	LIPA_AQUAE	P46136 aquilex aeo
897	4	33.3	262	1	THIM_ECOLI	P76423 escherichia	970	4	33.3	276	1	PLPB_PASHA	O08686 pasteurella
898	4	33.3	263	1	MAZG_HAETN	P44723 haemophilus	971	4	33.3	276	1	RSP4_CAEBL	P46769 caenorhabdi
899	4	33.3	263	1	SGS3_DROYA	P13728 drosophila	972	4	33.3	277	1	BHMT_PIG	O95332 sus scrofa
900	4	33.3	263	1	T278_THETH	P29748 thermus aqu	973	4	33.3	277	1	HXDB_NOTVI	P13263 notophthalm
901	4	33.3	263	1	TRPA_ANTSP	P13204 antilhamio	974	4	33.3	277	1	TRPA_HALVO	P18284 halobacteri
902	4	33.3	264	1	APAI_ANNAP	O42296 anas platyr	975	4	33.3	277	1	Y3IK_SSVI	P20203 sulfobobus
903	4	33.3	264	1	APAI_CHICK	P08250 gallus gall	976	4	33.3	277	1	Y4OR_RHISN	P55603 bradyrhizob
904	4	33.3	264	1	APAI_COTJA	P32918 coturnix co	977	4	33.3	278	1	FIXR_BRAJA	O05406 bradyrhizob
905	4	33.3	264	1	CXBL_XENIA	P08983 xenopus lae	978	4	33.3	278	1	T2D7_DROME	O27272 drosophila
906	4	33.3	264	1	DMPH_PSEBP	P49156 pseudomonas	979	4	33.3	278	1	T2N2_MEICO	P24617 neisseria g
907	4	33.3	264	1	GP3D_CHLMU	O46439 chlamydia m	980	4	33.3	278	1	VGIL_HCMV1	O06667 human cytom
908	4	33.3	264	1	IOD2_RANCA	P49896 rana catesb	981	4	33.3	278	1	VGIL_HCMV2	O06668 human cytom
909	4	33.3	264	1	PSBP_FRING	O49080 fritillaria	982	4	33.3	278	1	VGIL_HCMV3	O06669 human cytom

691	4	33.3	227	1	COX2_CANAU	047669	canis aureu	764	4	33.3	240	1	RSMB_CHICK	09pv94	gallus gall
692	4	33.3	227	1	COX2_CANME	047671	canis mesom	765	4	33.3	240	1	RSMB_ERIEU	09tub7	erianaceus e
693	4	33.3	227	1	COX2_CANSI	P98031	canis simen	766	4	33.3	240	1	RSMB_HUMAN	P14678	homo sapien
694	4	33.3	227	1	COX2_CHBR	047670	chrysocyon	767	4	33.3	240	1	RSMB_MONDO	09tub6	monodelphis
695	4	33.3	227	1	COX2_CUOAL	047668	cuon alpinu	768	4	33.3	240	1	RSMB_HUMAN	P14678	homo sapien
696	4	33.3	227	1	COX2_DUSTH	047672	dusticyon th	769	4	33.3	241	1	GLTL_ECOLI	P14076	escherichia
697	4	33.3	227	1	COX2_FELCA	P48890	felis silve	770	4	33.3	242	1	RASH_MSVA	P01115	harry murt
698	4	33.3	227	1	COX2_HALGR	P38590	halichoerus	771	4	33.3	242	1	C217_HUMAN	P57077	homo sapien
699	4	33.3	227	1	COX2_LYCPI	047674	lycaon pict	772	4	33.3	242	1	CCMC_RHOCA	P29961	rhodobacter
700	4	33.3	227	1	COX2_MACRO	P92662	macropus ro	773	4	33.3	242	1	FLGH_CAUCR	P22606	caulobacter
701	4	33.3	227	1	COX2_NICPR	047675	nictereautes	774	4	33.3	243	1	CAVT_BRALA	P05348	branchiosto
702	4	33.3	227	1	COX2_PHOVI	000528	phoca vitul	775	4	33.3	243	1	DENR_HUMAN	043583	homo sapien
703	4	33.3	227	1	COX2_PSECP	047676	pseudalopex	776	4	33.3	243	1	GSCA_XENLA	P29454	xenopus lae
704	4	33.3	227	1	COX2_PSECY	047677	pseudalopex	777	4	33.3	243	1	GSCB_XENLA	P53566	xenopus lae
705	4	33.3	227	1	COX2_PSECU	047678	pseudalopex	778	4	33.3	243	1	MUKE_HAEIN	P45186	haemophilus
706	4	33.3	227	1	COX2_SPEVE	047679	specthos ve	779	4	33.3	243	1	TRUA_MYCPN	050291	mycoplasma
707	4	33.3	227	1	COX2_VILMA	047680	vulpes macr	780	4	33.3	244	1	CAH_ERWCA	052538	erwinia car
708	4	33.3	227	1	COX2_VULVU	047681	vulpes vulp	781	4	33.3	244	1	HIO_CHITH	007134	chironomus
709	4	33.3	227	1	COX2_VULZE	047673	vulpes zerd	782	4	33.3	244	1	S40A_CHITE	005018	chironomus
710	4	33.3	227	1	FLPA_PYRHO	057811	pyrococcus	783	4	33.3	244	1	YK91_MYCTU	010700	mycobacteri
711	4	33.3	227	1	KCY_ECOLI	P23863	escherichia	784	4	33.3	244	1	YR01_CAEEL	010014	caenorhabdt
712	4	33.3	227	1	SVT_PSESY	P52833	pseudomonas	785	4	33.3	245	1	KAD_CHLTR	084130	chlamydia t
713	4	33.3	227	1	T2H2_HAEHA	P00643	haemophilus	786	4	33.3	245	1	UNG_MYCGE	P47343	mycoplasma
714	4	33.3	228	1	CAPB_STRAU	P39851	staphylococ	787	4	33.3	245	1	YH77_ARCFU	028497	archaeoglob
715	4	33.3	229	1	IRLR_BURPS	031395	burkholderi	788	4	33.3	246	1	DOGI_YEAST	P38774	saccharomyc
716	4	33.3	229	1	PRL_BOVIN	P01239	bos taurus	789	4	33.3	246	1	KAD_ARATH	082514	arabidopsis
717	4	33.3	229	1	PRL_CAPHI	028318	capra hircu	790	4	33.3	246	1	MCT2_SHEEP	P79204	ovis aries
718	4	33.3	229	1	PRL_SHEEP	P01240	ovis aries	791	4	33.3	246	1	RL4_HALMA	P12735	halotartula
719	4	33.3	229	1	Y4ME_RHISN	P55561	thizobium s	792	4	33.3	246	1	SLX6_HUMAN	095475	homo sapien
720	4	33.3	230	1	RT07_MAPO	P26867	marichantia	793	4	33.3	247	1	CUT3_MYCTU	006318	mycobacteri
721	4	33.3	230	1	YP2A_STRAU	P03866	staphylococ	794	4	33.3	247	1	GRAB_HUMAN	P10144	h granzyme
722	4	33.3	231	1	FLGH_PSEPU	052081	pseudomonas	795	4	33.3	247	1	MCT1_HUMAN	P21046	homo sapien
723	4	33.3	231	1	KCY_HAEIN	P43892	haemophilus	796	4	33.3	247	1	MCT1_MACFA	P56435	maccia fasc
724	4	33.3	231	1	PCRB_ARCFU	029844	archaeoglob	797	4	33.3	247	1	MCT1_PAPHA	P52195	papio hamad
725	4	33.3	231	1	RSMB_MOUSE	P27048	mus musculu	798	4	33.3	247	1	MCT2_MERUN	P50341	meriones un
726	4	33.3	232	1	CASB_PIG	P39037	sus scrofa	799	4	33.3	247	1	MCT3_RAT	P50339	rattus norv
727	4	33.3	232	1	FLGH_ECOLI	P75940	escherichia	800	4	33.3	247	1	MCT5_MOUSE	P21844	mus musculu
728	4	33.3	232	1	KLK_PIG	P00752	sus scrofa	801	4	33.3	247	1	PMX2_MOUSE	006318	mus musculu
729	4	33.3	233	1	BRAG_PSEAE	P21630	pseudomonas	802	4	33.3	247	1	RS3_CAEEL	P48152	caenorhabdt
730	4	33.3	233	1	PSMA_THDAC	P25156	thermoplasma	803	4	33.3	247	1	SUMT_PSEFL	P37725	pseudomonas
731	4	33.3	233	1	RL1_THEMA	P29333	thermoeoba	804	4	33.3	248	1	TPIS_CLOAB	052633	clostridium
732	4	33.3	233	1	SERA_ENTHI	P21138	entamoeba h	805	4	33.3	248	1	TRYP_FUSOX	P35049	fusarium ox
733	4	33.3	234	1	GCHL_SYNG	P55759	synchocyst	806	4	33.3	249	1	LYCES	P93206	lycopersico
734	4	33.3	234	1	RS3_ACTAC	P55827	actinobacil	807	4	33.3	249	1	HMX1_CHICK	P28361	gallus gall
735	4	33.3	234	1	RS3_HAEIN	P44372	haemophilus	808	4	33.3	249	1	MCT1_CANFA	P21842	canis famli
736	4	33.3	234	1	SODM_CANAL	013401	candida alb	809	4	33.3	249	1	PCNA_PIRAB	09uy88	pyrococcus
737	4	33.3	234	1	YGIB_ECOLI	P24195	escherichia	810	4	33.3	249	1	PCNA_PIRFU	073947	pyrococcus
738	4	33.3	235	1	AURB_CHIAU	P27197	chloroflexu	811	4	33.3	249	1	PCNA_PYROH	058398	pyrococcus
739	4	33.3	235	1	MSRA_HUMAN	09u168	homo sapien	812	4	33.3	249	1	REP2_ZYGBA	P13780	zygosacchar
740	4	33.3	235	1	VP26_VZVD	P09279	varicella-2	813	4	33.3	249	1	RU2A_ARATH	P43333	arabidopsis
741	4	33.3	235	1	YHHO_HAEIN	P44908	haemophilus	814	4	33.3	249	1	YBPT_BACSU	031458	baclillus su
742	4	33.3	236	1	CDBA_RAT	P07725	rattus norv	815	4	33.3	250	1	FCG3_BOVIN	P79107	bos taurus
743	4	33.3	236	1	GAMT_HUMAN	014353	homo sapien	816	4	33.3	250	1	FRI_SOYBN	P19976	glycine max
744	4	33.3	236	1	GAMT_MOUSE	035969	mus musculu	817	4	33.3	250	1	PSD8_CAEEL	023449	caenorhabdt
745	4	33.3	237	1	YMI3_CABEL	021018	caenorhabdt	818	4	33.3	250	1	TAD2_YEAST	P47058	saccharomyc
746	4	33.3	237	1	COX2_TRIRU	001566	trichophyto	819	4	33.3	250	1	TRPC_BACSU	P33316	homo sapien
747	4	33.3	237	1	FLAI_PYRHO	058281	pyrococcus	820	4	33.3	250	1	Y6Z7_PYRHO	058361	pyrococcus
748	4	33.3	237	1	GUN_ASPAC	P22669	aspergillus	821	4	33.3	251	1	COBK_MYCTU	010672	mycobacteri
749	4	33.3	237	1	MTRA_METTH	027227	methanobact	822	4	33.3	251	1	TPIS_LEIME	P48499	leishmania
750	4	33.3	237	1	MTRA_METTH	P80184	methanobact	823	4	33.3	251	1	TPIS_TRYCR	P52270	trypanosoma
751	4	33.3	237	1	PSAS_SOYBN	09m4t8	glycine max	824	4	33.3	251	1	TRPA_PYRKO	09y949	pyrococcus
752	4	33.3	237	1	RL23_MYCPN	P75578	mycoplasma	825	4	33.3	252	1	DUT_HUMAN	P33316	homo sapien
753	4	33.3	237	1	YGHS_ECOLI	046843	escherichia	826	4	33.3	252	1	GSC_HUMAN	P53915	homo sapien
754	4	33.3	238	1	ET3_HUMAN	P14138	homo sapien	827	4	33.3	253	1	EBSD_ENTFA	P36923	enterococcu
755	4	33.3	238	1	YT23_AGRVI	P70793	agrobacteri	828	4	33.3	253	1	FRI_PEA	P19975	pisum sativ
756	4	33.3	239	1	RIM9_YEAST	004734	saccharomyc	829	4	33.3	253	1	HEM4_METTH	026658	methanobact
757	4	33.3	239	1	TRBH_ECOLI	P19381	escherichia	830	4	33.3	253	1	KAD_CHLAMU	09pkf0	chlamydia m
758	4	33.3	239	1	UPPS_HAEIN	P44938	haemophilus	831	4	33.3	253	1	KDSB_HAEIN	P44490	haemophilus
759	4	33.3	239	1	WT1_SMIMA	P49953	smithosoma	832	4	33.3	253	1	PMX2_HUMAN	099611	homo sapien
760	4	33.3	240	1	8512_TRYCR	P18270	trypanosoma	833	4	33.3	253	1	RPSF_BACME	P35145	baclillus me
761	4	33.3	240	1	PARR_ECOLI	P13669	escherichia	834	4	33.3	253	1	SOJ_BACHD	09k3n0	baclillus ha
762	4	33.3	240	1	FX24_RHILV	P24230	thizobium l	835	4	33.3	253	1	SQJ_BACSU	P37522	baclillus su
763	4	33.3	240	1	H01_SYNG3	P72849	synchocyst	836	4	33.3	253	1	TPIS_COPJA	P21820	copits japo

545	4	33.3	189	1	PAAD_RICPR	Q9z09 rickettsia	618	4	33.3	209	1	RPOC_BUCAP	P41185 buchera ap
546	4	33.3	190	1	WS3_HUMAN	O00399 homo sapien	619	4	33.3	209	1	YC02_KLEPN	O48448 klebsiella
547	4	33.3	190	1	HBAY_ECOLI	P77717 escherichia	620	4	33.3	209	1	YDGI_BACSU	P96707 bacillus su
548	4	33.3	191	1	HUPE_RHIV	P27650 rhizobium l	621	4	33.3	209	1	YLZ3_CAEBL	O53446 caenorhabdi
549	4	33.3	191	1	MEEL_RABIT	P02602 oryctolagus	622	4	33.3	210	1	COBH_METTA	O58340 methanococ
550	4	33.3	191	1	PGHD_CANFA	O9x865 canis fam11	623	4	33.3	210	1	RS7_HALLA	P15763 halobacteri
551	4	33.3	191	1	RL3_HELPJ	O9z1r4 helicobacte	624	4	33.3	210	1	TIPI_YEAST	P27654 saccharomyc
552	4	33.3	191	1	RL3_HELPJ	P56031 helicobacte	625	4	33.3	210	1	Y121_HUMAN	O14135 homo sapien
553	4	33.3	192	1	GCH2_HELPJ	O08142 helicobacte	626	4	33.3	211	1	DEDD_ECOLI	P09549 escherichia
554	4	33.3	192	1	GCH2_HELPJ	O08315 helicobacte	627	4	33.3	211	1	GLPI_STIML	P45854 sinapis alb
555	4	33.3	192	1	PM1_HUMAN	P17152 homo sapien	628	4	33.3	211	1	TI6_MOUSE	P08505 mus musculu
556	4	33.3	192	1	ZAK4_HUMAN	O14206 homo sapien	629	4	33.3	211	1	SERB_METTA	O58989 methanococ
557	4	33.3	193	1	ASH2_HUMAN	O09929 homo sapien	630	4	33.3	211	1	TX10_HUMAN	O75193 homo sapien
558	4	33.3	193	1	H10_MOUSE	P10922 mus musculu	631	4	33.3	212	1	IFEA_CAEBL	O28888 caenorhabdi
559	4	33.3	193	1	H10_MOUSE	P43278 rattus norv	632	4	33.3	212	1	RAB2_HUMAN	O08886 homo sapien
560	4	33.3	194	1	HSR_XENLA	P22845 xenopus lae	633	4	33.3	212	1	RAB2_LYNST	O05975 lymanaea sta
561	4	33.3	194	1	PGHD_HORSE	O97921 equus cabal	634	4	33.3	212	1	RAB2_MOUSE	P33994 mus musculu
562	4	33.3	194	1	RASS_DICDI	P32254 dictyostell	635	4	33.3	212	1	RAB2_RABIT	O01971 oryctolagus
563	4	33.3	194	1	RS4_BOVIN	P79103 bos taurus	636	4	33.3	212	1	RAB2_RAT	P05712 rattus norv
564	4	33.3	194	1	RS4_HORSE	P55832 equus cabal	637	4	33.3	212	1	RL14_HUMAN	P50914 homo sapien
565	4	33.3	195	1	VOY8_CAEBL	P34665 caenorhabdi	638	4	33.3	212	1	RL1_AERPE	O9y9w6 aetopyrum p
566	4	33.3	195	1	HPPK_SYNT3	P72736 synechocyst	639	4	33.3	212	1	YTFB_ECOLI	P39310 escherichia
567	4	33.3	195	1	TPIS_LACSA	P48493 lactuca sat	640	4	33.3	213	1	CHRR_RHOSH	P04685 rhodobacter
568	4	33.3	195	1	Y133_AGRU	P05681 agrobacteri	641	4	33.3	213	1	KITH_RHOSI	O9z192 rhodothermu
569	4	33.3	195	1	Y123_CAEBL	P50437 caenorhabdi	642	4	33.3	213	1	RL14_RAT	P28600 bacillus st
570	4	33.3	196	1	AMEL_MOUSE	P45559 mus musculu	643	4	33.3	213	1	RL3_BACSF	P25869 african swi
571	4	33.3	196	1	NTRP_ENTHR	P43436 enterococcu	644	4	33.3	213	1	UBC_ASEW2	P32869 african swi
572	4	33.3	197	1	HAMI_YEAST	P47119 saccharomyc	645	4	33.3	213	1	YB15_YEAST	P38212 saccharomyc
573	4	33.3	197	1	TRFG_METJA	O57690 methanococ	646	4	33.3	214	1	FLA4_PYRO	O58285 pyrococcus
574	4	33.3	198	1	PR73_MMTVC	P03319 mouse mamma	647	4	33.3	214	1	NEUM_XENLA	O58860 xenopus lae
575	4	33.3	198	1	TNF4_MOUSE	P43488 mus musculu	648	4	33.3	214	1	RL18_AERPE	O9y1r4 aetopyrum p
576	4	33.3	198	1	Y1Y4_YEAST	P47089 saccharomyc	649	4	33.3	214	1	RSMB_RAT	P17136 rattus norv
577	4	33.3	199	1	NHAA_RHOSO	O53118 rhodococcus	650	4	33.3	215	1	SC14_SCHCO	P33795 schizophylli
578	4	33.3	200	1	SSUE_PSEPU	O85762 pseudomonas	651	4	33.3	215	1	COAT_PMV	P15596 papaya mosa
579	4	33.3	201	1	COAT_LVX	P27334 lilly virus	652	4	33.3	215	1	UBC_ASEB7	P27949 african swi
580	4	33.3	201	1	LEUD_ECOLI	P30126 escherichia	653	4	33.3	215	1	Y034_NPVAC	P21287 autographa
581	4	33.3	201	1	PYRE_HELPJ	O9z1x0 helicobacte	654	4	33.3	215	1	Y256_HAEIN	P42973 archaeglob
582	4	33.3	201	1	PYRE_HELPJ	P56162 helicobacte	655	4	33.3	215	1	YK1_YEAST	P53144 saccharomyc
583	4	33.3	201	1	RB1B_RAT	P10536 rattus norv	656	4	33.3	216	1	KCY_CHLPN	O9z7y5 chlamydia p
584	4	33.3	201	1	YPT1_PHTN	O01890 phytophthor	657	4	33.3	216	1	Y726_METTA	O58136 methanococ
585	4	33.3	202	1	AMEL_MONDO	Q28462 monodelphis	658	4	33.3	217	1	FLA2_METTA	O58302 methanococ
586	4	33.3	202	1	COAT_ELV	P35927 erysimum la	659	4	33.3	217	1	SOMA_CEREL	P55437 cervus elap
587	4	33.3	202	1	FTHC_HUMAN	P49914 homo sapien	660	4	33.3	218	1	GTAL_CAVPO	P81706 cavia porce
588	4	33.3	202	1	HRZA_TRIFL	P14530 trimeresunu	661	4	33.3	218	1	MEBB_BACSF	P16172 bacillus sp
589	4	33.3	202	1	RAB1_DISOM	P22125 discopoge o	662	4	33.3	218	1	MOGI_YEAST	P47123 saccharomyc
590	4	33.3	202	1	SDC4_RAT	P34901 rattus norv	663	4	33.3	219	1	FLA4_PYRAB	O9y13 pyrococcus
591	4	33.3	202	1	T2WZ_METTF	P29566 methanobact	664	4	33.3	219	1	FLA4_PYRO	O9z2w8 pyrococcus
592	4	33.3	204	1	BTF3_MOUSE	O64152 mus musculu	665	4	33.3	219	1	H1B_XENLA	P08893 xenopus lae
593	4	33.3	204	1	CLH5_CLAHE	P42059 cladosporiu	666	4	33.3	219	1	R1B7_ARCFU	O28272 archaeglob
594	4	33.3	205	1	DUT_RAT	P70583 rattus norv	667	4	33.3	219	1	VE03_ARCFU	O28869 archaeglob
595	4	33.3	205	1	HYFA_ECOLI	P23481 escherichia	668	4	33.3	222	1	AMTB_SECOE	P30271 secale cere
596	4	33.3	205	1	KAD_MICLU	P33107 micrococcus	669	4	33.3	222	1	KCY2_HAETN	P41893 haemophilus
597	4	33.3	205	1	RAB1_LYNST	O05974 lymanaea sta	670	4	33.3	223	1	Y12A_MARKO	O61728 marmota mon
598	4	33.3	205	1	RB1A_HUMAN	P11476 homo sapien	671	4	33.3	223	1	RNS2_SOLRU	O01796 solanum tub
599	4	33.3	205	1	RB1A_RAT	P05711 rattus norv	672	4	33.3	224	1	HXB6_HUMAN	P17509 homo sapien
600	4	33.3	205	1	RG84_HUMAN	P49798 homo sapien	673	4	33.3	224	1	HXB6_MOUSE	P09023 mus musculu
601	4	33.3	205	1	RG84_MOUSE	O08899 mus musculu	674	4	33.3	224	1	VV_MOUSE	P30927 mumps virus
602	4	33.3	205	1	RG84_RAT	P49799 rattus norv	675	4	33.3	224	1	VV_MOUSE	P30928 mumps virus
603	4	33.3	205	1	YNS0_YEAST	P42844 saccharomyc	676	4	33.3	224	1	VV_MOUSE	P33488 mumps virus
604	4	33.3	206	1	COBH_METTH	O26329 methanobact	677	4	33.3	224	1	YDHC_BACSU	O05494 bacillus su
605	4	33.3	206	1	Y086_CAEBL	P34622 caenorhabdi	678	4	33.3	225	1	ASR2_CRIGR	O04346 cricetus
606	4	33.3	207	1	FLA2_PYRO	O58283 pyrococcus	679	4	33.3	225	1	GP30_BPSP1	O38423 bacteriopho
607	4	33.3	207	1	TI6_MARKO	O35736 marmota mon	680	4	33.3	225	1	RS3_LEPIN	O9z3d0 leptospira
608	4	33.3	207	1	LEXA_AERHT	O41069 aeromonas h	681	4	33.3	225	1	XINA_THETA	O43097 thermomyces
609	4	33.3	207	1	PLCR_PSEAE	P40695 pseudomonas	682	4	33.3	225	1	Y574_AERPE	O9y8k4 aetopyrum p
610	4	33.3	208	1	CSF3_MOUSE	P09920 mus musculu	683	4	33.3	225	1	YB67_AERPE	O9y8u5 aetopyrum p
611	4	33.3	208	1	GCA3_HUMAN	O95843 homo sapien	684	4	33.3	226	1	14P_HUMAN	O14530 homo sapien
612	4	33.3	208	1	TI6_HORSE	O95181 equus cabal	685	4	33.3	226	1	ATP6_HELPJ	O9z115 helicobacte
613	4	33.3	208	1	NOLV_RHISN	P55716 rhizobium s	686	4	33.3	226	1	ATP6_HELPJ	P55085 helicobacte
614	4	33.3	208	1	RS3A_SULSO	O9u4d4 rhizobium s	687	4	33.3	226	1	HMWD_BRARE	O01704 brachydanio
615	4	33.3	208	1	SAOX_RHOCA	O52671 rhodobacter	688	4	33.3	226	1	LPQT_MYCFU	P96384 mycobacteri
616	4	33.3	208	1	SPC3_STRPU	P16537 strongyloe	689	4	33.3	226	1	OGG1_AOUAE	O66612 aquilifex ao
617	4	33.3	209	1	RL3_BACSU	P42920 bacillus su	690	4	33.3	227	1	COX2_CANAD	O47667 canis adust

399	4	33.3	150	1	RS13_METJA	P54019	methanococ	472	4	33.3	166	1	COF1_PIG	P10668	sus scrofa
400	4	33.3	151	1	HS11_WHEAT	P12810	tritlicum ae	473	4	33.3	166	1	COF1_RAT	P45592	rattus norv
401	4	33.3	151	1	SOD1_LYCES	P14830	lycopersico	474	4	33.3	166	1	TPX_BACSU	P80864	baacillus su
402	4	33.3	151	1	SP17_MACFA	O19021	macaca fasc	475	4	33.3	166	1	YE11_SCHPO	O13883	schizosacch
403	4	33.3	152	1	CORA_RAT	O63532	rattus norv	476	4	33.3	167	1	QCR4_BACSU	P46911	baacillus su
404	4	33.3	152	1	PYR1_PYROH	O58452	pyrococcus	477	4	33.3	167	1	YKQ3_YEAST	P35725	saccharomyc
405	4	33.3	152	1	RL9_SYNY3	P42352	synchocyst	478	4	33.3	168	1	HEM4_SALT	P37408	salmonella
406	4	33.3	153	1	H2B1_CHURE	P50565	chlamydomon	479	4	33.3	168	1	YNP7_YEAST	P33897	saccharomyc
407	4	33.3	153	1	HS13_SOYBN	P04793	glycine max	480	4	33.3	169	1	GP38_CANFA	O95152	canis famli
408	4	33.3	153	1	MYG_CARCR	P56208	caretta car	481	4	33.3	169	1	Y1S7_BACSU	O07393	baacillus su
409	4	33.3	153	1	MYG_CHEMY	P02202	cheilonia my	482	4	33.3	170	1	EMF7_ECOLI	P25394	escherichia
410	4	33.3	153	1	MYG_GRAE	P02201	graptlemys g	483	4	33.3	170	1	HEM4_PROMI	O51887	proteus mlt
411	4	33.3	153	1	PSAL_PORPU	P51222	porphyra pu	484	4	33.3	171	1	ATPF_HELPJ	O92477	helicobacte
412	4	33.3	153	1	RECX_PSEAE	P37860	pseudomonas	485	4	33.3	171	1	ATPF_HELPY	P56086	helicobacte
413	4	33.3	153	1	VG17_BPPH5	P15850	bacteriopho	486	4	33.3	171	1	IF3_LISMO	O53804	listeria mo
414	4	33.3	154	1	YPH4_CHRVI	P45373	chromatium	487	4	33.3	171	1	NUP4_BOVIN	P42029	bos taurus
415	4	33.3	154	1	HS11_LYCES	P30221	lycopersico	488	4	33.3	171	1	YSTM_RIET	O08815	thiobacillu
416	4	33.3	154	1	HS14_SOYBN	P04794	glycine max	489	4	33.3	172	1	HS20_NIPBR	O07460	nipoststrong
417	4	33.3	154	1	HS15_SOYBN	P04795	glycine max	490	4	33.3	173	1	RUB2_PSEOL	P00272	pseudomonas
418	4	33.3	154	1	PURR_RHOCA	O52710	rhodobacter	491	4	33.3	173	1	Y150_METJA	O57614	methanococ
419	4	33.3	155	1	BCCP_HAEIN	P43874	haemophilus	492	4	33.3	174	1	HSCB_BUCAI	P57659	buchnera ap
420	4	33.3	155	1	PRL_PHAVU	P25985	phaseolus v	493	4	33.3	174	1	NEUJ_RAT	P12760	rattus norv
421	4	33.3	155	1	PR2_PHAVU	P25986	phaseolus v	494	4	33.3	174	1	RBS1_WHEAT	P06871	tritlicum ae
422	4	33.3	155	1	RNH_SALTY	P23329	salmonella	495	4	33.3	174	1	RBS_HORVU	O40004	hordeum vul
423	4	33.3	156	1	CUS5_ARADI	P80518	araneus dia	496	4	33.3	174	1	VG17_BPPZA	P08389	bacteriopho
424	4	33.3	156	1	MAFK_HUMAN	O60675	homo sapien	497	4	33.3	174	1	YGT3_YEAST	P53102	saccharomyc
425	4	33.3	156	1	Y723_METJA	O58133	methanococ	498	4	33.3	175	1	LPEE_SALT	P43664	salmonella
426	4	33.3	157	1	FLIN_PSEAE	O51466	pseudomonas	499	4	33.3	175	1	RBS7_WHEAT	P26657	tritlicum ae
427	4	33.3	157	1	HS2C_CHURE	P12811	chlamydomon	500	4	33.3	175	1	RBS_AEGSQ	O38793	aegillops sq
428	4	33.3	157	1	PRTC_CANFA	O28278	canis famli	501	4	33.3	175	1	YGZ6_YEAST	P53054	saccharomyc
429	4	33.3	157	1	VE6_HPV36	P50810	human papil	502	4	33.3	176	1	CON8_NEUCR	P10169	neurospora
430	4	33.3	157	1	Y117_YEAST	P40502	saccharomyc	503	4	33.3	176	1	IPYR_AERPE	O95465	aeropyrum p
431	4	33.3	157	1	Y012_BPL2	P42547	bacteriopho	504	4	33.3	176	1	ITRY_ACACO	P34924	acacia conf
432	4	33.3	158	1	HS12_MEDSA	P27880	medicago sa	505	4	33.3	176	1	VEGE_HUMAN	P31025	homo sapien
433	4	33.3	158	1	ILVH_BUCAP	O85294	buchnera ap	506	4	33.3	176	1	Y017_MYCGE	P47263	mycoplasma
434	4	33.3	158	1	SAW2_SOYBN	P26967	glycine max	507	4	33.3	177	1	APT_MYCPN	P72588	mycoplasma
435	4	33.3	158	1	SH3B_DROME	O94965	drosophila	508	4	33.3	177	1	CYSC_SYNY3	P75340	synchocyst
436	4	33.3	159	1	CUS7_ARADI	P80519	araneus dia	509	4	33.3	178	1	ATPD_BACCA	P41011	baacillus ca
437	4	33.3	159	1	DUT_OREN2	P14597	orf virus (510	4	33.3	178	1	CASK_RAT	P04468	rattus norv
438	4	33.3	159	1	Y268_BORBU	O44756	borrella bu	511	4	33.3	179	1	14P_BOVIN	O18883	bos taurus
439	4	33.3	159	1	YBAK_ECOLI	P37175	escherichia	512	4	33.3	179	1	ATPD_BACP3	P09220	baacillus ps
440	4	33.3	159	1	YBAK_SALT	P37174	salmonella	513	4	33.3	179	1	RK27_TOBAC	P30125	nicotiana t
441	4	33.3	160	1	PETD_OOSI	P49489	odontella s	514	4	33.3	180	1	KCY_ARCFU	O28379	archaeoglob
442	4	33.3	160	1	PHAA_CYAPA	P00316	cyanothoria	515	4	33.3	180	1	YCA7_METJA	O58644	methanococ
443	4	33.3	160	1	RL10_METH	O27191	methanobact	516	4	33.3	180	1	YMER_STRAU	P08655	staphylococ
444	4	33.3	160	1	RL21_CAEEL	P34334	caenorhabdi	517	4	33.3	180	1	YPKW_THECU	P49654	thermomonas
445	4	33.3	161	1	HS16_SOYBN	P05478	glycine max	518	4	33.3	181	1	CASK_MOUSE	P06796	mus musculu
446	4	33.3	161	1	ID4_MOUSE	P41139	mus musculu	519	4	33.3	181	1	NADP_CAMJE	O9pmq3	campylobact
447	4	33.3	161	1	LE23_ARCFU	O29686	archaeoglob	520	4	33.3	181	1	NUSG_BUCAI	P57151	buchnera ap
448	4	33.3	161	1	VG41_HSVSA	O01027	herpesviru	521	4	33.3	181	1	Y856_METJA	O48266	methanococ
449	4	33.3	162	1	MAFG_HUMAN	O15525	homo sapien	522	4	33.3	182	1	RBS_MANES	O42915	manhot esc
450	4	33.3	162	1	MAFG_MOUSE	O54750	mus musculu	523	4	33.3	183	1	RL17_PODCA	P37380	podocoryne
451	4	33.3	163	1	HL_TETPH	P10156	tetrahymena	524	4	33.3	183	1	SYL_SUISO	O33768	sulfolobus
452	4	33.3	163	1	HMG5_DICDI	P54872	dicyostell	525	4	33.3	184	1	CAS3_MOUSE	O02862	mus musculu
453	4	33.3	163	1	ILVH_ECOLI	P00894	escherichia	526	4	33.3	184	1	NUSG_BORBU	O51335	schistosoma
454	4	33.3	163	1	ILVH_HAEIN	P45260	haemophilus	527	4	33.3	184	1	RL13_SCHMA	O95043	schistosoma
455	4	33.3	163	1	ILVH_SALT	P21622	salmonella	528	4	33.3	184	1	SM21_SCHMA	P32070	schistosoma
456	4	33.3	164	1	SP17_PAPHA	O95230	papio hamad	529	4	33.3	185	1	DPL_MOUSE	O60870	mus musculu
457	4	33.3	164	1	FLAY_HELPJ	O92453	helicobacte	530	4	33.3	185	1	EFPI_CHLTR	O84124	chlamydia t
458	4	33.3	164	1	FLAY_HELPY	O25776	helicobacte	531	4	33.3	185	1	SC6_SCHDO	O74300	schizopnyll
459	4	33.3	164	1	IM17_SCHPO	P87130	schizosacch	532	4	33.3	186	1	ARDH_LEIDO	O05885	leishmania
460	4	33.3	164	1	NOLB_RHIFR	P33208	rhizobium f	533	4	33.3	186	1	IF3_BORBU	O51208	borrella bu
461	4	33.3	164	1	OV17_ONCVO	P36991	onchocerca	534	4	33.3	187	1	Y730_METJA	O58140	methanococ
462	4	33.3	164	1	T2DA_XENLA	O91858	xenopus lae	535	4	33.3	187	1	DCM8_METSO	P08085	pseudomonas
463	4	33.3	164	1	TSTP_HSVSA	P18347	herpesviru	536	4	33.3	187	1	LEPU_BACSU	P42959	baacillus su
464	4	33.3	164	1	YOJ3_CAEEL	P34626	caenorhabdi	537	4	33.3	187	1	MADE_METEX	O49125	methyllobact
465	4	33.3	165	1	DEST_CHICK	P18359	gallus gall	538	4	33.3	187	1	MLEI_MOUSE	P05977	mus musculu
466	4	33.3	165	1	HL_TETPY	P12305	tetrahymena	539	4	33.3	187	1	TOD2_PSEPU	P13451	pseudomonas
467	4	33.3	165	1	RS13_SUISO	P95986	sulfolobus	540	4	33.3	187	1	Y160_THEMA	O92424	thermotoga
468	4	33.3	165	1	RS4Y_MACFU	P23528	macaca fusc	541	4	33.3	188	1	MLEI_RAT	P02600	rattus norv
469	4	33.3	166	1	COF1_HUMAN	P23528	homo sapien	542	4	33.3	189	1	INAE_HUMAN	P05015	homo sapien
470	4	33.3	166	1	COF1_MOUSE	P18760	mus musculu	543	4	33.3	189	1	NCS2_CAEEL	P36609	caenorhabdi
471	4	33.3	166	1	COF1_MOUSE	P18760	mus musculu	544	4	33.3	189	1	NCS2_CAEEL	P36609	caenorhabdi

253	4	33.3	90	1	Y032_HELPJ	Q9zn32	helicobacte	326	4	33.3	124	1	VNS4_CVMS	P29075	murine coro
254	4	33.3	92	1	RL5_MOUSE	P47962	mus musculu	327	4	33.3	125	1	FABL_AMBE	P81400	ambystoma m
255	4	33.3	93	1	IM09_ARATH	O9xy9y	arabidopsis	328	4	33.3	125	1	FABL_CHICK	P81426	gallus galli
256	4	33.3	93	1	YOIC_CAEEL	O03283	caenorhabdi	329	4	33.3	125	1	FLTO_SALT	P54699	salmonella
257	4	33.3	94	1	NLPD_SALDU	P33700	salmonella	330	4	33.3	125	1	HVIF_HUMAN	P06326	homo sapien
258	4	33.3	94	1	YNGC_CLOPE	P26834	clostridium	331	4	33.3	125	1	SDIS_COME	P00947	comamonas t
259	4	33.3	96	1	SASG_BACME	P02961	bacillus me	332	4	33.3	126	1	CU24_ARADI	P80516	araneus dia
260	4	33.3	96	1	YC4_TYLCU	P36812	tomato yell	333	4	33.3	127	1	CS21_EUGER	P12327	euglena gra
261	4	33.3	98	1	CYTB_MOUSE	O67426	mus musculu	334	4	33.3	127	1	CU26_ARADI	P80517	araneus dia
262	4	33.3	98	1	NLPD_SALT	P40827	salmonella	335	4	33.3	127	1	VFID_HAETN	P44455	haemophilus
263	4	33.3	98	1	P531_MOUSE	P70399	mus musculu	336	4	33.3	129	1	RL7_TREPA	O83268	treponema p
264	4	33.3	98	1	YC4_TYLCM	P27272	tomato yell	337	4	33.3	129	1	RM14_ACACA	P56167	acanthamoeb
265	4	33.3	99	1	GP45_BPSP1	O43939	bacterioph	338	4	33.3	130	1	NNDI_BACSU	P50618	bacillus su
266	4	33.3	99	1	IF1A_METHA	O27085	methanobact	339	4	33.3	130	1	SY28_MOUSE	O59112	mus musculu
267	4	33.3	99	1	RL12_METHA	P10623	methanococc	340	4	33.3	130	1	Y390_METTA	O58625	methanococc
268	4	33.3	99	1	Y13J_BPPI4	P39503	bacterioph	341	4	33.3	130	1	Y614_METTA	O56031	methanococc
269	4	33.3	99	1	YORB_PYRMO	P20297	pyrococcus	342	4	33.3	130	1	Y056_MYCTU	P71953	mycobacteri
270	4	33.3	100	1	REGN_BPPI2	P04891	bacterioph	343	4	33.3	131	1	YN09_YEAST	P34841	saccharomyc
271	4	33.3	101	1	RL5_RABIT	P19949	oryctolagus	344	4	33.3	132	1	HEX9_ADE40	P48312	human adeno
272	4	33.3	102	1	SGP3_CHRYI	O52055	chromatium	345	4	33.3	132	1	IF5A_METTA	O58625	methanococc
273	4	33.3	102	1	VE7_PAPVD	P03131	deer papill	346	4	33.3	132	1	VG24_BPMI5	O05231	mycobacteri
274	4	33.3	102	1	VE7_PAPVE	P11332	europae el	347	4	33.3	133	1	CND_SCHPO	O09190	schizosacch
275	4	33.3	103	1	ACBP_ANAPL	P45882	anas platyr	348	4	33.3	133	1	HEX9_ADE41	P35139	human adeno
276	4	33.3	103	1	LAC_CHICK	P20763	gallus gall	349	4	33.3	133	1	IL4_FELCA	P50530	felis silve
277	4	33.3	104	1	GAST_BOVIN	P01352	bos taurus	350	4	33.3	133	1	PROF_HELAN	O81982	heliandthus
278	4	33.3	104	1	GAST_SHEEP	O02686	ovis aries	351	4	33.3	134	1	H2B_ENTIV	P40284	entamoeba i
279	4	33.3	104	1	SY12_MOUSE	O67401	mus musculu	352	4	33.3	134	1	PRD4_HUMAN	O9nq94	homo sapien
280	4	33.3	104	1	YR7H_ECOLI	P21322	escherichia	353	4	33.3	134	1	VG24_BPMD2	O64218	mycobacteri
281	4	33.3	105	1	LAC_HUMAN	P01842	homo sapien	354	4	33.3	135	1	CTT1_MAIZE	P31726	zea mays (m
282	4	33.3	105	1	NDCL_BRAJA	P26024	bradyrhizob	355	4	33.3	135	1	P1LG_PSEAE	P46384	pseudomonas
283	4	33.3	105	1	YMO3_CAEEL	P34494	caenorhabdi	356	4	33.3	136	1	EXB2_XANCP	O34258	xanthomonas
284	4	33.3	106	1	CYC3_DESSA	P00135	desulfovibr	357	4	33.3	136	1	YB76_YEAST	P38322	saccharomyc
285	4	33.3	106	1	KACB_RABIT	P01839	oryctolagus	358	4	33.3	137	1	COX2_CANPA	O63855	canis famli
286	4	33.3	106	1	TBCA_YEAST	P46606	saccharomyc	359	4	33.3	137	1	NIFB_KLEBX	P56265	klebsiella
287	4	33.3	107	1	U139_ARATH	Q9sd88	arabidopsis	360	4	33.3	138	1	GC5H_PYRAB	O9y091	pyrococcus
288	4	33.3	108	1	HDEB_ECOLI	P26469	mus musculu	361	4	33.3	138	1	NEDR_MICVT	O02825	mticromonosp
289	4	33.3	109	1	CORT_MOUSE	P56469	mus musculu	362	4	33.3	139	1	RBS_PLECA	O08052	pleurochrys
290	4	33.3	109	1	PRVA_MOUSE	P33848	mus musculu	363	4	33.3	139	1	RS6_BORBU	O51142	borrelia bu
291	4	33.3	109	1	RBS_PROHO	P27569	prochloroth	364	4	33.3	140	1	Y14K_CSNV	P18920	chloris str
292	4	33.3	110	1	RPOM_THECE	O56254	thermococcu	365	4	33.3	140	1	YB60_HELPY	O25775	helicobacte
293	4	33.3	110	1	RS6_AOUAE	O64974	aquilex aeo	366	4	33.3	141	1	YFE3_CLOPA	O46425	clostridium
294	4	33.3	110	1	Y16F_BPPI4	P22916	bacterioph	367	4	33.3	142	1	HBAA_ANGAN	P80945	anguilla an
295	4	33.3	111	1	CKK4_SYNY3	P73474	synechocyst	368	4	33.3	142	1	IL3_CALVA	Q28334	callithrix
296	4	33.3	112	1	CLJ4_DROMI	O01774	tyrosophila	369	4	33.3	142	1	IL3_SAGOE	P51445	sagullinus oe
297	4	33.3	113	1	HCCI_CRYCO	O01239	cryptocodi	370	4	33.3	142	1	RECX_PSPBU	P37862	pseudomonas
298	4	33.3	113	1	RBSJ_MHEAT	P07398	trititum ae	371	4	33.3	142	1	YB87_MTCU	Q10870	mycobacteri
299	4	33.3	113	1	RLAI_DICDI	P22684	dicylosteli	372	4	33.3	143	1	PER_DROPI	Q25206	drosophila
300	4	33.3	113	1	Y12K_BPPHH	P23788	bacterioph	373	4	33.3	143	1	SGCA_ECOLI	P39363	escherichia
301	4	33.3	114	1	CU05_HOMAM	P81389	homarus ame	374	4	33.3	143	1	YS85_CAEEL	O09623	caenorhabdi
302	4	33.3	114	1	ERT3_RABIT	P19598	oryctolagus	375	4	33.3	144	1	CSF2_CEREL	P51748	cervus elap
303	4	33.3	114	1	PSSP_HUMAN	P08118	homo sapien	376	4	33.3	144	1	CSF2_SHEEP	P58773	ovis aries
304	4	33.3	115	1	GUAN_RAT	P28902	rattus norv	377	4	33.3	144	1	HEX9_ADEI2	P03284	human adeno
305	4	33.3	116	1	GCAD_BACCL	P42817	bacillus ca	378	4	33.3	144	1	RISB_PHONE	O01994	photobacter
306	4	33.3	116	1	GUAN_MOUSE	P33680	mus musculu	379	4	33.3	144	1	RS14_TRYBB	P19800	typanosoma
307	4	33.3	116	1	RM14_ACAPC	P34829	acanthamoeb	380	4	33.3	145	1	DH11_GOSHI	O09442	gossypium h
308	4	33.3	116	1	SP21_BACCO	P70871	bacillus co	381	4	33.3	145	1	RI19E_METTH	O27652	methanobact
309	4	33.3	117	1	HV1A_HUMAN	P01742	homo sapien	382	4	33.3	145	1	VNR9_YEAST	P53880	saccharomyc
310	4	33.3	117	1	HV1B_HUMAN	P01743	homo sapien	383	4	33.3	146	1	FLIU_BACSU	P20487	bacillus su
311	4	33.3	117	1	HV1G_HUMAN	P23083	homo sapien	384	4	33.3	146	1	H2B_TOBAC	P39354	nicotiana t
312	4	33.3	117	1	NLPD_SALTI	O56131	salmonella	385	4	33.3	147	1	GJB_PAREP	P80721	paraphimosto
313	4	33.3	119	1	NLT5_ORYSA	O65091	oryza sativ	386	4	33.3	147	1	PHEB_BACSU	P21204	bacillus su
314	4	33.3	119	1	RL24_LEPIN	O9x425	leptospira	387	4	33.3	147	1	YACA_ECOLI	P10409	bacillus su
315	4	33.3	120	1	CU19_ARADI	P80515	araneus dia	388	4	33.3	148	1	C552_THERH	P04164	thermus aqu
316	4	33.3	120	1	YRM7_CAEEL	O09416	caenorhabdi	389	4	33.3	148	1	CNRR_ALICU	P37973	alcaligenes
317	4	33.3	121	1	RLA2_TAESO	P50879	taenia soli	390	4	33.3	149	1	YXIE_BACSU	P42297	bacillus su
318	4	33.3	121	1	YHIT_AOUAE	O65536	aquilex aeo	391	4	33.3	149	1	LRPB_BACSU	P56659	bacillus su
319	4	33.3	123	1	RBS1_SPIOL	P00870	sphnacia oi	392	4	33.3	149	1	MLE3_MOUSE	P05978	mus musculu
320	4	33.3	123	1	Y949_METTA	O58359	methanococc	393	4	33.3	149	1	MLE3_RABIT	P02603	oryctolagus
321	4	33.3	124	1	GC5H_THEMA	O9xy55	thermotoga	394	4	33.3	149	1	MLE3_RAT	P02601	rattus norv
322	4	33.3	124	1	HVID_HUMAN	P01760	homo sapien	395	4	33.3	149	1	RL9_HELPJ	O62252	mus musculu
323	4	33.3	124	1	HVIE_HUMAN	P12940	hordeum vul	396	4	33.3	150	1	SP17_MOUSE	P27777	oryza sativ
324	4	33.3	124	1	IBB_HORVU	O52179	chromatium	397	4	33.3	150	1	RL9_HELPY	P56035	helicobacte
325	4	33.3	124	1	SGP2_CHRYI			398	4	33.3	150	1			

107	5	41.7	517	1	VL1_HPV25	002051	human papill	180	5	41.7	1172	1	AHM2_ARATH	064474	arabidopsis
108	5	41.7	518	1	VL1_HPV14	P36734	human papill	181	5	41.7	1196	1	ABL1_CAEEL	P03934	caenorhabd1
109	5	41.7	518	1	VL1_HPV21	P50787	human papill	182	5	41.7	1210	1	AF4_HUMAN	P51825	homo sapien
110	5	41.7	519	1	CBX2_MOUSE	P30658	mus musculus	183	5	41.7	1233	1	YE1E_YEAST	P43597	saccharomyc
111	5	41.7	525	1	VL1_HPV5B	P26537	human papill	184	5	41.7	1245	1	CSB2_BACTU	045712	baclillus th
112	5	41.7	526	1	VL1_HPV19	002050	human papill	185	5	41.7	1251	1	PIG2_HUMAN	P16885	homo sapien
113	5	41.7	556	1	C4G1_DROME	074161	drosophila alb	186	5	41.7	1253	1	POL2_SRY	P03315	semiliki for
114	5	41.7	562	1	CHS5_CANAL	093630	candida alb	187	5	41.7	1265	1	PIG3_RAT	P24135	rattus norv
115	5	41.7	566	1	UVRC_AQUAE	067887	aquifex aeo	188	5	41.7	1290	1	XCP2_XENLA	P50532	xenopus lae
116	5	41.7	572	1	GAG_IPHA	P04023	hamster int	189	5	41.7	1297	1	IRR_HUMAN	P14616	homo sapien
117	5	41.7	572	1	PTL1_STANU	P51183	staphylococ	190	5	41.7	1300	1	IRR_CAVPO	P14617	cavia porce
118	5	41.7	583	1	LAM3_XENLA	P10939	xenopus lae	191	5	41.7	1337	1	P152_YEAST	P39685	saccharomyc
119	5	41.7	583	1	LAM4_XENLA	P23420	xenopus lae	192	5	41.7	1472	1	A2MG_RAT	P36285	rattus norv
120	5	41.7	601	1	DNM1_MYCE	P47442	mycoplasma	193	5	41.7	1500	1	SSP5_STRGN	P16952	streptococ
121	5	41.7	604	1	BAP3_YEAST	P41815	saccharomyc	194	5	41.7	1540	1	RML_DROME	097714	drosophila
122	5	41.7	609	1	BAP2_YEAST	P38084	saccharomyc	195	5	41.7	1627	1	ADP1_MYCPN	P11311	mycoplasma
123	5	41.7	612	1	SYT_HELPJ	092mw3	helicobacte	196	5	41.7	1761	1	AKAC_HUMAN	002952	homo sapien
124	5	41.7	612	1	SYT_HELPJ	P56071	helicobacte	197	5	41.7	1794	1	YAVAL_SCHPO	010172	schizosacch
125	5	41.7	614	1	YEHQ_ECOLI	P33353	escherichia	198	5	41.7	1912	1	VIT1_CHICK	P87498	gallus gall
126	5	41.7	615	1	YBM2_SCHPO	010339	schizosacch	199	5	41.7	1928	1	MYSL_YEAST	P08964	saccharomyc
127	5	41.7	634	1	VEL_HPV51	P26544	human papill	200	5	41.7	2208	1	POLN_MANCV	069014	manchester
128	5	41.7	642	1	Z147_MOUSE	061510	mus musculus	201	5	41.7	2280	1	POLG_EMCV	P03304	encephalomy
129	5	41.7	642	1	DP3X_SALTY	P74876	salmonella	202	5	41.7	2292	1	POLG_EMCVB	P17593	encephalomy
130	5	41.7	642	1	HEMA_INCN	P07973	influenza c	203	5	41.7	2292	1	POLG_EMCVD	P17594	encephalomy
131	5	41.7	642	1	HEMA_INCP1	P07968	influenza c	204	5	41.7	2476	1	POLG_PIG	028993	sus scrofa
132	5	41.7	642	1	HEMA_INCP2	P07967	influenza c	205	5	41.7	3133	1	HMCT_BOMMO	P98092	bombyx mori
133	5	41.7	643	1	HEMA_INCP3	P06710	escherichia	206	5	33.3	32	1	ATP7_SPTOL	P17664	conus tulip
134	5	41.7	643	1	DP3X_ECOLI	015945	drosophila	207	5	33.3	42	1	TFXA_SPTOL	P80088	spinacia ol
135	5	41.7	644	1	ARNT_DROME	P07387	influenza c	208	5	33.3	42	1	TFXA_RHLIT	P42723	chizobium l
136	5	41.7	648	1	HEMA_INCNB	P87691	influenza c	209	5	33.3	44	1	Y5K3_VACCV	P18379	vaccinia vl
137	5	41.7	648	1	HEMA_INCYB	016643	homo sapien	210	5	33.3	48	1	TXA1_RADMA	P30831	radiantus
138	5	41.7	649	1	DREB_HUMAN	P03465	influenza c	211	5	33.3	48	1	TXA2_RADMA	P30831	radiantus
139	5	41.7	654	1	HEMA_INCCA	P07975	influenza c	212	5	33.3	48	1	TXA2_RADPA	P01554	radiantus
140	5	41.7	655	1	HEMA_INCIH	083134	creponema p	213	5	33.3	49	1	R332_BACLI	P35870	baclillus l1
141	5	41.7	658	1	UVRE_TREPA	P37710	enterococcu	214	5	33.3	50	1	R332_BACSU	006798	baclillus su
142	5	41.7	671	1	ALYS_ENTFA	P20811	bos taurus	215	5	33.3	53	1	ITH2_BOVIN	P56651	bos taurus
143	5	41.7	705	1	ICAL_BOVIN	P98070	xenopus lae	216	5	33.3	56	1	Y546_METJA	057966	methanococ
144	5	41.7	707	1	BMP1_XENLA	060048	listeria mo	217	5	33.3	59	1	TAT2_AQUAE	066477	aquifex aeo
145	5	41.7	711	1	CADA_LISMO	P12675	sus scrofa	218	5	33.3	60	1	YTR2_SPTAU	P22042	spirochaeta
146	5	41.7	723	1	ICAL_PIG	095208	ovis aries	219	5	33.3	62	1	UCRX_BOVIN	P00130	bos taurus
147	5	41.7	723	1	ICAL_SHEEP	P34478	caenorhabd1	220	5	33.3	63	1	ANP4_MACAM	P19609	macrozoarce
148	5	41.7	727	1	YMH4_CAEEL	P17629	saccharomyc	221	5	33.3	64	1	ANP2_MACAM	P19609	macrozoarce
149	5	41.7	750	1	HPRI_YEAST	095245	arabidopsis	222	5	33.3	65	1	YHSB_CLOAB	004353	clostridium
150	5	41.7	760	1	AHM4_ARATH	P53852	saccharomyc	223	5	33.3	65	1	YNOL_RHLFR	P33214	rhizobium f
151	5	41.7	767	1	YNY7_YEAST	061193	mus musculus	224	5	33.3	66	1	YGLR_STRKO	005954	streptomyce
152	5	41.7	778	1	RGL2_MOUSE	P53316	saccharomyc	225	5	33.3	66	1	YYCD_BACSU	P37480	baclillus su
153	5	41.7	781	1	YGS8_YEAST	P23358	escherichia	226	5	33.3	67	1	HUAI_METJA	057632	methanococ
154	5	41.7	791	1	PMS1_ECOLI	P54280	schizosacch	227	5	33.3	67	1	HUAI_METJA	058342	methanococ
155	5	41.7	794	1	PMS1_SCHPO	P95175	mycobacteri	228	5	33.3	67	1	HUAI_METJA	058655	methanococ
156	5	41.7	806	1	NUOG_MYCTU	005192	drosophila	229	5	33.3	67	1	HUAI_METJA	060254	methanococ
157	5	41.7	808	1	FTPB_DROME	P37370	saccharomyc	230	5	33.3	68	1	RL29_STRPN	094wv8	streptococ
158	5	41.7	817	1	VRP1_YEAST	P12296	mengo encep	231	5	33.3	68	1	TRPC_BACPU	P18268	baclillus pu
159	5	41.7	834	1	POLG_ENNGO	P19196	yeastinia en	232	5	33.3	70	1	F261_MOUSE	P70266	mus musculus
160	5	41.7	835	1	INVA_YEREN	099490	homo sapien	233	5	33.3	71	1	RL30_MYCLE	033001	mycobacteri
161	5	41.7	836	1	Y167_HUMAN	002910	drosophila	234	5	33.3	72	1	VG35_BPMU5	005245	mycobacteri
162	5	41.7	855	1	CPN_DROME	P32540	mengo encep	235	5	33.3	73	1	Y556_ARCFU	029655	archaeoglob
163	5	41.7	901	1	POLG_ENNG3	P22958	fusarium so	236	5	33.3	73	1	YB52_METJA	058852	methanococ
164	5	41.7	909	1	CTIA_FUSO	031151	zymomonas m	237	5	33.3	75	1	YCGI_ECOLI	P46131	escherichia
165	5	41.7	925	1	UVRA_ZYMO	P06166	oryctolagus	238	5	33.3	77	1	KEA2_ECOLI	P13964	escherichia
166	5	41.7	930	1	PRGR_RABIT	P06401	homo sapien	239	5	33.3	78	1	DSVD_DESVH	046502	desulfovibr
167	5	41.7	933	1	PRGR_HUMAN	095244	arabidopsis	240	5	33.3	78	1	Y113_RICPR	092635	rickettsia
168	5	41.7	951	1	AHM3_ARATH	094up9	homo sapien	241	5	33.3	80	1	GONI_CLAGA	P33439	clarifas gar
169	5	41.7	953	1	YA42_HUMAN	P47134	saccharomyc	242	5	33.3	82	1	RS16_SATFY	P36282	salmonella
170	5	41.7	954	1	BIR1_YEAST	040554	nicotiana t	243	5	33.3	82	1	TATA_VIBCH	P57051	vibrio chol
171	5	41.7	958	1	FE3A_TOBAC	013608	homo sapien	244	5	33.3	83	1	GVG1_HALNI	P24371	halobacteri
172	5	41.7	960	1	PEX6_HUMAN	014157	homo sapien	245	5	33.3	87	1	ANP5_MACAM	P07497	macrozoarce
173	5	41.7	963	1	Y144_HUMAN	P13497	homo sapien	246	5	33.3	87	1	ANP5_MACAM	P19607	macrozoarce
174	5	41.7	986	1	BMP1_HUMAN	P98063	mus musculus	247	5	33.3	87	1	ANPD_MACAM	P39730	saccharomyc
175	5	41.7	991	1	FE2P_MOUSE	P39730	saccharomyc	248	5	33.3	88	1	Y67_BPM7	P03801	bacterioph
176	5	41.7	1002	1	BMPI_YEAST	050365	mycoplasma	249	5	33.3	89	1	ACYP_ARCFU	029440	archaeoglob
177	5	41.7	1018	1	HMW1_MYCPN	000872	homo sapien	250	5	33.3	90	1	LEPPA_HUMAN	093968	homo sapien
178	5	41.7	1141	1	MYPS_HUMAN	P03833	klebsiella	251	5	33.3	90	1	RPOL_SULAC	P46217	sulfolobus
179	5	41.7	1171	1	NIFU_KLEPN			252	5	33.3	90	1			

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:43:01 ; Search time 20.38 Seconds
(without alignments)
20.170 Million cell updates/sec

Title: US-09-372-036-30
Perfect score: 12
Sequence: 1 STPVAPTOEVKK 12

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	12	100.0	P60_LISMO	P21171 listeria mo
2	6	50.0	PRSI_SOLRU	P17641 solanum tub
3	6	50.0	187 VGC_BPPHK	Q38042 bacterioph
4	6	50.0	453 1 GATV_HELPJ	Q92113 helicobacte
5	6	50.0	453 1 GATV_HELPJ	P56114 helicobacte
6	6	50.0	617 1 ABPI_SACEX	P38479 saccharomyc
7	6	50.0	985 1 ENV_FOAMV	P14351 human spuna
8	6	50.0	1133 1 ATX9_TETH	Q95050 tetrathymena
9	5	41.7	102 1 HCC2_CRYCO	Q01238 cryptocodi
10	5	41.7	103 1 KAC4_RABIT	P01840 oryctolagus
11	5	41.7	174 1 RPCL_BPMU	P06019 bacterioph
12	5	41.7	178 1 YEL5_YEAST	P43617 saccharomyc
13	5	41.7	185 1 EEP1_CHLTPN	Q92900 chlamydia p
14	5	41.7	200 1 RL29_MYCGE	P47405 mycoplasma
15	5	41.7	201 1 IMMU_BPSPB	P06650 bacterioph
16	5	41.7	206 1 VAD1_TREPA	O83443 treponema p
17	5	41.7	209 1 VG40_BPPH8	P14817 bacterioph
18	5	41.7	217 1 V33P_ADEA1	P19416 human adeno
19	5	41.7	217 1 YD67_SCHPO	Q10319 schizosacch
20	5	41.7	218 1 RPE_TREPA	O57119 treponema p
21	5	41.7	228 1 TRKA_PYRHO	O66107 pyrococcus
22	5	41.7	239 1 KLU2_CAVPO	P13233 cavia porce
23	5	41.7	239 1 SOD3_PLEBO	P50060 plectonema
24	5	41.7	246 1 Y984_CAMEE	P45491 campylobact
25	5	41.7	250 1 YG87_MYCPN	Q50315 mycoplasma
26	5	41.7	251 1 CB24_ARATH	P27521 arabidopsis
27	5	41.7	261 1 HB21_HUMAN	P01920 homo sapien
28	5	41.7	261 1 HB24_HUMAN	P10557 chlamydia t
29	5	41.7	263 1 GP3D_CHLTR	P10558 homo sapien
30	5	41.7	268 1 HB2X_HUMAN	P05538 homo sapien
31	5	41.7	270 1 URED_SYNY3	P73047 synechocyst
32	5	41.7	296 1 YB27_YEAST	P38279 saccharomyc
33	5	41.7	305 1 LMD2_PHOLE	Q06878 photobacter

34	5	41.7	309 1	POLG_HCVH7	P27955 hepatitis c
35	5	41.7	309 1	URIC_SOYBN	P04670 glycine max
36	5	41.7	309 1	URID_SOYBN	P04104 glycine max
37	5	41.7	314 1	ACCO_MALDO	O00985 malus domes
38	5	41.7	321 1	SELR_NPVOP	O65328 oryza pseu
39	5	41.7	323 1	PF27_MOUSE	P52875 mus musculu
40	5	41.7	325 1	MODD_MYCBO	O30620 mycobacteri
41	5	41.7	325 1	MODD_MYCRU	O50906 mycobacteri
42	5	41.7	327 1	EMT2_MOUSE	O61672 m equillipra
43	5	41.7	327 1	YB56_XENLA	P21574 xenopus lae
44	5	41.7	346 1	TRPA_MAIZE	P42390 zea mays (m
45	5	41.7	354 1	YMA3_MYCBO	Q02279 mycobacteri
46	5	41.7	356 1	HIS8_ECOLI	P06986 escherichia
47	5	41.7	359 1	HIS8_SALTY	P10369 salmonella
48	5	41.7	360 1	WMT2_CAEEL	P34889 caenorhabdi
49	5	41.7	362 1	SRK2_SPOLA	P42688 spongillia l
50	5	41.7	366 1	RPOO_REOVD	P03526 reovirus (t
51	5	41.7	366 1	RPOO_REOVL	P12002 reovirus (t
52	5	41.7	366 1	YB85_YEAST	P07940 reovirus (t
53	5	41.7	367 1	MTCL_CHVT3	O04806 saccharomyc
54	5	41.7	367 1	NTIM_BOVAN	P36216 chlorella v
55	5	41.7	377 1	TTL_BOVIN	P19041 podospira a
56	5	41.7	377 1	TTL_BOVIN	P38584 bos taurus
57	5	41.7	379 1	YMH7_CAEEL	P38160 sus scrofa
58	5	41.7	380 1	YGV5_YEAST	P34474 caenorhabdi
59	5	41.7	386 1	GAG_HV1W2	P53334 saccharomyc
60	5	41.7	388 1	GAG_HV1W2	P05889 human immun
61	5	41.7	390 1	EMRA_ECOLI	P27303 escherichia
62	5	41.7	391 1	THAB_PAROL	Q91242 parallelchly
63	5	41.7	400 1	CYH2_HUMAN	O99418 homo sapien
64	5	41.7	400 1	CYH2_MOUSE	P97695 mus musculu
65	5	41.7	415 1	YLN2_CAEEL	O18964 caenorhabdi
66	5	41.7	428 1	SRK_HUMAN	P98077 homo sapien
67	5	41.7	432 1	BAC_XENLA	P24781 xenopus lae
68	5	41.7	442 1	TIG_CHLTR	O84713 chlamydia t
69	5	41.7	445 1	GLMM_HELPJ	Q9amz2 helicobacte
70	5	41.7	445 1	GLMM_HELPJ	P25177 helicobacte
71	5	41.7	452 1	YDQ4_SCHPO	O14197 schizosacch
72	5	41.7	453 1	YDQ4_SCHPO	P34656 caenorhabdi
73	5	41.7	458 1	KRA_XENLA	P51126 xenopus lae
74	5	41.7	465 1	REBA_VIBCH	O07024 vibrio chol
75	5	41.7	468 1	PCOI_MOUSE	Q61398 mus musculu
76	5	41.7	468 1	PCOI_RAT	O08628 rattus norv
77	5	41.7	470 1	GLNA_FREDI	P33035 fremyella d
78	5	41.7	473 1	GLNA_SYNY3	P77961 synechocyst
79	5	41.7	473 1	SYE_AQUAE	O67271 aquilex aeo
80	5	41.7	473 1	YCLC_BACSU	P94405 bacillus su
81	5	41.7	474 1	VPQC_STRD7	O94697 streptomyc
82	5	41.7	474 1	VP61_NPVOP	O10270 oryza pseu
83	5	41.7	481 1	PE0_LISIN	O01836 listeria in
84	5	41.7	484 1	SGAT_ECOLI	P39301 escherichia
85	5	41.7	488 1	EXON_HSV6U	P24447 human herpe
86	5	41.7	488 1	EXON_HSV6Z	P52448 human herpe
87	5	41.7	488 1	PE24_RABIT	O26691 oryctolagus
88	5	41.7	490 1	SUCP_LEUME	O59495 leucostococ
89	5	41.7	498 1	ACHP_HUMAN	P30926 homo sapien
90	5	41.7	498 1	YCIC_ECOLI	P78061 escherichia
91	5	41.7	501 1	YH92_CAEEL	O22256 caenorhabdi
92	5	41.7	503 1	GAG_HV1JR	P20873 human immun
93	5	41.7	504 1	GAG_HV1MA	P20873 human immun
94	5	41.7	504 1	IRE5_HUMAN	O13568 homo sapien
95	5	41.7	509 1	CP77_BOVIN	O50185 bos taurus
96	5	41.7	509 1	PSBB_GUTH	O78511 guillardia
97	5	41.7	509 1	VLI_HV49	P36742 human papil
98	5	41.7	510 1	PUR1_YEAST	P04046 saccharomyc
99	5	41.7	512 1	VLI_HPV24	P50790 human papil
100	5	41.7	514 1	VLI_HPV08	P06417 human papil
101	5	41.7	514 1	VLI_HPV47	P24242 human papil
102	5	41.7	515 1	VLI_HPV50	P50818 human papil
103	5	41.7	516 1	VLI_HPV05	P06917 human papil
104	5	41.7	516 1	VLI_HPV20	P50786 human papil
105	5	41.7	516 1	VLI_HPV36	P50812 human papil
106	5	41.7	517 1	VLI_HPV12	P36733 human papil

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OY 2 TPVAP 6
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 Db 164 TPVAP 168

RESULT 48

S07291
 repressor protein ci - phage Mu
 C/Species: phage Mu
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999
 C/Accession: S07291
 R/Pileups, H.: Kamp, D.; Kahmann, R.; Braeuer, B.; Dellus, H.
 Mol. Gen. Genet. 186, 315-321, 1982
 A/Title: Nucleotide sequence of the immunity region of bacteriophage Mu.
 A/Reference number: S07291; MUID:83012203
 A/Accession: S07291
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-174 <PRI>
 A/Cross-references: EMBL:V01464; NID:915807; PIDN:CAA24711.1; PID:915808
 C/Keywords: DNA binding; transcription regulation

Query Match 41.7%; Score 5; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYK 12
 |||||
 Db 168 OEYK 172

RESULT 49

D86699
 hypothetical protein yfii [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C/Species: Lactococcus lactis subsp. lactis
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
 C/Accession: D86699
 R/Bolotin, A.; Muncher, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. in press, 2001
 A/Title: The complete genome sequence of the lactic acid bacterium.
 A/Reference number: A86625
 A/Accession: D86699
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-175 <STO>
 A/Cross-references: GB:AE005176; NID:912723488; PIDN:AAK04694.1; GSPDB:GND0146
 A/Experimental source: strain IL1403
 C/Genetics:
 A/Gene: yfii

Query Match 41.7%; Score 5; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYK 12
 |||||
 Db 94 OEYK 98

RESULT 50

T50849
 hypothetical protein 110K5.14 [imported] - sorghum (fragment)
 C/Species: Sorghum bicolor (sorghum)
 C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
 C/Accession: T50849
 R/Tikhonov, A.P.; SanMiguel, P.J.; Nakajima, Y.; Gorenstein, N.M.; Bennetzen, J.L.; Ayre
 Proc. Natl. Acad. Sci. U.S.A. 96, 7409-7414, 1999
 A/Title: Colinearity and its exceptions in orthologous adh regions of maize and sorghum.
 A/Reference number: Z25261; MUID:99307423
 A/Accession: T50849
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-175 <TIK>
 A/Cross-references: EMBL:AF124045; PIDN:AAD43043.1
 A/Experimental source: cultivar BTx623
 C/Genetics:
 A/Map position: J
 A/Note: 110K5.14

Query Match 41.7%; Score 5; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
 |||||
 Db 68 TPVAP 72

Search completed: August 15, 2001, 12:34:44
 Job time: 109 sec

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: J33327
 R:Madsen, C.; Wamsley, P.; O'Brien, D.
 submitted to the EMBL Data Library, July 1998
 A:Description: The sequence of *Caenorhabditis elegans* cosmid C40D2.
 A:Reference number: 221323
 A:Accession: J33327
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-147 <MAD>
 A:Cross-references: EMBL:AF07530; PIDN:AMC26267.1; GSPDB:GN00020; CESP:C40D2.4
 C:Genetics:
 A:Gene: CESP:C40D2.4
 A:Map position: 2
 A:Introns: 45/3; 58/1; 75/1; 102/3

Query Match 41.7%; Score 5; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTOE 9
 |||||
 Db 53 APTOE 57

RESULT 44
 725638
 hypothetical protein C46H11.5 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: J25638
 R:Miller, N.; Bradshaw, H.; Wamsley, P.
 submitted to the EMBL Data Library, February 1997
 A:Description: The sequence of *C. elegans* cosmid C46H11.
 A:Reference number: 220061
 A:Accession: J25638
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-157 <MLI>
 A:Cross-references: EMBL:U88314; PIDN:AA842359.1; GSPDB:GN00019; CESP:C46H11.5
 A:Experimental source: strain Bristol N2; clone C46H11
 C:Genetics:
 A:Gene: CESP:C46H11.5
 A:Map position: 1
 A:Introns: 12/1; 44/2

Query Match 41.7%; Score 5; DB 2; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTOE 9
 |||||
 Db 86 APTOE 90

RESULT 45
 965568
 hypothetical protein F6D8.6 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: C96568
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Holt, T.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719
 A:Accession: C96568
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-161 <STO>
 A:Cross-references: GB:AE005173; NID:95903065; PIDN:AAD55624.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F6D8.6
 A:Map position: 1

Query Match 41.7%; Score 5; DB 2; Length 161;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAP 7
 |||||
 Db 40 PVAP 44

RESULT 46
 S61230
 cytochrome-c biosynthesis heme-carrier protein cycJ - *Rhizobium leguminosarum*
 C:Species: *Rhizobium leguminosarum*
 C:Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 29-Sep-1999
 C:Accession: S61230
 R:Delgado, M.J.; Yeaman, K.H.; Wu, G.; Vargas, C.; Davies, A.; Poole, R.K.; Johnston, submitted to the EMBL Data Library, July 1995
 A:Description: Characterization of the *cycHKL* genes involved in cytochrome c biogenesis
 A:Reference number: S61229
 A:Accession: S61230
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-165
 A:Cross-references: EMBL:X89726; NID:9967064; PIDN:CAA61877.1; PID:9967066
 C:Superfamily: Escherichia coli cytochrome-c biosynthesis heme-carrier protein cme
 C:Keywords: carrier protein; chromoprotein; heme; iron; metalloprotein
 F124/Binding site: heme (His) (covalent) #status predicted

Query Match 41.7%; Score 5; DB 2; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
 |||||
 Db 45 TPVAP 49

RESULT 47
 S11770
 ImaA protein - *Listeria monocytogenes*
 C:Species: *Listeria monocytogenes*
 C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 24-Nov-1999
 C:Accession: S11770
 R:Goehmann, S.; Leimister-Waechter, M.; Schiltz, E.; Goebel, W.; Chakraborty, T.
 Mol. Microbiol. 4, 1091-1099, 1990
 A:Title: Characterization of a *Listeria monocytogenes*-specific protein capable of inducing apoptosis
 A:Reference number: S11770; MUID:91041717
 A:Accession: S11770
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-170 <GOE>
 C:Genetics:
 A:Gene: ImaA
 C:Superfamily: *Listeria monocytogenes* ImaA protein

Query Match 41.7%; Score 5; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Reference number: 225035
 A:Accession: T50083
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1133 <SAU>
 A:Cross-references: EMBL:AL13984; PIDN:CAB61215.1; GSPDB:GN00066; SPDB:SPAC1556.04c
 A:Experimental source: strain 972H(-); cosmid c1556
 C:Genetics:
 A:Gene: SPDB:SPAC1556.04c
 A:Map position: 1
 A:Introns: 47/1; 67/3; 95/2; 121/3
 C:Superfamily: cytidine deaminase

Query Match 41.7%; Score 5; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYK 12
 |||||
 DB 11 OEYK 15

RESULT 39
 B60497
 MHC class II histocompatibility antigen RT1 D-I beta chain precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 12-Aug-1996
 C:Accession: B60497
 R:Holowachuk, E.M.; Greer, M.K.
 Diabets 38, 267-271, 1989
 A:Title: Unaltered class II histocompatibility antigens and pathogenesis of IDDM in BB
 A:Reference number: A60497; MUID:89121214
 A:Accession: B60497
 A:Molecule type: mRNA
 A:Residues: 1-134 <HOL>
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
 F:1-27/Domain: signal sequence #status predicted <SIG>

Query Match 41.7%; Score 5; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPYA 5
 |||||
 DB 21 STPYA 25

RESULT 40
 A81676
 conserved hypothetical protein TC0687 [imported] - Chlamydia muridarum (strain N199)
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MOpn
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
 C:Accession: A81676
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150235
 A:Accession: A81676
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-134 <RET>
 A:Cross-references: GB:AE002337; GB:AE002160; NID:g7190714; PIDN:AAF39504.1; PID:g719071
 C:Genetics:
 A:Experimental source: strain N199 (MOpn)
 C:Superfamily: Escherichia coli dosage-dependent dnaX suppressor protein dksa

Query Match 41.7%; Score 5; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYK 12
 |||||
 DB 41 OEYK 45

RESULT 41
 E72580
 hypothetical protein APE1924 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: E72580
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
 A:Reference number: A72450; MUID:99310339
 A:Accession: E72580
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-141 <KAW>
 A:Cross-references: DDBJ:AP000062; NID:95105244; PIDN:BAA80930.1; PID:d1044716; PID:g
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1924

Query Match 41.7%; Score 5; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VAPPO 8
 |||||
 DB 66 VAPPO 70

RESULT 42
 G72384
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: G72384
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: G72384
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-147 <ARN>
 A:Cross-references: GB:AE001717; GB:AE000512; NID:g4980871; PIDN:AAD35456.1; PID:g498
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM0369

Query Match 41.7%; Score 5; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEYK 12
 |||||
 DB 127 OEYK 131

RESULT 43
 T33327
 hypothetical protein C40D2.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans

A:Accession: G72066
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-124 <ARN>
 A:Cross-references: GB:AE001638, GB:AE001363; NID:94376819; PIDN:AA18674.1; PID:9437682
 A:Experimental source: strain CML029
 C:Genetics:
 A:Gene: dksA
 C:Superfamily: Escherichia coli dosage-dependent dnaK suppressor protein dksA

Query Match 41.7%; Score 5; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVKK 12
 |||||
 DB 31 QEVKK 35

RESULT 34

T24876
 hypothetical protein T13F2.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C:Accession: T24876
 R:Swingburne, J.
 Submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19947
 A:Accession: T24876
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-124 <MIL>
 A:Cross-references: EMBL, Z81122; PIDN:CA803353.1; GSPDB:GN00022; CESP:T13F2.2
 A:Experimental source: clone T13F2
 C:Genetics:
 A:Gene: CESP:T13F2.2
 A:Map position: 4
 A:Introns: 27/3; 61/3; 91/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match 41.7%; Score 5; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVKK 12
 |||||
 DB 39 QEVKK 43

RESULT 35

I54454
 lymphocyte antigen - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
 C:Accession: I54454
 R:Hiratawa, A.; Seyfried, C.E.; Nepom, G.T.; Milner, E.C.
 Immunogenetics 29, 186-190, 1989
 A>Title: Sequence analysis of HLA class II domains: characterization of the DQw3 family
 A:Reference number: I54454; MUID:89173071
 A:Accession: I54454
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-126 <RES>
 A:Cross-references: GB:M25325; NID:9619801; PIDN:AAA59675.1; PID:9619802
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 41.7%; Score 5; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SRPVA 5
 |||||
 DB 26 SRPVA 30

RESULT 36

D86684
 prophage p11 protein 41, tail component [imported] - Lactococcus lactis subsp. lactis
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
 C:Accession: D86684
 R:Boletín, A.; Winkler, P.; Mauger, S.; Jallón, O.; Malarne, K.; Weissenbach, J.; Eh
 Genome Res. In Press, 2001
 A>Title: The complete genome sequence of the lactic acid bacterium.
 A:Reference number: AB6625
 A:Accession: D86684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-131 <STO>
 A:Cross-references: GB:AE005176; NID:912723355; PIDN:AKK04574.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: p1141

Query Match 41.7%; Score 5; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTQEV 10
 |||||
 DB 3 PTQEV 7

RESULT 37

B81600
 conserved hypothetical protein CP0218 [imported] - Chlamydomonas reinhardtii (strain A
 C:Species: Chlamydomonas reinhardtii
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
 C:Accession: B81600
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
 , C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzbe
 Nuclear Acids Res. 28, 1397-1406, 2000
 A>Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
 A:Reference number: AB1500; MUID:20150255
 A:Accession: B81600
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-132 <REA>
 A:Cross-references: GB:AE002183; GB:AE002161; NID:97189146; PIDN:ARF38087.1; PID:9718
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CP0218
 C:Superfamily: Escherichia coli dosage-dependent dnaK suppressor protein dksA

Query Match 41.7%; Score 5; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVKK 12
 |||||
 DB 39 QEVKK 43

RESULT 38

T50083
 probable cytidine deaminase [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
 C:Accession: T50083
 R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, November 1999

A:Residues: 1-114 <QVE>
A:Cross-references: EMBL:AL049862; GSPDB:GNO0061; ATSP:FI8B3.180
A:Experimental source: cultivar Columbia; BAC clone FI8B3
C:Genetics:
A:Gene: ATSP:FI8B3.180
A:Map position: 3
C:Superfamily: Arabidopsis hypothetical protein FI8B3.180

Query Match 41.7%; Score 5; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVKK 12
|||||
DB 43 QEVKK 47

RESULT 29
B49094
methylmalonyl-CoA decarboxylase (EC 4.1.1.41) delta chain - Veillonella parvula
C:Species: Veillonella parvula
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C:Accession: B49094
R:Huder, J.B.; Dimroth, P.
J. Biol. Chem. 268, 24564-24571, 1993
A:Title: Sequence of the sodium ion pump methylmalonyl-CoA decarboxylase from Veillonella
A:Reference number: A49094, MUID:94043308
A:Accession: B49094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <HND>
A:Cross-references: GB:L22208; NID:9415592; PIDN:AAC36821.1; PID:9415594
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 41.7%; Score 5; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
|||||
DB 60 TPVAP 64

RESULT 30
A72293
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: A72293
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200, MUID:99287316
A:Accession: A72293
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <ARN>
A:Cross-references: GB:AE001770; GB:AE000512; NID:94981658; PIDN:AAD36200.1; PID:9498167
C:Genetics:
A:Experimental source: strain MSB8
A:Gene: TM1124

Query Match 41.7%; Score 5; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPYA 5
|||||

DB 30 STPYA 34

RESULT 31
B86557
Dnak suppressor [imported] - Chlamydia pneumoniae (strain J139)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: B86557
R:Shiral, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: B86557
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <STO>
A:Cross-references: GB:BA000008; NID:98978905; PIDN:BA98740.1; GSPDB:GNO0142
A:Experimental source: strain J138
C:Genetics:
A:Gene: dksA
C:Superfamily: Escherichia coli dosage-dependent dnak suppressor protein dksA

Query Match 41.7%; Score 5; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVKK 12
|||||
DB 31 QEVKK 35

RESULT 32
A71518
probable dnak suppressor - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jun-2000
C:Accession: A71518
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A:Reference number: A71570; MUID:99000809
A:Accession: A71518
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <ARN>
A:Cross-references: GB:AE001314; GB:AE001273; NID:93328833; PIDN:AAC68004.1; PID:9332
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: dksA
C:Superfamily: Escherichia coli dosage-dependent dnak suppressor protein dksA

Query Match 41.7%; Score 5; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVKK 12
|||||
DB 31 QEVKK 35

RESULT 33
G72066
dnak suppressor - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jun-2000
C:Accession: G72066
R:Rahman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606

Db 31 STPVA 35

RESULT 24

B56581
 major basic nuclear protein, variant HCC2 - dinoflagellate (Cryptocodinium cohnii) (fr
 N:Alternate names: protein alpha chain p14
 C:Species: Cryptocodinium cohnii
 C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
 C:Accession: B56581; S14640; S14644
 R:Salta-Rovira, M.; Geraud, M.L.; Caput, D.; Jacques, F.; Soyier-Gobillard, M.O.; Vermet,
 Chromosoma 100, 510-518, 1991
 A:Title: Molecular cloning and immunolocalization of two variants of the major basic nuc
 A:Reference number: A56581; MUID:92111321
 A:Accession: B56581
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <SAL>
 A:Cross-references: EMBL:X58444; NID:q17962; PIDN:CAA41350.1; PID:q17963
 A:Note: sequence extracted from NCBI backbone (NCBIN:77122, NCBIIP:77123)
 C:Keywords: DNA binding; nucleus

Query Match 41.7%; Score 5; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OEVRK 12
 |||||
 Db 43 OEVRK 47

RESULT 25

K4RB
 19 kappa-B4 chain C region - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Jan-1991 #sequence_revision 15-Oct-1982 #text_change 16-Aug-1996
 C:Accession: A93971; A93891; A92176; A02122
 R:Emorline, L.; Dreher, K.; Kindt, T.J.; Max, E.
 Proc. Natl. Acad. Sci. U.S.A. 80, 5709-5713, 1983
 A:Title: Rabbit immunoglobulin kappa genes: structure of a germline b4 allotype J-C locu
 A:Reference number: A93971; MUID:83300036
 A:Accession: A93971
 A:Molecule type: DNA
 A:Residues: 1-103 <EMO>
 A:Note: the sequence was determined from the germline gene
 R:Heidmann, O.; Auftray, C.; Cazeneuve, P.A.; Rougeon, F.
 Proc. Natl. Acad. Sci. U.S.A. 78, 5802-5806, 1981
 A:Title: Nucleotide sequence of constant and 3' untranslated regions of a kappa immunogl
 A:Reference number: A93891; MUID:82060334
 A:Accession: A93891
 A:Molecule type: mRNA
 A:Residues: 1-103 <HER>
 R:Chen, K.C.S.; Kindt, T.J.; Krause, R.M.
 J. Biol. Chem. 250, 3289-3296, 1975
 A:Title: Primary structure of the L chain from a rabbit homogeneous antibody to streptoc
 A:Reference number: A92176; MUID:75133568
 A:Accession: A92176
 A:Molecule type: protein
 A:Residues: 1-57, 'D', '59-103 <CHR>
 A:Note: this chain was obtained from antibody to the specific carbohydrate of group C st
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:19-87/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 5; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7

Db 2 PVAPT 6

RESULT 26

F53275
 Ig kappa-1 chain C region b95 allotype - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: F53275
 R:Ayadi, H.; Marche, P.N.; Cazeneuve, P.A.
 Immunogenetics 34, 201-207, 1991
 A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
 A:Reference number: A53275; MUID:91372868
 A:Accession: F53275
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-104 <AYA>
 A:Note: sequence inconsistent with nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIIP:56170)
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-87/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 5; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
 |||||
 Db 2 PVAPT 6

RESULT 27

T14788
 hypothetical protein DKFZP564A122.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14788
 R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, August 1999
 A:Reference number: Z18178
 A:Accession: T14788
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-112 <DUE>
 A:Cross-references: EMBL:AL110269
 A:Experimental source: fetal brain; clone DKFZP564A122
 C:Genetics:
 A:Note: DKFZP564A122.1

Query Match 41.7%; Score 5; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTOEV 10
 |||||
 Db 91 PTOEV 95

RESULT 28

T08411
 hypothetical protein F18B3.180 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
 C:Accession: T08411
 R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16409
 A:Accession: T08411
 A:Molecule type: DNA

T30302
 P-type ATPase - Tetrahymena thermophila
 C:Species: Tetrahymena thermophila
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 07-Dec-1999
 C:Accession: T30302
 R:Wang, S.; Takeyasu, K.
 Submitted to the EMBL Data Library, November 1995
 A:Description: The starvation-induced P-type ATPase in Tetrahymena thermophila.
 A:Reference number: 220815
 A:Accession: T30302
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1133 <MAN>
 A:Cross-references: EMBL:U41063; NID:g1545827; PID:g1545828; PIDN:AAB08071.1
 C:Genetics:
 A:Genetic code: SGCS
 A>Note: TPA9

Query Match 50.0%; Score 6; DB 2; Length 1133;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEYKK 12
 |||||
 Db 1099 TOEYKK 1104

RESULT 20
 E64664
 Outer membrane protein - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: E64664
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatlek, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467
 A:Accession: E64664
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1230 <TOM>
 A:Cross-references: GB:AE000621; GB:AE000511; NID:g2314301; PIDN:AAD08205.1; PID:g231431

Query Match 50.0%; Score 6; DB 2; Length 1230;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEYKK 12
 |||||
 Db 173 TOEYKK 178

RESULT 21
 E75264
 Hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: E75264
 R:White, O.; Eisen, J.A.; Hefelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamthayan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: E75264
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-75 <WHI>

A:Cross-references: GB:AE002081; GB:AE000513; NID:g6460337; PIDN:AAF12064.1; PID:g646
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2520
 A:Map position: 1

Query Match 41.7%; Score 5; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VAPTO 8
 |||||
 Db 24 VAPTO 28

RESULT 22
 T29802
 Hypothetical protein C06E4.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T29802
 R:Du, Z.; Gattung, S.
 Submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C06E4.
 A:Reference number: 220688
 A:Accession: T29802
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <DUZ>
 A:Cross-references: EMBL:U41277; PIDN:AAA82477.1; CESP:C06E4.2
 C:Genetics:
 A:Gene: CESP:C06E4.2
 A:Introns: 31/1

Query Match 41.7%; Score 5; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VAPTO 8
 |||||
 Db 40 VAPTO 44

RESULT 23
 T34429
 Hypothetical protein F55C7.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T34429
 R:Du, Z.; Le, T.
 Submitted to the EMBL Data Library, November 1996
 A:Description: The sequence of C. elegans cosmid F55C7.
 A:Reference number: 221524
 A:Accession: T34429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-88 <DUZ>
 A:Cross-references: EMBL:U80436; PIDN:AAC71107.1; GSPDB:GN00019; CESP:F55C7.2
 A:Experimental source: strain Bristol N2; clone F55C7
 C:Genetics:
 A:Gene: CESP:F55C7.2
 A:Map position: 1
 A:Introns: 18/3

Query Match 41.7%; Score 5; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPYA 5
 |||||

submitted to the EMBL Data Library, October 1997
A:Reference number: Z19673

A:Accession: T23087
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <MIL>
A:Cross-references: EMBL:Z99942; PIDN:CAB17068.1; GSPDB:GN00028; CESP:HL3N06.2
A:Experimental source: clone HL3N06
C:Genetics:
A:Gene: CESP:HL3N06.2
A:Map position: X
A:Introns: 17/1; 294/1; 331/3; 364/1; 414/2; 432/2

Query Match 50.0%; Score 6; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
|||||
Db 73 TPVAPT 78

RESULT 15
S42719
actin-binding protein ABP1 - Saccharomyces exiguus
C:Species: Saccharomyces exiguus
C:Date: 07-Sep-1994 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S42719
R:Langre, U.; Steiner, S.; Grollig, F.; Wagner, G.; Philippson, P.
Biochim. Biophys. Acta 1217, 214-218, 1994
A:Title: Cloning and sequencing of a gene coding for an actin binding protein of Sacchar
A:Reference number: S42719; MUID:94154001
A:Accession: S42719
A:Molecule type: DNA
A:Residues: 1-617 <LAN>
A:Cross-references: EMBL:X73977; NID:G433513; PIDN:CAA52156.1; PID:G433514
C:Superfamily: actin-binding protein ABP1; SH3 homology
C:Keywords: actin binding; cytoskeleton
F:564-613/Domain: SH3 homology <SH3>

Query Match 50.0%; Score 6; DB 2; Length 617;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
|||||
Db 412 TOEVKK 417

RESULT 16
S66953
hypothetical protein YOR070C - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein Q2931
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
C:Accession: S66953
R:Bonin, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66929
A:Accession: S66953
A:Molecule type: DNA
A:Residues: 1-637 <BOH>
A:Cross-references: EMBL:Z74978; NID:G1420220; PID:E251984; PID:G1420221; GSPDB:GN00015;
C:Genetics:
A:Gene: MIPS:YOR070C
A:Map position: 15R

Query Match 50.0%; Score 6; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 TPVAPT 7
|||||
Db 181 TPVAPT 186

RESULT 17
HB4913
probable ATP-dependent RNA helicase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: HB4913
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Unayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: HB4913
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-748 <STO>
A:Cross-references: GB:AE002093; NID:G2275211; PIDN:AAB63833.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g47330
A:Map position: 2

Query Match 50.0%; Score 6; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPRQ 8
|||||
Db 725 PVAPRQ 730

RESULT 18
VCLJSP
env polyprotein - human foamy virus
N:Alternate names: coat polyprotein
C:Species: human foamy virus
A>Note: host Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: C29685
R:Fluegel, R.M.; Rehwilm, A.; Maurer, B.; Darai, G.
EMBO J. 6, 2077-2084, 1987
A:Title: Nucleotide sequence analysis of the env gene and its flanking regions of the
A:Reference number: A91074; MUID:88004420
A:Accession: C29685
A:Molecule type: genomic RNA
A:Residues: 1-985 <FLU>
A:Cross-references: GB:X05591; GB:Y00070; NID:G61759; PIDN:CAA29086.1; PID:G61762
C:Genetics:
A:Gene: env
C:Superfamily: foamy virus env polyprotein
C:Keywords: coat protein; polyprotein; transmembrane protein
F:64-87/Domain: transmembrane #status predicted <TM1>
F:579-595/Domain: transmembrane #status predicted <TM2>
F:936-972/Domain: transmembrane #status predicted <TM3>

Query Match 50.0%; Score 6; DB 1; Length 985;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12
|||||
Db 181 TOEVKK 186

RESULT 19

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-293 <NH1>
A:Cross-references: GB:AE001940; GB:AE000513; NID:g6458577; PIDN:AAF10447.1; PID:g645858
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0864
A:Map position: 1

Query Match 50.0%; Score 6; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVAPT 6
|||||
DB 227 TPVAPT 232

RESULT 10
T34992
probable lipoprotein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34992
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: 221550
A:Accession: T34992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-447 <OLI>
A:Cross-references: EMBL:AL031182; PIDN:CAA20169.1; GSPDB:GN00070; SCOEDB:SC4A2.17C
C:Genetics:
A:Gene: SCOEDB:SC4A2.17C

Query Match 50.0%; Score 6; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
|||||
DB 63 TPVAPT 68

RESULT 11
F64623
amidase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: F64623
R:Tomb, J.F.; White, O.; Kervilave, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.; Nature 388, 539-547, 1997
A:Authors: Mellin, E.; Hayes, W.S.; Bordovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: F64623
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-453 <ROM>
A:Cross-references: GB:AE000594; GB:AE000511; NID:g2313957; PIDN:AND07880.1; PID:g231396
C:Superfamily: Indoleacetamide hydrolase

Query Match 50.0%; Score 6; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7

DB 373 TPVAPT 378
|||||

RESULT 12
A71891
glu-tRNA amidotransferase, chain A - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
C:Accession: A71891
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MUID:99120557
A:Accession: A71891
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-453 <ARN>
A:Cross-references: GB:AE001507; GB:AE001439; NID:g4155326; PIDN:AAD06348.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: gata
C:Superfamily: Indoleacetamide hydrolase

Query Match 50.0%; Score 6; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7
|||||
DB 373 TPVAPT 378

RESULT 13
H85574
hypothetical protein Z0891 [Imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: H85574
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobeck, E.J.; Davis, N.W.; Llim, A.; Diallanita, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-456 <STO>
A:Cross-references: GB:AE005174; NID:g12513654; PIDN:AAG55060.1; GSPDB:GN00145; UNGP:
A:Experimental source: strain O157:H7, substrain EDL533
C:Genetics:
A:Gene: Z0891

Query Match 50.0%; Score 6; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VAPTOE 9
|||||
DB 378 VAPTOE 383

RESULT 14
T23087
hypothetical protein H13N06.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T23087
R:Lennard, N.

DB 29 TOEVKK 34

RESULT 5

STH-21 protein - potato
C:Species: Solanum tuberosum (potato)
C:Date: 13-Jan-1995 #sequence_revision 09-May-1997 #text_change 20-Aug-1999
C:Accession: S35162; S11869
R:Maton, D.P.; Prescott, G.; Bertrand, C.; Camirand, A.; Brisson, N.
Plant Mol. Biol. 22, 279-291, 1993
A:Title: Identification of cis-acting elements involved in the regulation of the pathogen
A:Reference number: S35161; MUID:93283632
A:Accession: S35162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <MAT>
A:Cross-references: EMBL:M29042; NID:q169577; PIDN:AAA02829.1; PID:q169578
C:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1990
C:Genetics:
A:Gene: STH-21
A:Introns: 57/1
C:Superfamily: pathogenesis-related protein

Query Match 50.0%; Score 6; DB 2; Length 155;

Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7

DB 12 TPVAPT 17

RESULT 6

JC4806
core protein G - phage phi-K
C:Species: Phage phi-K
C:Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 20-Jun-2000
C:Accession: JC4806; B04253; A04253
R:Kodaira, K.; Oki, M.; Kakikawa, M.; Kimoto, H.; Taketo, A.
J. Biochem. 119, 1062-1069, 1996
A:Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant ph
A:Reference number: JC4804; MUID:96424987
A:Accession: JC4806
A:Status: nucleic acid sequence not shown
A:Cross-references: EMBL:X60323; NID:q1478118; PIDN:CAA42892.1; PID:q1478127
R:Stins, J.; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628, 1979
A:Title: drug (primase)-dependent origins of DNA replication. Nucleotide sequences of th
A:Reference number: A92247; MUID:80049950
A:Accession: B04253
A:Molecule type: DNA
A:Residues: 165-187 <SIM>
C:Comment: This protein is one of the structural components of the bacteriophage capsid.
C:Genetics:
A:Gene: G
C:Superfamily: phage phi-X174 gene G protein
C:Keywords: capsid protein

Query Match 50.0%; Score 6; DB 2; Length 187;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7

DB 25 TPVAPT 30

RESULT 7

C86847
transcription regulator Tena [imported] - Lactococcus lactis subsp. lactis (strain IL
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86847
R:Boitlin, A.; Winker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: C86847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <STO>
A:Cross-references: GB:AE005176; NID:q12724803; PIDN:AAK05877.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: tena
C:Superfamily: transcription activator tena

Query Match 50.0%; Score 6; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAPT 7

DB 103 TPVAPT 108

RESULT 8

F71504
hypothetical protein CT504 - Chlamydia trachomatis (serotype D, strain UM3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1998 #text_change 18-Aug-2000
C:Accession: F71504
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A:Reference number: A71570; MUID:99000809
A:Accession: F71504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <ARN>
A:Cross-references: GB:AE001323; GB:AE001273; NID:g3328931; PIDN:AA68105.1; PID:g3332
A:Experimental source: serotype D, strain UM-3/Cx
C:Genetics:
A:Gene: CT504
C:Superfamily: conserved hypothetical protein TC0791

Query Match 50.0%; Score 6; DB 2; Length 288;

Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAP 6

DB 131 STPVAP 136

RESULT 9

F75466
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75466
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75466

979 4 33.3 128 2 H84223
980 4 33.3 128 2 JN0727
981 4 33.3 128 2 S75366
982 4 33.3 128 2 T05635
983 4 33.3 128 2 T32789
984 4 33.3 129 2 A33548
985 4 33.3 129 2 S36260
986 4 33.3 129 2 S46393
987 4 33.3 129 2 B71350
988 4 33.3 129 2 S53806
989 4 33.3 129 2 S37713
990 4 33.3 129 2 F83764
991 4 33.3 130 1 F64376
992 4 33.3 130 1 C69883
993 4 33.3 130 2 PC6025
994 4 33.3 130 2 S08079
995 4 33.3 130 2 F25733
996 4 33.3 130 2 G70813
997 4 33.3 130 2 S77271
998 4 33.3 130 2 D70966
999 4 33.3 130 2 T29887
1000 4 33.3 130 2 F64348

ALIGNMENTS

RESULT 1
A:1487
protein p60 precursor - Listeria monocytogenes
N:Alternate names: Invasion-associated protein
C:Species: Listeria monocytogenes
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1996
R:Koehler, S.; Letmeister-Waechter, M.; Chakraborty, T.; Lottspeich, F.; Goebel, W.
Infect. Immun. 58, 1943-1950, 1990
A:Title: The gene coding for protein p60 of Listeria monocytogenes and its use as a spec
A:Reference number: A41487; MUID:90256283
A:Accession: A41487
A:Molecule type: DNA
A:Residues: 1484 <KOE>
A:Cross-references: GB:X52268
A:Accession: B41487
A:Molecule type: protein
A:Residues: 28-49 <KO2>
C:Genetics:
A:Gene: lbp
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-484/Product: protein 60 #status predicted <MAT>

Query Match 100.0%; Score 12; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAPTOEVKK 12
|||||
Db 146 STVPAPTOEVKK 157

RESULT 2
D81259
probable tonB transport protein Cj1630 [imported] - Campylobacter jejuni (strain NCTC 11
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: D81259
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912
A:Accession: D81259
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-227 <PAR>
A:Cross-references: GB:AL111168; GB:AL111168; NID:g96968971; PIDN:CAB73618.1; PID:g9696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: tonB2; Cj1630

Query Match 58.3%; Score 7; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTOEVKK 11
|||||
Db 105 APTOEVKK 111

RESULT 3
F83231
hypothetical protein PA3307 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83231
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardly, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82850; MUID:20437337
A:Accession: F83231
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STO>
A:Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AA06695.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3307

Query Match 50.0%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPTQ 8
|||||
Db 27 PVAPTQ 32

RESULT 4
T37186
probable regulatory protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T37186
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T37186
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-116 <SEE>
A:Cross-references: EMBL:AL096823; PIDN:CAB46971.1; GSPDB:GN00070; SCOEDB:SCQ11.16
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCQ11.16
C:Superfamily: Streptomyces ambifaciens replication activator protein pra

Query Match 50.0%; Score 6; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVKK 12

833	4	33.3	115	2	E45213	Ca2+-transporting	906	4	33.3	122	2	PC4279	anti-SS-A/Ro 60k p
834	4	33.3	115	2	PH1560	Ig heavy chain V r	907	4	33.3	122	2	PC4280	anti-SS-A/Ro 60k p
835	4	33.3	115	2	PH1557	Ig heavy chain V r	908	4	33.3	122	2	PH1426	Ig heavy chain V r
836	4	33.3	115	2	G72568	hypothetical prote	909	4	33.3	122	2	PH0958	Ig heavy chain V r
837	4	33.3	115	2	E70702	hypothetical prote	910	4	33.3	122	2	S36271	Ig heavy chain V r
838	4	33.3	115	2	E84684	hypothetical prote	911	4	33.3	122	2	C49590	Ig heavy chain V r
839	4	33.3	115	2	E86809	hypothetical prote	912	4	33.3	122	2	B49590	Ig heavy chain V r
840	4	33.3	115	2	D84501	hypothetical prote	913	4	33.3	122	2	T22096	hypothetical prote
841	4	33.3	115	2	E84512	probable MYB famli	914	4	33.3	123	1	RKSPS	ribulose-bisphosph
842	4	33.3	115	2	PC2230	hobo-like transpos	915	4	33.3	123	2	D33548	Ig heavy chain V-I
843	4	33.3	116	1	B46279	guanylin precursor	916	4	33.3	123	2	PH1413	Ig heavy chain V r
844	4	33.3	116	2	S31698	Ig heavy chain pre	917	4	33.3	123	2	PH1423	Ig heavy chain V r
845	4	33.3	116	2	PH0959	Ig heavy chain V r	918	4	33.3	123	2	S38492	Ig heavy chain - h
846	4	33.3	116	2	S36261	Ig heavy chain V r	919	4	33.3	123	2	C36006	Ig heavy chain V r
847	4	33.3	116	2	S31667	Ig heavy chain V r	920	4	33.3	123	2	S44108	Ig heavy chain V-D
848	4	33.3	116	2	PN0618	ribosomal protein	921	4	33.3	123	2	E64418	conserved hypotet
849	4	33.3	116	2	UC5188	sporulation-specif	922	4	33.3	123	2	G71143	hypothetical prote
850	4	33.3	116	2	PC4228	N-acetylglucosamin	923	4	33.3	123	2	H75059	hypothetical prote
851	4	33.3	116	2	G70831	hypothetical prote	924	4	33.3	123	2	B75546	hypothetical prote
852	4	33.3	116	2	S70726	replication activa	925	4	33.3	123	2	G71189	hypothetical prote
853	4	33.3	116	2	T33195	hypothetical prote	926	4	33.3	123	2	C71423	hypothetical prote
854	4	33.3	116	2	H72489	hypothetical prote	927	4	33.3	123	2	A05125	hypothetical prote
855	4	33.3	117	1	GLHUEU	Ig heavy chain V-I	928	4	33.3	123	2	T20279	hypothetical prote
856	4	33.3	117	1	HVHU35	Ig heavy chain pre	929	4	33.3	124	1	TIBHB	trypsin inhibitor
857	4	33.3	117	1	HVHU35	Ig heavy chain pre	930	4	33.3	124	1	M1HUNL	Ig heavy chain V-I
858	4	33.3	117	2	T02872	probable lipid tra	931	4	33.3	124	1	M1HUST	Ig heavy chain V-I
859	4	33.3	117	2	S19669	Ig heavy chain V r	932	4	33.3	124	1	MNTHMS	nonstructural prot
860	4	33.3	117	2	S19670	Ig heavy chain V r	933	4	33.3	124	2	S19665	Ig heavy chain V r
861	4	33.3	117	2	A28846	Ig heavy chain pre	934	4	33.3	124	2	E72403	Ig heavy chain V r
862	4	33.3	117	2	PT0371	Ig gamma chain pre	935	4	33.3	124	2	B70472	conserved hypotet
863	4	33.3	117	2	S21668	Ig kappa chain V r	936	4	33.3	124	2	H72263	conserved hypotet
864	4	33.3	117	2	S31680	Ig heavy chain V r	937	4	33.3	124	2	G75116	hypothetical prote
865	4	33.3	117	2	S18551	Ig heavy chain V r	938	4	33.3	124	2	B82196	RsB1 protein VC14
866	4	33.3	117	2	S18553	Ig heavy chain V r	939	4	33.3	124	2	T36292	hypothetical prote
867	4	33.3	117	2	S18552	Ig heavy chain V r	940	4	33.3	125	1	S1PSDR	steroid Delta-15om
868	4	33.3	117	2	B82614	hypothetical prote	941	4	33.3	125	1	HVHUMO	Ig heavy chain V-I
869	4	33.3	117	2	H86640	ribonuclease P (EC	942	4	33.3	125	2	PH1410	Ig heavy chain V r
870	4	33.3	117	2	E75537	conserved hypotet	943	4	33.3	125	2	PH0957	Ig heavy chain V r
871	4	33.3	118	2	PH1666	Ig heavy chain V r	944	4	33.3	125	2	A64502	hypothetical prote
872	4	33.3	118	2	S36265	Ig heavy chain V r	945	4	33.3	125	2	S78697	probable export pr
873	4	33.3	118	2	S12440	Ig lambda chain (M	946	4	33.3	125	2	H86722	hypothetical prote
874	4	33.3	118	2	S12441	Ig lambda chain (K	947	4	33.3	125	2	T38537	probable single-st
875	4	33.3	118	2	S12442	Ig lambda chain (K	948	4	33.3	126	2	PH1417	Ig heavy chain V r
876	4	33.3	118	2	T35747	hypothetical prote	949	4	33.3	126	2	PH1418	Ig heavy chain V r
877	4	33.3	118	2	T07905	low-carbon dioxide	950	4	33.3	126	2	PH1424	Ig heavy chain V r
878	4	33.3	118	2	S34346	hypothetical prote	951	4	33.3	126	2	PH1412	Ig heavy chain V r
879	4	33.3	119	2	S08077	Ig kappa chain pre	952	4	33.3	126	2	B33548	Ig heavy chain V r
880	4	33.3	119	2	JN0295	Ig heavy chain V-D	953	4	33.3	126	2	T24181	Ig heavy chain V-I
881	4	33.3	119	2	PH0961	Ig heavy chain V r	954	4	33.3	126	2	A56657	hypothetical prote
882	4	33.3	119	2	S44106	Ig heavy chain V-D	955	4	33.3	126	2	G83571	pFEMP2/MESA protei
883	4	33.3	119	2	S58445	lipooprotein D - Sa	956	4	33.3	126	2	H75433	conserved hypotet
884	4	33.3	119	2	T00151	hypothetical prote	957	4	33.3	127	1	C64140	hypothetical prote
885	4	33.3	119	2	E83674	hypothetical prote	958	4	33.3	127	2	PH1414	probable glycyL ra
886	4	33.3	119	2	G86843	hypothetical prote	959	4	33.3	127	2	PH1415	Ig heavy chain V r
887	4	33.3	119	2	D64002	hypothetical prote	960	4	33.3	127	2	PH1421	Ig heavy chain V r
888	4	33.3	119	2	E72526	hypothetical prote	961	4	33.3	127	2	PH1411	Ig heavy chain V r
889	4	33.3	120	2	S21667	Ig kappa chain V r	962	4	33.3	127	2	PH1420	Ig heavy chain V r
890	4	33.3	120	2	S21666	Ig kappa chain V r	963	4	33.3	127	2	PH0955	Ig heavy chain V r
891	4	33.3	120	2	PH0962	Ig heavy chain V r	964	4	33.3	127	2	S34014	Ig heavy chain V r
892	4	33.3	120	2	T29774	hypothetical prote	965	4	33.3	127	2	S00653	Ig heavy chain V r
893	4	33.3	120	2	D71039	hypothetical prote	966	4	33.3	127	2	F82197	chlrophyll a/b-b1
894	4	33.3	120	2	T23978	hypothetical prote	967	4	33.3	127	2	RSB2	protein VC14
895	4	33.3	120	2	C85849	unknown protein en	968	4	33.3	127	2	G83870	arabinogalactan-pr
896	4	33.3	120	2	A12539	hypothetical prote	969	4	33.3	128	2	169024	inner spore coat p
897	4	33.3	121	2	E70313	histidine triad-li	970	4	33.3	128	2	S16685	MHC sex-limited pr
898	4	33.3	121	2	A29678	T-cell receptor ga	971	4	33.3	128	2	PH0952	Ig heavy chain V r
899	4	33.3	121	2	S20783	Ig heavy chain V r	972	4	33.3	128	2	S76468	Ig heavy chain V r
900	4	33.3	121	2	A49590	Ig heavy chain V r	973	4	33.3	128	2	T22276	hypothetical prote
901	4	33.3	121	2	UC4622	ribosomal phosphop	974	4	33.3	128	2	D75575	hypothetical prote
902	4	33.3	121	2	D75089	hypothetical prote	975	4	33.3	128	2	S76955	hypothetical prote
903	4	33.3	121	2	T32888	hypothetical prote	976	4	33.3	128	2	D72481	hypothetical prote
904	4	33.3	121	2	S74021	hypothetical prote	977	4	33.3	128	2	H70435	hypothetical prote
905	4	33.3	121	2	S75660	hypothetical prote	978	4	33.3	128	2	T15911	hypothetical prote

687	4	33.3	101	2	S12424	Ig heavy chain V r
688	4	33.3	101	2	S12428	Ig heavy chain V r
689	4	33.3	101	2	S12431	hypothetical prote
690	4	33.3	101	2	H65009	hypothetical prote
691	4	33.3	101	2	B72079	hypothetical prote
692	4	33.3	101	2	F86544	hypothetical prote
693	4	33.3	101	2	S76550	hypothetical prote
694	4	33.3	101	2	T19560	hypothetical prote
695	4	33.3	102	1	W7MLDP	E7 protein - deer
696	4	33.3	102	1	W7MLDP	E7 protein - Europ
697	4	33.3	102	2	PH1232	Ig heavy chain V r
698	4	33.3	102	2	PH1234	Ig heavy chain V r
699	4	33.3	102	2	PH1235	Ig heavy chain V r
700	4	33.3	102	2	PH1237	Ig heavy chain V r
701	4	33.3	102	2	PH1238	Ig heavy chain V r
702	4	33.3	102	2	PH1239	Ig heavy chain V r
703	4	33.3	102	2	PH1240	Ig heavy chain V r
704	4	33.3	102	2	PH1243	Ig heavy chain V r
705	4	33.3	102	2	PH1248	Ig heavy chain V r
706	4	33.3	102	2	PH1262	Ig heavy chain V r
707	4	33.3	102	2	PH1264	Ig heavy chain V r
708	4	33.3	102	2	PH1268	Ig heavy chain V r
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711	4	33.3	102	2	PH1281	Ig heavy chain V r
712	4	33.3	102	2	PH1244	Ig heavy chain V r
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714	4	33.3	102	2	PH1249	Ig heavy chain V r
715	4	33.3	102	2	PH1252	Ig heavy chain V r
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718	4	33.3	102	2	PH1259	Ig heavy chain V r
719	4	33.3	102	2	PH1260	Ig heavy chain V r
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722	4	33.3	102	2	PH1266	Ig heavy chain V r
723	4	33.3	102	2	PH1267	Ig heavy chain V r
724	4	33.3	102	2	PH1275	Ig heavy chain V r
725	4	33.3	102	2	PH1278	Ig heavy chain V r
726	4	33.3	102	2	PH1279	Ig heavy chain V r
727	4	33.3	102	2	PH1281	Ig heavy chain V r
728	4	33.3	102	2	PH1282	Ig heavy chain V r
729	4	33.3	102	2	PH1271	Ig heavy chain V r
730	4	33.3	102	2	PH1272	Ig heavy chain V r
731	4	33.3	102	2	PH1273	Ig heavy chain V r
732	4	33.3	102	2	H69841	conserved hypotet
733	4	33.3	102	2	S28361	hypothetical prote
734	4	33.3	102	2	F84709	probable glutaredo
735	4	33.3	102	2	T39407	hypothetical prote
736	4	33.3	103	2	B26167	Ig lambda chain C
737	4	33.3	103	2	B60608	myosin heavy chain
738	4	33.3	103	2	T51238	parvalbumin - mous
739	4	33.3	103	2	T51248	ACBP/DBI - duck
740	4	33.3	103	2	G75513	conserved hypotet
741	4	33.3	104	1	GMBO	gastlin precursor
742	4	33.3	104	1	PH1665	Ig heavy chain V r
743	4	33.3	104	2	S69899	Ig heavy chain V r
744	4	33.3	104	2	J00863	hypothetical 11.6k
745	4	33.3	104	2	A83871	hypothetical prote
746	4	33.3	104	2	B81787	probable inner mem
747	4	33.3	105	1	L2HU	Ig lambda chain C
748	4	33.3	105	2	S47430	spdd protein - Str
749	4	33.3	105	2	T36213	hypothetical prote
750	4	33.3	105	2	T49655	modc protein - Bra
751	4	33.3	105	2	S27493	KO2D10.3 protein -
752	4	33.3	105	2	S44838	outer membrane pro
753	4	33.3	106	1	D82734	cytochrome c3 - De
754	4	33.3	106	1	CCDV3S	Ig kappa-2 chain C
755	4	33.3	106	1	K4RBS	nonstructural prot
756	4	33.3	106	1	B48354	Ig heavy chain V r
757	4	33.3	106	2	S20774	Ig kappa-B4 chain
758	4	33.3	106	2	G20907	hypothetical prote
759	4	33.3	106	2	G72632	
760	4	33.3	106	2	S64649	RBL2 protein - yea
761	4	33.3	107	2	S40290	protein-tyrosine-p
762	4	33.3	107	2	S76718	hypothetical prote
763	4	33.3	107	2	T45621	hypothetical prote
764	4	33.3	107	2	B64845	hypothetical prote
765	4	33.3	107	2	F83182	hypothetical prote
766	4	33.3	107	2	E83040	DNA-binding protei
767	4	33.3	107	2	G81080	hypothetical prote
768	4	33.3	108	2	PH1664	Ig heavy chain V r
769	4	33.3	108	2	C49056	T-cell receptor al
770	4	33.3	108	2	S51687	protein-tyrosine-p
771	4	33.3	108	2	T51146	ring-box protein 1
772	4	33.3	108	2	A86675	hypothetical prote
773	4	33.3	108	2	S61627	hypothetical prote
774	4	33.3	108	2	D72662	hypothetical prote
775	4	33.3	108	2	A72516	hypothetical prote
776	4	33.3	108	2	T26681	hypothetical prote
777	4	33.3	108	2	F84479	En/Spm-like transp
778	4	33.3	108	2	A72704	hypothetical prote
779	4	33.3	109	2	S16437	ribulose-bisphosph
780	4	33.3	109	2	PH1672	Ig heavy chain V r
781	4	33.3	109	2	PH1671	Ig heavy chain V r
782	4	33.3	109	2	PH1671	Ig heavy chain V r
783	4	33.3	109	2	D71279	hypothetical prote
784	4	33.3	109	2	F84010	hypothetical prote
785	4	33.3	109	2	T34639	hypothetical prote
786	4	33.3	109	2	T51864	probable heat-shoc
787	4	33.3	110	1	A37414	parvalbumin - mous
788	4	33.3	110	2	PH1669	Ig heavy chain V r
789	4	33.3	110	2	PH1670	Ig heavy chain V r
790	4	33.3	110	2	G70305	ribosomal protein
791	4	33.3	110	2	S50100	transcription-asso
792	4	33.3	110	2	A55263	hypothetical 12.8k
793	4	33.3	110	2	JV0102	hypothetical prote
794	4	33.3	110	2	T30125	probable PE protel
795	4	33.3	110	2	D70610	hypothetical prote
796	4	33.3	110	2	T27823	hypothetical prote
797	4	33.3	110	2	T46071	hypothetical prote
798	4	33.3	110	2	T48382	hypothetical prote
799	4	33.3	110	2	G72696	hypothetical prote
800	4	33.3	111	2	S21925	Ig heavy chain V r
801	4	33.3	111	2	T16302	hypothetical prote
802	4	33.3	111	2	A81673	conserved hypotet
803	4	33.3	111	2	S17200	protein kinase (EC
804	4	33.3	111	2	D72646	hypothetical prote
805	4	33.3	112	2	E82540	conserved hypotet
806	4	33.3	112	2	S30269	protein hdbp precu
807	4	33.3	112	2	F86023	hypothetical prote
808	4	33.3	112	2	S77344	carbon dioxido con
809	4	33.3	112	2	A71515	hypothetical prote
810	4	33.3	112	2	T01515	hypothetical prote
811	4	33.3	112	2	A64976	galactitol utilisz
812	4	33.3	112	2	C83938	hypothetical prote
813	4	33.3	112	2	C86415	hypothetical prote
814	4	33.3	113	1	RKWT55	ribulose-bisphosph
815	4	33.3	113	1	R6DOP1	acidic ribosomal p
816	4	33.3	113	2	PH1428	Ig heavy chain V r
817	4	33.3	113	2	PH1663	Ig heavy chain V r
818	4	33.3	113	2	PC1281	MS5 protein - hepa
819	4	33.3	113	2	S11640	hypothetical prote
820	4	33.3	113	2	A56581	major basic nuclea
821	4	33.3	113	2	A83429	hypothetical prote
822	4	33.3	113	2	D83320	hypothetical prote
823	4	33.3	113	2	A83697	hypothetical prote
824	4	33.3	113	2	T08623	hypothetical prote
825	4	33.3	113	2	S66805	probable sensor xl
826	4	33.3	113	2	T49533	hypothetical prote
827	4	33.3	113	2	PC2231	hobo-like transpos
828	4	33.3	113	2	B71088	hypothetical prote
829	4	33.3	114	2	S07898	endothelin 3 - rab
830	4	33.3	114	2	PH1667	Ig heavy chain V r
831	4	33.3	114	2	A34567	beta-microseminopr
832	4	33.3	115	1	JN0318	guanylin precursor

541	4	33.3	65	2	S35024	hypothetical prote	614	4	33.3	86	2	F85748	unknown protein en
542	4	33.3	66	2	S65971	yydD protein - Bac	615	4	33.3	86	2	A70005	conserved hypotet
543	4	33.3	66	2	PN0644	hypothetical prote	616	4	33.3	87	1	PF0ECP	antifreeze protein
544	4	33.3	67	2	I47395	histone H1 I-1 (cl	617	4	33.3	87	2	B31075	antifreeze protein
545	4	33.3	67	2	G72372	hypothetical prote	618	4	33.3	87	2	C31075	antifreeze protein
546	4	33.3	67	2	A64321	archaeal histone -	619	4	33.3	87	2	T27141	hypothetical prote
547	4	33.3	67	2	A64457	archaeal histone -	620	4	33.3	87	2	S27040	hypothetical prote
548	4	33.3	67	2	D64416	archaeal histone -	621	4	33.3	88	1	O6BP77	Vat-1 protein - Pa
549	4	33.3	67	2	D64513	archaeal histone -	622	4	33.3	88	2	S60815	gene 6.7 protein -
550	4	33.3	68	1	A55457	lactococcal histone	623	4	33.3	88	2	P85717	M protein precursor
551	4	33.3	68	2	JH0100	lactococcal histone	624	4	33.3	88	2	P85717	hypothetical prote
552	4	33.3	68	2	S37677	lactococcal histone	625	4	33.3	88	2	A85743	hypothetical prote
553	4	33.3	69	2	S28195	small acid-soluble	626	4	33.3	88	2	A83659	Bm1p2 protein - Ba
554	4	33.3	69	2	PC7068	tissue kallikrein	627	4	33.3	89	2	A83659	hypothetical prote
555	4	33.3	69	2	AB2489	synaptotagmin II p	628	4	33.3	90	2	B69352	hypothetical prote
556	4	33.3	69	2	AB2489	cold shock DNA-bn	629	4	33.3	90	2	S78047	ribosomal protein
557	4	33.3	69	2	H69383	conserved hypotet	630	4	33.3	90	2	B71983	similar to late em
558	4	33.3	70	2	S74243	50S ribosomal prot	631	4	33.3	91	2	D86503	hypothetical prote
559	4	33.3	70	2	A47395	6-phosphofructo-2-	632	4	33.3	91	2	B96574	hypothetical prote
560	4	33.3	70	2	S56769	histone H1 I-1 (N-	633	4	33.3	92	2	C72119	hypothetical prote
561	4	33.3	71	2	C82807	RNA-directed RNA p	634	4	33.3	92	2	C82174	ribosomal protein
562	4	33.3	71	2	T45384	30S ribosomal prot	635	4	33.3	92	2	PA4620	similar to late em
563	4	33.3	72	2	S28196	ribosomal protein	636	4	33.3	92	2	T34744	hypothetical prote
564	4	33.3	72	2	PQ0613	tissue kallikrein	637	4	33.3	92	2	T51187	small zinc finger-
565	4	33.3	72	2	PQ0613	ferritin 5 - compe	638	4	33.3	92	2	JU0239	nuclear matrix pro
566	4	33.3	72	2	PQ0615	ferritin 2 - compe	639	4	33.3	93	2	B85537	unknown [imported]
567	4	33.3	72	2	S30980	ferritin 1 - compe	640	4	33.3	93	2	T45593	small zinc finger-
568	4	33.3	72	2	S75519	gene 35 protein -	641	4	33.3	94	2	SA9470	hypothetical prote
569	4	33.3	72	2	E69386	hypothetical prote	642	4	33.3	94	2	B84539	hypothetical prote
570	4	33.3	72	2	E69523	hypothetical prote	643	4	33.3	94	2	G36943	chemoreceptor prot
571	4	33.3	72	2	T48971	hypothetical prote	644	4	33.3	95	2	SA43903	hypothetical prote
572	4	33.3	73	2	D69319	conserved hypotet	645	4	33.3	95	2	S68231	PHG22 protein prec
573	4	33.3	73	2	T44814	hypothetical prote	646	4	33.3	95	2	B32830	homeotic protein H
574	4	33.3	73	2	H69035	conserved hypotet	647	4	33.3	95	2	A56644	inverted repeat co
575	4	33.3	73	2	G64443	hypothetical prote	648	4	33.3	95	2	H81119	conserved hypotet
576	4	33.3	73	2	T20911	hypothetical prote	649	4	33.3	95	2	G81901	hypothetical prote
577	4	33.3	73	2	E82788	hypothetical prote	650	4	33.3	95	2	C69905	hypothetical prote
578	4	33.3	74	2	E69028	hypothetical prote	651	4	33.3	96	2	S10069	regulatory protein
579	4	33.3	75	2	T12080	low molecularweig	652	4	33.3	96	2	T16179	hypothetical prote
580	4	33.3	75	2	C85636	hypothetical prote	653	4	33.3	97	1	USBSBW	small acid-soluble
581	4	33.3	75	2	A64842	hypothetical prote	654	4	33.3	97	2	PH0870	Ig heavy chain v r
582	4	33.3	76	2	T17673	yeast protein - Bsc	655	4	33.3	97	2	I51262	Ig heavy chain v r
583	4	33.3	76	2	B83402	hypothetical prote	656	4	33.3	97	2	A69061	aggrecan chondroit
584	4	33.3	76	2	A75309	hypothetical prote	657	4	33.3	98	2	PH1429	hypothetical prote
585	4	33.3	76	2	I39960	hypothetical prote	658	4	33.3	98	2	PH1274	Ig heavy chain v r
586	4	33.3	77	2	H69328	hypothetical prote	659	4	33.3	98	2	PH0877	Ig heavy chain v r
587	4	33.3	77	2	D85940	nifu protein (nifu	660	4	33.3	98	2	A30523	Ig heavy chain v r
588	4	33.3	77	2	S00970	hypothetical prote	661	4	33.3	98	2	PH0871	Ig heavy chain v r
589	4	33.3	77	2	E82612	krclal protein - pl	662	4	33.3	98	2	S24680	Ig heavy chain v1
590	4	33.3	78	2	S61468	hypothetical prote	663	4	33.3	98	2	S46463	Ig heavy chain v1
591	4	33.3	78	2	G71720	p83/100 protein -	664	4	33.3	98	2	S26910	Ig heavy chain v r
592	4	33.3	78	2	S72745	hypothetical prote	665	4	33.3	98	2	S26914	Ig heavy chain v r
593	4	33.3	78	2	T16325	B117_F2_71 protei	666	4	33.3	98	2	S26918	Ig heavy chain v r
594	4	33.3	79	2	T30118	hypothetical prote	667	4	33.3	98	2	S26938	Ig heavy chain v r
595	4	33.3	80	1	RHIDLS	hypothetical prote	668	4	33.3	98	2	S26909	Ig heavy chain v r
596	4	33.3	80	2	F72306	gonadoliberin I pr	669	4	33.3	98	2	S26919	Ig heavy chain v r
597	4	33.3	80	2	D75366	conserved hypotet	670	4	33.3	98	2	S26913	Ig heavy chain v r
598	4	33.3	81	2	T29888	hypothetical prote	671	4	33.3	98	2	S26912	Ig heavy chain v r
599	4	33.3	82	2	S37173	hypothetical prote	672	4	33.3	98	2	S26911	Ig heavy chain v r
600	4	33.3	82	2	G82366	ribosomal protein	673	4	33.3	98	2	S26920	Ig heavy chain v r
601	4	33.3	82	2	T29889	tata protein VC008	674	4	33.3	98	2	S26921	Ig heavy chain v r
602	4	33.3	82	2	T29893	hypothetical prote	675	4	33.3	98	2	S26915	Ig heavy chain v r
603	4	33.3	82	2	T29891	hypothetical prote	676	4	33.3	98	2	S26907	Ig heavy chain v r
604	4	33.3	82	2	T33088	hypothetical prote	677	4	33.3	98	2	I49562	Ig heavy chain v r
605	4	33.3	83	2	C47188	hypothetical prote	678	4	33.3	98	2	S22592	alpha-1 type III c
606	4	33.3	83	2	T08238	MHC class II histo	679	4	33.3	98	2	T24286	hypothetical prote
607	4	33.3	83	2	J01124	gas-vesicle operon	680	4	33.3	99	1	OCQYBW	hypothetical prote
608	4	33.3	84	2	AS3012	serum response fac	681	4	33.3	99	2	H69000	translation initia
609	4	33.3	84	2	T09540	proline rich prote	682	4	33.3	99	2	C29826	hypothetical t1k p
610	4	33.3	84	2	S61465	p83/100 protein -	683	4	33.3	100	2	T08763	hypothetical prote
611	4	33.3	84	2	S61466	p83/100 protein -	684	4	33.3	100	2	B72540	hypothetical prote
612	4	33.3	84	2	T47420	hypothetical prote	685	4	33.3	100	2	B49598	hypothetical prote
613	4	33.3	84	2	E82709	hypothetical prote	686	4	33.3	100	2	S77878	hypothetical prote

395	5	41.7	1070	2	T25836	hypothetical prote	468	5	41.7	2292	2	S55401	capsid polypepten
396	5	41.7	1071	2	T34385	hypothetical prote	469	5	41.7	2325	2	T02235	acetyl-CoA carboxy
397	5	41.7	1072	2	T04926	starch synthase ho	470	5	41.7	2447	2	T16870	hypothetical prote
398	5	41.7	1073	2	T01955	hypothetical prote	471	5	41.7	2476	2	T34022	zonadhesin - pig
399	5	41.7	1092	2	T33717	carbamoyl-phosphat	472	5	41.7	2541	2	T29340	hypothetical prote
400	5	41.7	1093	2	T50652	AP-3 complex beta-3	473	5	41.7	2796	2	JC4743	fatty-acid synthas
401	5	41.7	1094	2	T50651	AP-3 complex beta-3	474	5	41.7	3131	2	T39553	vacuolar protein s
402	5	41.7	1098	2	S38100	hypothetical prote	475	5	41.7	3131	2	S39842	enantiin synthetas
403	5	41.7	1105	2	T18295	Ap-3 adaptor compl	476	5	41.7	3133	2	S52093	hemocytin - silkw
404	5	41.7	1108	2	T38673	probable transcrip	477	5	41.7	4162	2	T42633	connectin/titin -
405	5	41.7	1113	2	H84105	hypothetical prote	478	5	41.7	4957	2	T03455	ALR protein - huma
406	5	41.7	1119	2	T50995	related to cytoske	479	5	41.7	5262	2	T03454	ALR protein - huma
407	5	41.7	1123	2	S36846	myosin-binding pro	480	5	41.7	6642	2	T29757	protein UNC-89 - C
408	5	41.7	1127	1	E71156	endopeptidase Ia h	481	5	41.7	6839	2	S57242	twitchin (similarl
409	5	41.7	1132	2	B82538	ribonuclease E Xp2	482	5	41.7	7160	2	T27935	hypothetical prote
410	5	41.7	1138	2	S24614	myosin-binding pro	483	4	33.3	12	2	A33099	163k exomarginen
411	5	41.7	1150	1	A53289	kinesin-like prote	484	4	33.3	21	1	A35225	conanotkin T - con
412	5	41.7	1171	1	Q0K8FP	pyruvate (flavodox	485	4	33.3	22	2	C39800	calcium-activated
413	5	41.7	1172	2	F84572	probable cadmlum-t	486	4	33.3	23	2	F61491	seed protein ws-6
414	5	41.7	1196	2	T23832	protein-tyrosine k	487	4	33.3	23	2	PS0446	potassium channel
415	5	41.7	1199	2	S20969	AF-4 protein, spli	488	4	33.3	27	2	S55234	flavodoxin isoform
416	5	41.7	1210	2	I39410	serine/proline-ric	489	4	33.3	30	2	B60291	30k serine protein
417	5	41.7	1213	2	A58198	web1 protein homol	490	4	33.3	32	2	S21245	H+-transporting At
418	5	41.7	1217	2	T25894	hypothetical prote	491	4	33.3	32	2	S13897	alkaline phosphata
419	5	41.7	1224	2	T40765	probable membrane	492	4	33.3	33	2	I22565	R-phycoerythrin ga
420	5	41.7	1228	2	S59681	hypothetical prote	493	4	33.3	36	2	I57728	phosphatase - Escheric
421	5	41.7	1233	2	S56271	hypothetical prote	494	4	33.3	38	2	S40096	chlorophyll a/b-D1
422	5	41.7	1240	2	T04193	delta endotoxin -	495	4	33.3	38	2	T31479	hypothetical prote
423	5	41.7	1245	2	T18211	neutonal cell cycl	496	4	33.3	40	2	B69408	hypothetical prote
424	5	41.7	1251	2	A56677	phospholipase C (E	497	4	33.3	41	2	B54357	muconate cyclisom
425	5	41.7	1252	2	S02004	structural polypro	498	4	33.3	41	4	I68622	hypothetical myell
426	5	41.7	1253	1	VHW	1-phosphatidylinos	499	4	33.3	42	2	A47116	trifolliotoxin precu
427	5	41.7	1265	2	A34163	insulin receptor-t	500	4	33.3	44	1	MMWZK4	K4 protein - vacci
428	5	41.7	1268	2	B36502	C-terminal domain-	501	4	33.3	44	2	S56313	GutB-2a protein
429	5	41.7	1268	2	T31420	transferrin-like p	502	4	33.3	45	2	T33464	hypothetical prote
430	5	41.7	1274	2	T10729	probable calmoduli	503	4	33.3	47	2	E47395	histone H1 II-1 (c
431	5	41.7	1276	2	T02711	chromosomal protei	504	4	33.3	48	1	TZAR2	toxin RpiI - sea a
432	5	41.7	1290	2	A55094	insulin receptor-t	505	4	33.3	48	2	JN0355	neurotoxin I - sea
433	5	41.7	1300	2	A36502	acetyl-CoA carboxy	506	4	33.3	48	2	T12940	hypothetical prote
434	5	41.7	1306	2	S42659	nuclear pore membr	507	4	33.3	49	2	S39857	ribosomal protein
435	5	41.7	1337	2	A53824	hypothetical prote	508	4	33.3	49	2	B56448	collin-like prote
436	5	41.7	1341	2	T17885	cell surface antiq	509	4	33.3	49	2	B86888	50S ribosomal prot
437	5	41.7	1415	2	T21244	hypothetical prote	510	4	33.3	49	2	PC4007	hypothetical prote
438	5	41.7	1418	2	T37264	zyg-9 protein - Ca	511	4	33.3	50	2	B60718	phospholipase A2 h
439	5	41.7	1440	2	T27942	lin-15B protein -	512	4	33.3	50	2	F84075	hypothetical prote
440	5	41.7	1472	2	A26122	alpha-2-macroglobu	513	4	33.3	51	2	S47401	outer membrane pro
441	5	41.7	1473	2	A35186	sallivary agglutini	514	4	33.3	52	2	A57336	ropA protein - Khl
442	5	41.7	1534	2	A56734	ribosome receptor,	515	4	33.3	52	2	A38942	chemoreceptor prot
443	5	41.7	1536	2	A43607	cell surface antiq	516	4	33.3	52	2	A69330	ISORF2-like protei
444	5	41.7	1582	2	T15308	hypothetical prote	517	4	33.3	52	2	T00141	hypothetical prote
445	5	41.7	1625	2	T02921	acetyl-CoA carboxy	518	4	33.3	53	2	S66602	aldehyde oxidase (
446	5	41.7	1637	1	IUYMAP	adhesin P1 precurs	519	4	33.3	53	2	F47395	histone H1 II-1 (c
447	5	41.7	1635	2	A41480	adhesin P1, group	520	4	33.3	53	2	B47395	histone H1 II-1 (c
448	5	41.7	1684	2	JW0057	gravin - human	521	4	33.3	53	2	C47395	histone H1 II-1 (c
449	5	41.7	1685	2	T02750	acetyl-CoA carboxy	522	4	33.3	53	2	D47395	histone H1 II-2 (c
450	5	41.7	1698	2	T13800	coracle gene prote	523	4	33.3	53	2	G47395	histone H1 II-2 (c
451	5	41.7	1711	2	T31337	1,4-beta-glucanase	524	4	33.3	53	2	A72614	hypothetical prote
452	5	41.7	1723	2	S58880	receptor DSC-205 -	525	4	33.3	54	2	B36943	chemoreceptor prot
453	5	41.7	1785	2	A45546	major merozoite su	526	4	33.3	55	2	T03337	gene e30 protein -
454	5	41.7	1794	2	T38459	hypothetical diver	527	4	33.3	56	2	I56605	I7 alpha-hydroxya
455	5	41.7	1819	2	A71928	cag island protein	528	4	33.3	56	2	B64368	hypothetical prote
456	5	41.7	1846	2	T10670	hypothetical prote	529	4	33.3	58	2	I79344	interferon alpha O
457	5	41.7	1912	2	T29088	vitellogenin I pre	530	4	33.3	59	2	JT0289	phosphoprotein Pp3
458	5	41.7	1927	2	G64585	cag pathogenicity	531	4	33.3	60	2	B70306	conserved hypotet
459	5	41.7	1928	2	S46773	myosin heavy chain	532	4	33.3	60	2	S53364	mucin 5AC (clone J
460	5	41.7	1963	2	T49914	callose synthase c	533	4	33.3	61	2	T43672	hypothetical prote
461	5	41.7	2144	2	S71490	ashl protein - fru	534	4	33.3	62	1	CCBO17	ubiquinol--cytochr
462	5	41.7	2254	2	D86215	protein T6D22.14 l	535	4	33.3	62	2	T44918	hypothetical prote
463	5	41.7	2272	2	T18572	gag, pol and env p	536	4	33.3	62	2	T26847	hypothetical prote
464	5	41.7	2290	1	GNNYE	genome polypepten	537	4	33.3	63	2	E31075	antifreeze protein
465	5	41.7	2292	1	GNNYED	genome polypepten	538	4	33.3	64	2	D31075	antifreeze protein
466	5	41.7	2292	1	GNNYEB	genome polypepten	539	4	33.3	64	2	H82849	hypothetical prote
467	5	41.7	2292	2	S35961	capsid polypepten	540	4	33.3	65	2	G69542	hypothetical prote

249	5	41.7	518	2	S36472	L2 protein - human	322	5	41.7	691	2	H81313	ATP-dependent DNA
250	5	41.7	519	2	S23796	modifier-3 protein	323	5	41.7	700	2	T13577	hypothetical prote
251	5	41.7	519	2	T45038	hypothetical prote	324	5	41.7	701	1	S33709	DHR39-short protei
252	5	41.7	525	1	PIWUa5	L1 protein - human	325	5	41.7	707	2	JC2218	procollagen C-endo
253	5	41.7	528	2	E86795	unknown protein F2	326	5	41.7	711	2	A85352	calpastatin, cardil
254	5	41.7	530	2	D83291	probable MFS trans	327	5	41.7	713	2	A28706	procollagen C-endo
255	5	41.7	532	2	S40983	hypothetical prote	328	5	41.7	730	1	BMHU1	hypothetical prote
256	5	41.7	534	2	C69146	hypothetical prote	329	5	41.7	739	2	T29407	hypothetical prote
257	5	41.7	537	2	D86520	CTP synthetase [im	330	5	41.7	746	2	T19287	glucan 1,4-alpha-g
258	5	41.7	537	2	A72103	CTP synthetase - C	331	5	41.7	748	2	T49633	hypothetical prote
259	5	41.7	537	2	E81568	CTP synthase CP052	332	5	41.7	748	2	S54505	hypothetical prote
260	5	41.7	537	2	E96606	hypothetical prote	333	5	41.7	750	2	H70628	probable pknq prot
261	5	41.7	539	2	I49065	lymphoid-restrict	334	5	41.7	752	1	S51866	HPR1 protein - yea
262	5	41.7	539	2	T02508	hypothetical prote	335	5	41.7	755	2	S42462	structural polypro
263	5	41.7	542	2	T29707	hypothetical prote	336	5	41.7	763	2	T44735	serine/threonine-s
264	5	41.7	543	2	T00513	cytochrome P450 ho	337	5	41.7	767	2	S63220	probable membrane
265	5	41.7	546	2	S36450	L1 protein - human	338	5	41.7	768	2	T37601	probable transcript
266	5	41.7	547	2	B56573	nuclear pore compl	339	5	41.7	771	2	T26176	hypothetical prote
267	5	41.7	550	2	C86704	conserved hypotat	340	5	41.7	775	2	E83400	pyrroloquinoline q
268	5	41.7	553	2	C75318	hypothetical prote	341	5	41.7	781	1	S64576	hypothetical prote
269	5	41.7	556	2	D86262	hypothetical prote	342	5	41.7	792	2	S20554	pyruvate, water dik
270	5	41.7	556	2	T47511	probable transport	343	5	41.7	792	2	E85778	phosphoenolpyruvat
271	5	41.7	557	2	A70480	cardamoyl-phosphat	344	5	41.7	794	2	T37989	DNA mismatch repai
272	5	41.7	557	2	B83962	hypothetical prote	345	5	41.7	806	2	H70647	probable NADH dehy
273	5	41.7	557	2	A00629	protein-tyrosine k	346	5	41.7	808	1	S33708	nuclear steroid/ch
274	5	41.7	558	2	E86016	probable enzyme z4	347	5	41.7	811	2	PN0689	connectin 1 - chic
275	5	41.7	558	2	S75104	hypothetical prote	348	5	41.7	815	2	H96494	protein F7F22.2 [i
276	5	41.7	562	2	G84221	NADH dehydrogenase	349	5	41.7	816	2	T17257	hypothetical prote
277	5	41.7	566	2	C70482	repair excision nu	350	5	41.7	817	2	S51342	verpitolin - yeast
278	5	41.7	567	2	B86481	hypothetical prote	351	5	41.7	822	2	G69010	conserved hypotet
279	5	41.7	570	2	F70332	proline-CRMA synth	352	5	41.7	823	1	A58788	procollagen C-endo
280	5	41.7	572	1	FOHYH	retrovirus-related	353	5	41.7	829	2	T33283	hypothetical prote
281	5	41.7	573	2	T21653	hypothetical prote	354	5	41.7	834	2	E69380	methyl-accepting c
282	5	41.7	573	2	S66710	probable membrane	355	5	41.7	835	2	S11442	livaslin Yersinia
283	5	41.7	574	1	S76132	protein kinase pkn	356	5	41.7	835	2	C86444	hypothetical prote
284	5	41.7	578	2	T33916	hypothetical prote	357	5	41.7	842	2	S49124	carbon-monoxide de
285	5	41.7	580	2	C96597	Rubisco subunit b1	358	5	41.7	865	2	A47282	calcium-binding pr
286	5	41.7	581	2	E75383	conserved hypotet	359	5	41.7	871	2	H81430	translaton Initia
287	5	41.7	583	2	S01301	lamin I-III - Afri	360	5	41.7	871	2	D86355	protein T16E15.12
288	5	41.7	583	2	T30131	hypothetical prote	361	5	41.7	873	2	A47283	calphothin - fruit
289	5	41.7	585	2	E85809	hypothetical prote	362	5	41.7	877	2	E81847	pyruvate dehydroge
290	5	41.7	587	2	F85084	probable ath1a-11	363	5	41.7	887	2	E81094	pyruvate dehydroge
291	5	41.7	599	2	D81367	heat shock pyruvate	364	5	41.7	899	2	S51341	S501 protein - yea
292	5	41.7	601	1	A64222	gene NDI intron 4	365	5	41.7	900	1	GNNYV	genome polyprotein
293	5	41.7	603	2	S06059	probable amino aci	366	5	41.7	912	2	H71931	hypothetical prote
294	5	41.7	604	2	S54032	stmr protein - Str	367	5	41.7	919	2	C66578	YopC/gen secretion
295	5	41.7	604	2	S25203	cadmium efflux ATP	368	5	41.7	919	2	F72045	type III secretion
296	5	41.7	605	2	E69153	probable amino aci	369	5	41.7	920	5	T43263	probable excludu
297	5	41.7	609	2	S45930	theonine--tRNA li	370	5	41.7	925	2	T33732	hypothetical prote
298	5	41.7	612	2	G71972	probable exocyst c	371	5	41.7	929	2	G71420	protein F7G19.9 [i
299	5	41.7	612	2	C64535	hypothetical 68.5K	372	5	41.7	930	2	A25923	progesterone recep
300	5	41.7	615	2	T37981	probable exocyst c	373	5	41.7	931	2	D86222	protein F7G19.9 [i
301	5	41.7	622	2	A64980	hypothetical 68.5K	374	5	41.7	933	1	QRHUP	progesterone recep
302	5	41.7	634	1	MIWL51	El protein - human	375	5	41.7	940	2	T01834	hypothetical prote
303	5	41.7	634	2	I49642	estrogen-responsiv	376	5	41.7	951	2	T08987	probable cadmium-t
304	5	41.7	637	2	S74677	hypothetical prote	377	5	41.7	954	2	S57108	hypothetical prote
305	5	41.7	641	2	T03095	homeoprotein Sail	378	5	41.7	958	2	S47179	hypothetical prote
306	5	41.7	643	1	DIEC36	DNA-directed DNA p	379	5	41.7	969	2	A75634	McB-related prote
307	5	41.7	643	1	G85344	hypothetical prote	380	5	41.7	980	2	S71090	peroxisome biogene
308	5	41.7	646	2	G69871	hypothetical prote	381	5	41.7	982	2	T43699	DNA mismatch repai
309	5	41.7	649	2	JN0809	drebrin E (clone 9	382	5	41.7	986	1	B58788	procollagen C-endo
310	5	41.7	651	2	T15624	hypothetical prote	383	5	41.7	990	2	I15168	nucleolar phosphop
311	5	41.7	651	2	T21175	hypothetical prote	384	5	41.7	990	2	T12678	hypothetical prote
312	5	41.7	651	2	T14763	hypothetical prote	385	5	41.7	991	2	I49540	procollagen C-endo
313	5	41.7	654	1	HMIVC8	hemagglutinin prec	386	5	41.7	998	2	H75005	ATP-dependent prot
314	5	41.7	655	2	S07412	hemagglutinin-este	387	5	41.7	1000	2	B72385	hypothetical prote
315	5	41.7	662	2	T20570	hypothetical prote	388	5	41.7	1001	2	T00532	probable cadmium-t
316	5	41.7	668	2	C71365	probable excludu	389	5	41.7	1001	2	T29105	myosin-B - Toxopla
317	5	41.7	668	2	H86729	exinuclease ABC s	390	5	41.7	1002	2	S70292	FUN12 protein - ye
318	5	41.7	670	2	T34548	hypothetical prote	391	5	41.7	1004	2	H70673	probable mbtd prot
319	5	41.7	671	2	A38109	autolysin - Entero	392	5	41.7	1018	1	S73720	cytadherence acces
320	5	41.7	682	2	C84295	UDP-sugar hydrolas	393	5	41.7	1021	2	I39207	leukoocyte surface
321	5	41.7	683	2	E86358	hypothetical prote	394	5	41.7	1025	2	E86355	hypothetical prote

103	5	41.7	276	2	T29894	hypothetical prote
104	5	41.7	287	2	E75159	hypothetical prote
105	5	41.7	288	2	A81009	hypothetical prote
106	5	41.7	289	2	C70400	ferredoxin oxidore
107	5	41.7	291	2	S42420	replication protei
108	5	41.7	293	2	T09758	myb-related protei
109	5	41.7	293	2	A82690	phosphatidylerine
110	5	41.7	296	2	S46018	probable membrane
111	5	41.7	296	2	G84747	AT-hook DNA-bindin
112	5	41.7	298	2	T36900	probable integral
113	5	41.7	299	2	A82063	uroporphyrin-III C
114	5	41.7	302	2	A96841	hypothetical prote
115	5	41.7	305	2	JN0518	acylttransferase (E
116	5	41.7	305	2	F83966	dihydrocorate deh
117	5	41.7	307	1	S75769	hypothetical prote
118	5	41.7	308	2	E75409	probable antibioti
119	5	41.7	309	1	A25776	urate oxidase (EC
120	5	41.7	311	2	H84746	hypothetical prote
121	5	41.7	314	2	S22513	ethylene-forming e
122	5	41.7	315	2	T25171	hypothetical prote
123	5	41.7	315	2	T26422	hypothetical prote
124	5	41.7	318	2	T00112	glycosyltransferas
125	5	41.7	321	2	U80772	37k glycoprotein -
126	5	41.7	321	2	D70070	transcription regu
127	5	41.7	323	2	A31351	probable transmemb
128	5	41.7	325	2	D70666	probable modd prot
129	5	41.7	327	2	JC4195	36k hydrophobic nu
130	5	41.7	327	2	H82554	conserved hypothet
131	5	41.7	335	2	T31559	hypothetical prote
132	5	41.7	335	2	T31560	hypothetical prote
133	5	41.7	335	2	T31561	hypothetical prote
134	5	41.7	335	2	G75309	lytb protein - Del
135	5	41.7	335	2	H75518	probable cytochrom
136	5	41.7	335	2	T37262	probable tyrosine
137	5	41.7	336	1	B38274	Y box-binding prot
138	5	41.7	337	2	T46742	ornithine carboxam
139	5	41.7	339	2	G75529	peptide ABC transp
140	5	41.7	340	2	D86837	ornithine carboxam
141	5	41.7	342	2	T45456	probable membrane
142	5	41.7	343	2	T14245	NADH dehydrogenase
143	5	41.7	343	2	H82171	probable multidrug
144	5	41.7	346	2	S56655	tryptophan synthas
145	5	41.7	355	2	C70457	hypothetical prote
146	5	41.7	356	1	XNECHC	histidinol-phospha
147	5	41.7	356	2	D85827	histidinol-phospha
148	5	41.7	359	1	XNEBHC	histidinol-phospha
149	5	41.7	360	2	T26037	hypothetical prote
150	5	41.7	360	2	S32695	Wnt-2 protein - Ca
151	5	41.7	362	2	S24551	protein-tyrosine k
152	5	41.7	366	1	MNXRSD	sigma NS protein -
153	5	41.7	366	1	MNXRST	sigma NS protein -
154	5	41.7	366	1	MNXRST	sigma NS protein -
155	5	41.7	366	2	C27401	sigma NS protein -
156	5	41.7	366	2	S53073	hypothetical prote
157	5	41.7	367	1	A46355	site-specific DNA-
158	5	41.7	367	2	T18185	probable silte-spec
159	5	41.7	367	2	S46336	env polypeptide -
160	5	41.7	368	2	S06058	NADH dehydrogenase
161	5	41.7	375	2	T51333	transcription fact
162	5	41.7	376	2	S04497	surface antigen PA
163	5	41.7	379	2	A45443	tubulin--tyrosine
164	5	41.7	380	2	D84214	NADH dehydrogenase
165	5	41.7	386	2	S64614	probable membrane
166	5	41.7	389	2	D84068	RNA helicase BH334
167	5	41.7	390	2	F65048	multidrug resistan
168	5	41.7	390	2	F85916	multidrug resistan
169	5	41.7	391	2	I51097	thyroid hormone re
170	5	41.7	394	2	T18752	hypothetical prote
171	5	41.7	395	2	D83782	aspartate aminotra
172	5	41.7	402	2	JH0403	procollagen I C-pr
173	5	41.7	410	2	D70599	hypothetical prote
174	5	41.7	415	2	T20335	hypothetical prote
175	5	41.7	416	2	G69748	conserved hypothet
176	5	41.7	418	2	F83986	transporter BH2694
177	5	41.7	421	2	D81098	gcpe protein NM813
178	5	41.7	421	2	H81843	conserved hypothet
179	5	41.7	421	2	T14773	hypothetical prote
180	5	41.7	422	2	G70984	probable papas pro
181	5	41.7	423	2	H84257	Htt13 transducer I
182	5	41.7	423	2	T44258	transducer protein
183	5	41.7	423	2	S73020	hypothetical prote
184	5	41.7	428	2	S28468	mannose-1-phosphat
185	5	41.7	432	1	A41056	brachyury homolog
186	5	41.7	435	2	T19687	hypothetical prote
187	5	41.7	440	2	D64616	N-acetyluramoyl-L
188	5	41.7	442	2	D71481	probable trigger f
189	5	41.7	443	2	E71135	hypothetical prote
190	5	41.7	445	2	D71977	phosphoglucosamine
191	5	41.7	445	2	C38537	urec protein - Hel
192	5	41.7	448	2	B56558	retinoic acid rece
193	5	41.7	451	2	B96774	hypothetical prote
194	5	41.7	452	2	T38962	hypothetical prote
195	5	41.7	453	2	S40943	hypothetical prote
196	5	41.7	459	2	A41977	retinoic acid rece
197	5	41.7	461	2	T42513	1D-myo-inositol-tr
198	5	41.7	462	2	B86262	hypothetical prote
199	5	41.7	464	2	A56558	retinoic acid rece
200	5	41.7	465	2	H82345	mannose-1-phosphat
201	5	41.7	469	2	H71897	probable probable
202	5	41.7	470	2	T15946	hypothetical prote
203	5	41.7	471	2	JC1403	glutamate--ammonia
204	5	41.7	473	2	D70405	glutamate--ammonia
205	5	41.7	473	2	S75141	glutamate--ammonia
206	5	41.7	474	2	H69761	conserved hypothet
207	5	41.7	474	2	T10271	capsid-associated
208	5	41.7	475	2	T44997	conserved hypothet
209	5	41.7	475	2	D86209	protein F22G5.18 I
210	5	41.7	475	2	A85523	hypothetical prote
211	5	41.7	476	2	B44997	merozoite surface
212	5	41.7	476	2	T25736	hypothetical prote
213	5	41.7	477	2	A75545	amidophosphoribosy
214	5	41.7	478	2	A32555	major merozoite su
215	5	41.7	482	2	A44997	merozoite surface
216	5	41.7	482	2	T32564	hypothetical prote
217	5	41.7	484	2	D65230	hypothetical 52.9
218	5	41.7	484	2	A86116	hypothetical prote
219	5	41.7	488	1	QOEBHS	alkaline exonuclea
220	5	41.7	488	2	T44030	alkaline exonuclea
221	5	41.7	488	2	T44215	alkaline exonuclea
222	5	41.7	488	2	F86209	protein F22G5.14 I
223	5	41.7	490	2	P00164	sucrose phosphoryl
224	5	41.7	492	2	T43859	uroporphyrinogen I
225	5	41.7	493	2	T12044	probable legumain
226	5	41.7	496	2	T30976	hypothetical prote
227	5	41.7	498	2	D64878	probable glutamate
228	5	41.7	498	2	G02421	nicotinic acetylch
229	5	41.7	498	2	G85755	glutamate--ammonia
230	5	41.7	500	2	S77243	hypothetical prote
231	5	41.7	501	2	T27513	hypothetical prote
232	5	41.7	504	2	T34995	probable integral
233	5	41.7	504	2	G02474	interferon regulat
234	5	41.7	505	2	T01667	gag polyprotein
235	5	41.7	505	2	B64560	poly E-rich protei
236	5	41.7	505	2	B46629	mucin 6, gastric (
237	5	41.7	507	2	G01614	zinc finger protei
238	5	41.7	508	2	T19350	hypothetical prote
239	5	41.7	509	1	S04346	steroid 17alpha-mo
240	5	41.7	509	2	S36572	LI protein - human
241	5	41.7	510	2	S53970	amidophosphoribosy
242	5	41.7	512	2	T33463	probable serine ca
243	5	41.7	514	1	PIWL8	LI protein - human
244	5	41.7	514	1	PIWL47	LI protein - human
245	5	41.7	516	1	PIWL5	LI protein - human
246	5	41.7	516	2	T09364	cytochrome P450 ho
247	5	41.7	517	2	S36496	LI protein - human
248	5	41.7	517	2	S36543	LI protein - human

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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:34:40 ; Search time 33.87 Seconds
(without alignments)
26.988 Million cell updates/sec

Title: US-09-372-036-30
Perfect score: 12
Sequence: 1 SRPVAPTOEVKK 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	484	2	A14187	protein p60 precu
2	58.3	227	2	D81259	probable tonb tran
3	50.0	102	2	E83231	hypothetical prote
4	50.0	116	2	T37186	probable regulator
5	50.0	155	2	S35162	SRP-21 protein - p
6	50.0	187	2	JC4806	core protein G - p
7	50.0	218	2	C68647	transcription regu
8	50.0	288	2	F71504	hypothetical prote
9	50.0	293	2	F75466	hypothetical prote
10	50.0	447	2	T34992	probable lipoprote
11	50.0	453	1	F64623	amidase - Helicoba
12	50.0	453	2	A71891	glu-tRNA amidotran
13	50.0	456	2	H85574	hypothetical prote
14	50.0	460	2	T33087	hypothetical prote
15	50.0	617	2	S42719	actin-binding prot
16	50.0	637	2	S66953	hypothetical prote
17	50.0	748	2	H84913	probable ATP-depen
18	50.0	985	1	VCLJSP	env polypeptide -
19	50.0	1133	2	T30302	P-type ATPase - Te
20	50.0	1230	2	E64664	outer membrane pro
21	50.0	75	2	E75264	hypothetical prote
22	50.0	82	2	T29802	hypothetical prote
23	50.0	88	2	T34429	hypothetical prote
24	50.0	102	2	B56581	major basic nuclea
25	50.0	103	1	K4RB	Ig kappa-B4 chain
26	50.0	104	2	F53275	Ig kappa-1 chain C
27	50.0	112	2	T14788	hypothetical prote
28	50.0	114	2	T08411	hypothetical prote
29	50.0	115	2	B49094	methylmalonyl-CoA

30	5	41.7	117	2	A72293	conserved hypothet
31	5	41.7	124	2	B86557	Dnak suppressor [I
32	5	41.7	124	2	A71518	probable dnak supp
33	5	41.7	124	2	G72066	dnak suppressor
34	5	41.7	124	2	T24876	hypothetical prote
35	5	41.7	126	2	I54454	Lymphocyte antigen
36	5	41.7	131	2	D86684	prophage p11 prote
37	5	41.7	132	2	B81600	conserved hypothet
38	5	41.7	133	2	T50083	probable cyclidine
39	5	41.7	134	2	B60497	MHC class II histo
40	5	41.7	134	2	A81676	conserved hypothet
41	5	41.7	141	2	E72580	hypothetical prote
42	5	41.7	147	2	G72384	conserved hypothet
43	5	41.7	147	2	T33327	hypothetical prote
44	5	41.7	157	2	T25638	hypothetical prote
45	5	41.7	161	2	C96568	hypothetical prote
46	5	41.7	165	2	S61230	cytochrome-c biosy
47	5	41.7	170	2	S11770	lma protein - Lis
48	5	41.7	174	2	S07291	repressor protein
49	5	41.7	175	2	D86639	hypothetical prote
50	5	41.7	175	2	T50849	hypothetical prote
51	5	41.7	177	1	S57789	hypothetical prote
52	5	41.7	178	2	S56300	hypothetical prote
53	5	41.7	179	2	G84789	hypothetical prote
54	5	41.7	185	2	H86513	elongation factor
55	5	41.7	185	2	G72110	translational elonga
56	5	41.7	185	2	D96572	protein F12M16.6 [
57	5	41.7	190	2	H75162	anthranilate synth
58	5	41.7	193	2	H86404	probable lipid tra
59	5	41.7	196	2	A41050	repressor protein
60	5	41.7	199	2	F68832	hypothetical prote
61	5	41.7	200	2	F64217	ribosomal protein
62	5	41.7	201	1	IMBPSB	immunity protein -
63	5	41.7	201	2	S69748	hypothetical prote
64	5	41.7	206	2	A71326	probable V-type At
65	5	41.7	206	2	H83587	conserved hypothet
66	5	41.7	209	2	S04827	gene 40A protein -
67	5	41.7	211	2	T22122	hypothetical prote
68	5	41.7	217	2	S10212	late 33k protein -
69	5	41.7	217	2	T37859	probable transcrip
70	5	41.7	218	2	G71260	probable ribulose-
71	5	41.7	221	2	H86860	protein serine/chr
72	5	41.7	223	2	G82478	hypothetical prote
73	5	41.7	224	2	A31459	MHC class II histo
74	5	41.7	224	2	T12797	immunity protein d
75	5	41.7	227	2	H71214	hypothetical prote
76	5	41.7	228	2	F75390	hypothetical prote
77	5	41.7	239	2	A27207	lysine kallikrein
78	5	41.7	241	2	S75154	urease accessory p
79	5	41.7	245	2	F71474	hypothetical prote
80	5	41.7	246	2	I40763	hypothetical prote
81	5	41.7	246	2	B81373	hypothetical prote
82	5	41.7	250	2	S62838	hypothetical prote
83	5	41.7	251	2	T45707	CHLOROPHYLL A-B BI
84	5	41.7	251	2	C84036	succinate dehydrog
85	5	41.7	252	2	A86449	hypothetical prote
86	5	41.7	253	2	E71198	hypothetical prote
87	5	41.7	253	2	A75159	hypothetical prote
88	5	41.7	254	2	T33323	protein-1-isoaspar
89	5	41.7	260	2	T18909	hypothetical prote
90	5	41.7	261	1	HLHDB	MHC class II histo
91	5	41.7	261	1	HLHUC	MHC class II histo
92	5	41.7	261	1	B37044	MHC class II histo
93	5	41.7	261	2	I54480	HLA DQ-beta - huma
94	5	41.7	261	2	T51222	hypothetical prote
95	5	41.7	263	2	C69887	hypothetical prote
96	5	41.7	264	2	C37386	hypothetical prote
97	5	41.7	264	2	S01922	hypothetical prote
98	5	41.7	267	2	T32063	hypothetical prote
99	5	41.7	268	2	D29312	MHC class II histo
100	5	41.7	269	2	I54432	MHC class II histo
101	5	41.7	271	2	T16590	hypothetical prote
102	5	41.7	276	2	S75249	esterase s110992 -

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PR 18-JUN-1999;	99US-0139456.	PR 18-AUG-1999;	99US-0149426.
PR 18-JUN-1999;	99US-0139457.	PR 20-AUG-1999;	99US-0149722.
PR 18-JUN-1999;	99US-0139458.	PR 20-AUG-1999;	99US-0149723.
PR 18-JUN-1999;	99US-0139459.	PR 20-AUG-1999;	99US-0149929.
PR 18-JUN-1999;	99US-0139460.	PR 23-AUG-1999;	99US-0149902.
PR 18-JUN-1999;	99US-0139461.	PR 23-AUG-1999;	99US-0149930.
PR 18-JUN-1999;	99US-0139462.	PR 25-AUG-1999;	99US-0150566.
PR 18-JUN-1999;	99US-0139463.	PR 26-AUG-1999;	99US-0150884.
PR 18-JUN-1999;	99US-0139750.	PR 27-AUG-1999;	99US-0151065.
PR 18-JUN-1999;	99US-0139763.	PR 27-AUG-1999;	99US-0151066.
PR 21-JUN-1999;	99US-0139817.	PR 27-AUG-1999;	99US-0151080.
PR 22-JUN-1999;	99US-0139899.	PR 30-AUG-1999;	99US-0151303.
PR 23-JUN-1999;	99US-0140353.	PR 31-AUG-1999;	99US-0151438.
PR 23-JUN-1999;	99US-0140354.	PR 01-SEP-1999;	99US-0151930.
PR 24-JUN-1999;	99US-0140695.	PR 07-SEP-1999;	99US-0152363.
PR 28-JUN-1999;	99US-0140823.	PR 10-SEP-1999;	99US-0153070.
PR 29-JUN-1999;	99US-0140991.	PR 13-SEP-1999;	99US-0153758.
PR 30-JUN-1999;	99US-0141287.	PR 15-SEP-1999;	99US-0154018.
PR 01-JUL-1999;	99US-0141842.	PR 16-SEP-1999;	99US-0154039.
PR 01-JUL-1999;	99US-0142154.	PR 20-SEP-1999;	99US-0154779.
PR 02-JUL-1999;	99US-0142055.	PR 22-SEP-1999;	99US-0155139.
PR 06-JUL-1999;	99US-0142390.	PR 23-SEP-1999;	99US-0155486.
PR 08-JUL-1999;	99US-0142803.	PR 24-SEP-1999;	99US-0155659.
PR 09-JUL-1999;	99US-0142920.	PR 28-SEP-1999;	99US-0156458.
PR 12-JUL-1999;	99US-0142977.	PR 29-SEP-1999;	99US-0156596.
PR 13-JUL-1999;	99US-0143542.	PR 04-OCT-1999;	99US-0157117.
PR 14-JUL-1999;	99US-0143624.	PR 05-OCT-1999;	99US-0157753.
PR 15-JUL-1999;	99US-0144005.	PR 06-OCT-1999;	99US-0157865.
PR 16-JUL-1999;	99US-0144085.	PR 07-OCT-1999;	99US-0158029.
PR 16-JUL-1999;	99US-0144086.	PR 08-OCT-1999;	99US-0158232.
PR 19-JUL-1999;	99US-0144325.	PR 12-OCT-1999;	99US-0158369.
PR 19-JUL-1999;	99US-0144331.	PR 13-OCT-1999;	99US-0159293.
PR 19-JUL-1999;	99US-0144332.	PR 13-OCT-1999;	99US-0159294.
PR 19-JUL-1999;	99US-0144333.	PR 13-OCT-1999;	99US-0159295.
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PR 20-JUL-1999;	99US-0144335.	PR 14-OCT-1999;	99US-0159330.
PR 20-JUL-1999;	99US-0144632.	PR 14-OCT-1999;	99US-0159331.
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PR 21-JUL-1999;	99US-0144814.	PR 18-OCT-1999;	99US-0159638.
PR 21-JUL-1999;	99US-0145086.	PR 21-OCT-1999;	99US-0159584.
PR 21-JUL-1999;	99US-0145087.	PR 21-OCT-1999;	99US-0160741.
PR 22-JUL-1999;	99US-0145085.	PR 21-OCT-1999;	99US-0160767.
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PR 03-AUG-1999;	99US-0147038.	PR 28-OCT-1999;	99US-0161995.
PR 04-AUG-1999;	99US-0147204.	PR 29-OCT-1999;	99US-0162142.
PR 04-AUG-1999;	99US-0147302.		
PR 05-AUG-1999;	99US-0147192.		
PR 05-AUG-1999;	99US-0147260.		
PR 06-AUG-1999;	99US-0147303.		
PR 06-AUG-1999;	99US-0147416.		
PR 09-AUG-1999;	99US-0147493.		
PR 09-AUG-1999;	99US-0147935.		
PR 10-AUG-1999;	99US-0148171.		
PR 11-AUG-1999;	99US-0148319.		
PR 12-AUG-1999;	99US-0148341.		
PR 13-AUG-1999;	99US-0148565.		
PR 13-AUG-1999;	99US-0148684.		
PR 16-AUG-1999;	99US-0149368.		
PR 17-AUG-1999;	99US-0149175.		

Query Match 41.7%; Score 5; DB 21; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RPVAP 6
Db 6 lrpvap 10

Search completed: August 15, 2001, 12:35:47
Job time: 172 sec

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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
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PR 12-OCT-1999; 99US-0158365.
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PR 21-OCT-1999; 99US-0160814.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 5; DB 21; Length 152;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
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Db 95 pvapt 99
RESULT 50
AAG12578
ID AAG12578 standard; Protein; 158 AA.
XX
AC AAG12578;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 11746.
XX
DE Zea mays protein fragment SEQ ID NO: 11746.
XX
KM Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130049.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.

Query Match 41.7%; Score 5; DB 21; Length 151;
Best Local Similarity 100.0%; Pred. No. 3,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 npvap 6
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DB 50 npvap 54

RESULT 49
AAG54453
ID AAG54453 standard; Protein; 152 AA.

XX AAG54453;

DT 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 69433.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132566.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

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PR 18-MAY-1999; 99US-0134768.

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PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

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PR 10-JUN-1999; 99US-0138540.

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PR 02-JUL-1999; 99US-0142055.
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PR 06-AUG-1999; 99US-0147416.
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 PR 25-AUG-1999; 99US-0150566.
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 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151338.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
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 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
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 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 41.78; Score 5; DB 21; Length 148;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 APR0E 9
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 Db 93 aptge 97

RESULT 48
 AAB43699
 ID AAB43699 standard; Protein; 151 AA.

AC AAB43699;

DT 08-FEB-2001 (first entry)

DE Human cancer associated protein sequence SEQ ID NO:1144.

XX Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnereary; immunomodulator;
 KW antidiabetic; antitastmatic; antirheumatic; antiarthritic; antiviral;
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
 KW dermatological; neuroprotective; thrombolytic; coagulant; neotropic;
 KW vasotropic; antiposietic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening.

OS Homo sapiens.

PN WO200055350-A1.

PD 21-SEP-2000.

PE 08-MAR-2000; 2000MO-US05882.

PF 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI; 2000-587533/55.

DR N-PSDB; AAC77908.

PT Novel isolated nucleic acids comprising sequences encoding peptides
 useful for treating or diagnosing e.g. cancer -

PS Claim 11; Page 1760-1761; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given
 XX in AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnereary; immunomodulator;
 CC antidiabetic; antitastmatic; antirheumatic; antiarthritic;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC neotropic; vasotropic; antiposietic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention.

XX Sequence 151 AA;

PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 5; DB 21; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APTOE 9
Db 93 aptge 97

RESULT 47
AAG53842

ID AAG53842 standard; Protein; 148 AA.

AC AAG53842;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68587.

XX protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OY 8 QEVK 12
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 Db 63 gevkk 67

RESULT 43

AAV36760
 ID AAV36760 standard; Protein; 135 AA.

XX
 AC AAV36760;

XX
 DT 07-OCT-1999 (first entry)

XX
 DE Amino acid sequence of a Chlamydia trachomatis protein.

XX
 DE Vaccine; eye disease; conventional trachoma; nongonococcal urethritis; genital diseases; perlethepatitis;
 KM paratrachoma; inclusion conjunctivitis; genital diseases; perlethepatitis;
 KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
 KM bartholinitis; pneumopathy; venereal lymphogranulomatosis.

XX
 OS Chlamydia trachomatis.

XX
 PN MO928475-A2.

XX
 PD 10-JUN-1999.

XX
 PF 27-NOV-1998; 98MO-IB01939.

XX
 PR 04-NOV-1998; 98US-0107077.

XX
 PR 28-NOV-1997; 97FR-0015041.
 PR 17-DEC-1997; 97FR-0016034.
 XX

PA (GEST) GENSET.
 XX
 PI Griffiths R;
 XX
 DR WPI; 1999-371125/31.

XX
 PT Genome sequence of Chlamydia trachomatis

PS
 Disclosure; Page 662-663; 1755pp; English.

CC AAV36754-Y37949 are encoded by open reading frames (ORFs) of the genome
 CC of Chlamydia trachomatis (see AA201425). The polypeptides can be used as
 CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nongonococcal urethritis,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC perlethepatitis, bartholinitis; pneumopathy in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the invention
 CC may be of use in treating these diseases.

XX
 SQ Sequence 135 AA;

Query Match 41.7%; Score 5; DB 20; Length 135;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QEVK 12
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 Db 42 gevkk 46

RESULT 44

AAAG08989
 ID AAAG08989 standard; Protein; 142 AA.

XX
 AC AAAG08989;

XX
 DT 17-OCT-2000 (first entry)

XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 6743.

XX
 DE Protein identification: signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.

XX
 OS Arabidopsis thaliana.

XX
 PN EP1033405-A2.

XX
 PD 06-SEP-2000.

XX
 PF 25-FEB-2000; 2000EP-0301439.

XX
 PR 25-FEB-1999; 99US-0121825.

XX
 PR 05-MAR-1999; 99US-0123180.

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PF 25-FEB-2000; 2000EP-0301439.
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PR 24-SEP-1999; 99US-0155659.


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XX DE Staphylococcus aureus protein of unknown function.
XX
XX DE Staphylococcus aureus protein; immune response induction; eye infection;
XX antibody production; T-cell immune response; gastrointestinal infection;
XX respiratory infection; inhibitor; bacterial infection; cardiac infection;
XX central nervous system; kidney infection; urinary tract infection;
XX antimicrobial compound identification; broad spectrum antibiotic;
XX therapy.
XX
XX OS Staphylococcus aureus.
XX
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..130
XX FT /note= "residues designated X are unspecified, and
XX FT represented as Xaa in the specification"
XX
XX PF EP841394-A2.
XX PD 13-MAY-1998.
XX
XX PF 24-SEP-1997; 97EP-0307485.
XX
XX PR 24-SEP-1996; 96US-0027032.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX PI Black MT, Burnham MKR, Hodgson JE, Knowles DFC;
XX PI Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M;
XX PI Ward JM;
XX
XX DR WPI: 1998-252940/23.
XX
XX DR N-PSDB; AAY3451.
XX
XX PT New nucleic acid sequences from Staphylococcus aureus WCHU29 -
XX PT useful in vaccines and for treatment of bacterial infections of e.g.
XX PT respiratory tract and central nervous system
XX
XX PS Claim 11: Page 312; 390pp; English.
XX
XX CC This sequence represents a Staphylococcus aureus protein of unknown
XX CC function, and is encoded by a DNA sequence of the invention.
XX CC The DNA sequences were isolated from Staphylococcus aureus WCHU29
XX CC (NCIMB 40771). Host cells containing the DNA sequences are used to
XX CC produce polypeptides or fragments. The proteins are used in the treatment
XX CC of disease, for inducing an immune response by administering them, to
XX CC produce antibody and/or T-cell immune response. Antagonists of the
XX CC proteins are used for the inhibition of bacterial polypeptides.
XX CC Conditions which may be treated include bacterial infections, especially
XX CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
XX CC urinary tract, skin, bones and joints. The proteins can also be used to
XX CC identify antimicrobial compounds which are broad spectrum antibiotics,
XX CC especially useful in the treatment of H. pylori infection.
XX
XX SQ Sequence 130 AA:

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Query Match 41.7%; Score 5; DB 19; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4 VAPRO 8
DB 108 vaprcq 112

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RESULT 41
ID AAY35155 standard; Protein: 132 AA.
AC AAY35155;
XX

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DT 13-SEP-1999 (first entry)
XX
XX DE Chlamydia pneumoniae transmembrane protein sequence.
XX
XX DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
XX vaccine; neutralising epitope.
XX
XX OS Chlamydia pneumoniae.
XX
XX PN W09927105-A2.
XX
XX PD 03-JUN-1999.
XX
XX PF 20-NOV-1998; 98WO-1B01890.
XX
XX PR 04-NOV-1998; 98US-0107078.
XX PR 21-NOV-1997; 97FR-0014673.
XX
XX PA (GEST ) GENSET.
XX
XX PI Griffiths R;
XX
XX DR WPI: 1999-357842/30.
XX
XX PT Genome sequence of Chlamydia pneumoniae
XX PT
XX PS Page 1021; Disclosure: 1912pp; English.
XX
XX CC AAY34584-Y35879 represent the proteins encoded by all the open reading
XX CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
XX CC C. pneumoniae causes respiratory disease such as pneumonia and
XX CC bronchitis and is thought to be a contributing factor in heart
XX CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX CC nodosum or pharyngitis. The polypeptides encoded by the open reading
XX CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
XX CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX CC nucleotide sequences can also be used as immunogenic compositions,
XX CC especially where the vector directs the expression of a neutralising
XX CC epitope of C. pneumoniae.
XX
XX SQ Sequence 132 AA:

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Query Match 41.7%; Score 5; DB 20; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 8 QEVKK 12
DB 39 gevkk 43

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RESULT 42
ID AAG59953 standard; Protein: 134 AA.
XX
XX AC AAG59953;
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XX DT 18-OCT-2000 (first entry)
XX
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 77605.
XX
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX
XX OS Arabidopsis thaliana.
XX
XX PN EP1033405-A2.
XX
XX PD 06-SEP-2000.
XX

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PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 5; DB 21; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
Db 68 pvapt 72

RESULT 40
AAW77657
ID AAW77657 standard; Protein: 130 AA.
XX AAW77657;
AC
XX
DT 30-OCT-1998 (first entry)
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KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KM antiviral; antibacterial; antifungal; antirhumatic; antihypoid;
 KM antinaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KM cardiovascular disease; diabetes mellitus; hypochyroidism; SCID; AIDS;
 KM cholesterol ester storage; systemic lupus erythematosus; infection;
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antinflammatory disease; coagulation;
 KM thrombosis; contraceptive.
 OS Homo sapiens.
 XX MO200058473-A2.
 PN 05-OCT-2000.
 PD 31-MAR-2000; 2000MO-US08621.
 PF 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX (CURA-) CURAGEN CORP.
 PA Shinkets RA, Leach M;
 XX MPI: 2000-602362/57.
 DR N-PSDB; AAC74473.
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX Claim 11; Page 449; 5507pp; English.
 XX AAC74446 to AAC77606 encode the proteins given in ABA40237 to ABA43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiparasitic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;
 CC antihypoid; and antinaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypochyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX Sequence 125 AA:
 SQ

Query Match 41.7%; Score 5; DB 21; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
 Db 14 tpvap 18

RESULT 39
 AAG54454
 ID AAG54454 standard; Protein; 125 AA.
 XX AAG54454;
 AC 18-OCT-2000 (first entry)
 DT 18-OCT-2000 (first entry)
 XX Zea mays protein fragment SEQ ID NO: 69434.
 DE Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence; corn.
 XX Zea mays subsp. mays.
 OS Zea mays subsp. mays.
 XX EPI033405-A2.
 PN 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-0301439.
 PF 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
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PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 5; DB 21; Length 121;
Best Local Similarity 100.0%; Pred. No. 2,7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVAPT 7
DB 64 pvapt 68

RESULT 38
AAB40264
ID AAB40264 standard; Protein; 125 AA.
XX
XX AAB40264;
AC
XX
XX
DT 08-FEB-2001 (first entry)
XX
XX Human ORFX ORF28 polypeptide sequence SEQ ID NO:56.
DE Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
KW vulnerability; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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Query Match 41.78; Score 5; DB 21; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 8 OEKK 12
DB 43 qevkk 47

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RESULT 37
AAG54455
ID AAG54455 standard; Protein: 121 AA.
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AC AAG54455;

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XX 18-OCT-2000 (first entry)
DT
XX
XX Zea mays protein fragment SEQ ID NO: 69435.
DE
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
PD
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PE
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 25-MAR-1999; 99US-0126264.
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PR 01-APR-1999; 99US-0127462.
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RESULT 36
AAG59954
ID AAG59954 standard: Protein; 114 AA.
XX
AC AAG59954;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77606.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PM EP103405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 5; DB 21; Length 114;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 OEKK 12
Db 43 gevkk 47
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PR 25-OCT-1999; 990S-0161404.
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PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161921.
PR 28-OCT-1999; 990S-0161922.
PR 28-OCT-1999; 990S-0161923.
PR 29-OCT-1999; 990S-0162142.

Query Match 41.7%; Score 5; DB 21; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
DB 83 stcpva 87

RESULT 34
AAV11113

ID AAV11113 standard; Protein; 114 AA.

XX AAV11113;

DT 08-JUN-1999 (first entry)

DE H. pylori ORF hp6e10363_30517031_f3_3 secreted protein.

XX Vaccine; probe: diagnostic; ORF; cell envelope protein;

KW secreted protein; cytoplasmic protein; cellular protein.

OS Helicobacter pylori.

PN WO9624475-A1.

PD 11-JUN-1998.

PF 05-DEC-1997; 97WO-US22104.

XX 14-JUL-1997; 97US-0891928.

PR 05-DEC-1996; 96US-0759625.

PR 25-MAR-1997; 97US-0823745.

XX (ASTR) ASTRA AB.

PI Alm RA, Castriotta LM, Dolg PC, Kabok Z, Smith D;

DR MPI; 1998-333051/29.

XX N-PSDB; AAX30642.

PT New isolated Helicobacter pylori nucleic acids - used to develop

PR products for the diagnosis, prevention and treatment of infection by

CC H. pylori and other Helicobacter species

PS Claims 37, 41; Page 278-279; 339pp; English.

XX Recombinant or substantially pure preparations of H. pylori polypeptides

CC are disclosed, together with the nucleic acids encoding them. In all,

CC 97 ORFs are shown. The proteins are variously cell envelope proteins,

CC cytoplasmic proteins, secreted proteins or other cellular proteins.

CC Vaccines containing the nucleic acids or proteins are claimed, as are

CC probes containing at least 8 nucleotides from the nucleic acid

CC sequences. The vaccines are useful for treating or reducing the risk of

CC H. pylori infections, and the probes can be used diagnostically for

CC detecting the presence of Helicobacter in a sample. The products are

CC also of use in screening for compounds having the ability to interfere

CC with the H. pylori life cycle or to inhibit H. pylori infection.

Query Match 41.7%; Score 5; DB 19; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
DB 99 stcpva 103

RESULT 35

AA612210

ID AAG12210 standard; Protein; 114 AA.

AC AAG12210;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 11234.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

PN EP103405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 990S-0121825.

PR 05-MAR-1999; 990S-0123180.

PR 09-MAR-1999; 990S-0122548.

PR 23-MAR-1999; 990S-0125788.

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 69350.
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154029.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158368.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.

XX 08-FEB-2001.
 PD 28-JUL-2000; 2000MO-US20538.
 PF 30-JUL-1999; 99US-0146634.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Resnick MA, Inga A;
 PI WPI; 2001-123321/13.
 DR
 XX
 PT New isolated mutated human p53 polypeptides for inducing toxicity in a
 PT cell, treating cancer and identifying compounds that mimic toxic or
 PT supertransactivating mutations -
 PS Claim 33; Page -; 144pp; English.
 CC The present invention provides a number of peptides derived from the
 CC human p53 protein and containing specific mutations. These are useful for
 CC isolating supertransactivating and toxic p53 mutants, and for inhibiting
 CC cell growth and treating cancer. The present sequence is a peptide
 CC derived from the wild-type human p53 protein shown in AAB72878.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from that given in Genbank acc. no. X02469 (see AAB72878).
 CC
 SO Sequence 102 AA;

Query Match 41.7%; Score 5; DB 22; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PVAPT 7
 |||||
 Db 23 pvapt 27

RESULT 30
 AAM75784
 ID AAM75784 standard; Protein; 107 AA.
 AC AAM75784;
 XX
 DT 18-JAN-1999 (first entry)
 XX
 DE Human lymphocyte surface receptor cytoplasmic domain.
 XX
 KW TAC1; transmembrane activator and CAML-interactor;
 KW calcium signal-modulating cyclophilin ligand; human;
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte;
 KW infection; cancer; rheumatoid arthritis; autoimmune disease;
 KW glomerulonephritis; immunosuppressive; graft versus host disease;
 KW transplant rejection; therapy; signal transduction.
 KW
 OS Homo sapiens.
 XX
 PN WO9839361-A1.
 PD 11-SEP-1998.
 XX
 PF 03-MAR-1998; 98MO-US04270.
 XX
 PR 03-MAR-1997; 97US-0810572.
 XX
 PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 XX
 PI Bram RJ, Von Bulow G;
 XX WPI; 1998-506346/43.
 DR N-PSDB; AAV57329.
 XX

PT New isolated transmembrane activator protein - used to develop
 PT products for treating e.g. infections, cancers, autoimmune and
 PT inflammatory conditions, transplant rejection or graft-versus-host
 PT disease
 PS Claim 6; Page 72; 89pp; English.
 CC This polypeptide comprises the C-terminal, i.e. cytoplasmic,
 CC domain of novel human transmembrane activator and CAML-interactor
 CC protein TAC1 (see AAM75783). TAC1 is a lymphocyte receptor protein
 CC that is involved in the calcium activation pathway. It is normally
 CC present in B-lymphocytes, and to a much lesser extent in immature
 CC T-lymphocytes, and can therefore be targeted to specifically
 CC regulate B cell responses without affecting T cell activity. The
 CC cytoplasmic domain of TAC1 mediates signal transduction via
 CC Ca2+-dependent and Ca2+-independent mechanisms and includes the
 CC CAML-binding region of TAC1. Methods are claimed for identifying a
 CC ligand for TAC1 and for identifying immunosuppressive drugs that
 CC selectively block the action of B lymphocytes without affecting
 CC mature T lymphocytes. TAC1 can be activated to increase immune
 CC system activity, e.g. for treating infections or cancers. It can
 CC be blocked to provide immunosuppression, e.g. for treating
 CC autoimmune and inflammatory conditions such as immune complex-
 CC induced vasculitis, glomerulonephritis, haemolytic anaemia,
 CC myasthenia gravis, type II collagen-induced arthritis, experimental
 CC allergic and hyperacute xenograft rejection, rheumatoid arthritis,
 CC systemic lupus erythematosus, transplant rejection, cancer or
 CC graft versus host disease.
 CC
 SO Sequence 107 AA;

Query Match 41.7%; Score 5; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 APTQE 9
 |||||
 Db 53 aptqe 57

RESULT 31
 AAG12211
 ID AAG12211 standard; Protein; 110 AA.
 AC AAG12211;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 11235.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 KW
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.

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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157153.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 41.7%; Score 5; DB 21; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 STRVA 5
DB 69 strva 73

```

RESULT 28

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AAV82898
ID AAV82898 standard; Protein; 101 AA.

```

```

AC AAV82898;

```

```

DT 24-JUL-2000 (first entry)

```

```

DE CUB domain from BMP-1 protein of mouse.

```

```

XX BPC-1; oncogene; oncogenic; cancer; prostate; bladder; antibody;
XX antisenese; vaccine; detection; prognosis; drug screening; BMP-1;
XX mouse.
XX
OS Mus musculus.
XX

```

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PN WO200009691-A2.
XX
XX 24-FEB-2000.
PD
XX 10-AUG-1999; 99WO-US18250.
PF
XX 10-AUG-1998; 98US-0095982.
XX
XX (UROG-) UROGENESYS INC.
PA (AFAR/) AFAR D E.
PA (HUBE/) HUBERT R. S.
PA (LEON/) LEONG K.
PA (RAIT/) RAITANO A. B.
PA (SAFE/) SAFEFRAN D. C.
PA (JAKO/) JAKOBOVITS A.
XX
XX Afar DE, Hubert RS, Leong K, Raitano AB, Safefran DC, Jakobovits A;
PI WPI; 2000-206006/18.
XX
XX New isolated BPC-1 polypeptides, useful for developing products for the
PT diagnosis, staging, prognosis and treatment of cancers, particularly
PT prostate or bladder cancer.
PS
XX Disclosure: Figure 3; 79pp; English.
XX
XX BPC-1 polypeptides and polynucleotides can be used for the detection
XX of BPC-1 polypeptides and polynucleotides in biological samples, this
XX is particularly useful for detecting cancers expressing BPC-1, e.g.
XX prostate cancer or bladder cancer. Antibodies directed against BPC-1
XX or antisense polynucleotides can be used for treating such cancers.
XX The BPC-1 polypeptides can also be used in vaccines for treating or
XX inhibiting the development of a cancer expressing BPC-1. The
XX polypeptides and polynucleotides can also be used for detection,
XX prognosis, drug screening and predicting susceptibility to developing
XX cancer. In normal human tissues BPC-1 is only expressed in certain
XX tissues of the brain, however, it is expressed at high levels in
XX prostate cancer cells and bladder cancer cells. The BPC-1 polypeptide
XX comprises a CUB domain which is expressed in prostate and bladder
XX carcinoma cells and which shows sequence similarity with CUB domains
XX from other known proteins. This is a CUB domain from the BMP-1
XX protein of a mouse. It shows 36.3% identity with the
XX BPC-1 CUB domain 3 in 102 residues overlap.
SQ Sequence 101 AA.

```

```

Query Match 41.7%; Score 5; DB 21; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 4 VAPTO 8
DB 23 vaptq 27

```

RESULT 29

```

AAB72875
ID AAB72875 standard; Protein; 102 AA.

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AC AAB72875;

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DT 09-MAY-2001 (first entry)

```

```

DE Human p53 A76T/V122A mutated peptide.

```

```

XX Human; p53 mutation; mutant; muten; gene therapy; supertransactivating;
XX cancer.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
XX WO200109325-A2.
XX

```

XX Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay: genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134321.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145513.
PR 27-JUL-1999; 99US-0145518.
PR 27-JUL-1999; 99US-0145519.
PR 28-JUL-1999; 99US-0145551.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147208.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.

PR 12-SEP-1997; 97US-0058668.
 PR 12-SEP-1997; 97US-0058669.
 PR 12-SEP-1997; 97US-0058750.
 PR 12-SEP-1997; 97US-0058751.
 PR 12-SEP-1997; 97US-0058752.
 PR 12-SEP-1997; 97US-0058753.
 PR 02-OCT-1997; 97US-0060834.
 PR 02-OCT-1997; 97US-0060841.
 PR 02-OCT-1997; 97US-0060844.
 PR 02-OCT-1997; 97US-0060845.
 PR 02-OCT-1997; 97US-0061059.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;
 PI Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
 PI Yu GJ;
 DR WPI; 1999-080881/07.
 DR N-PSDB; AAX04315.
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 PS
 PS Claim 11; Page 266; 380pp; English.
 CC
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC protein (e.g. AAX04302) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 86 novel genes and their fragments (nucleic
 CC acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 86
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAX04311 for described uses).
 CC
 CC Sequence 27 AA;
 SQ
 QY Query Match 41.7%; Score 5; DB 20; Length 27;
 Db Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PVAPT 7
 Db 9 pvapt 13
 XX
 XX
 XX
 XX
 DE Secreted protein encoded by gene 9 clone HSIDY06.
 XX
 XX
 KM Human; secreted protein; gene therapy; protein therapy; tissue; cancer;
 KM tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS;
 KM developmental abnormality; foetal deficiency; Alzheimer's disease;
 KM cognitive disorder; schizophrenia; immunological disorder; mood disorder;
 KM immune deficiency disease; respiratory disorder; arthritis; skeletal;
 KM haematopoietic disorder; neural; osteoporosis; metabolic disorders;
 KM cardiovascular; endocrine; gastrointestinal; asthma; diagnosis.
 XX
 XX Homo sapiens.
 OS

XX
 PN MO9901020-A2.
 XX
 PD 14-JAN-1999.
 XX
 PF 30-JUN-1998; 98WO-US13608.
 XX
 PR 12-SEP-1997; 97US-0058663.
 PR 01-JUL-1997; 97US-0051381.
 PR 01-JUL-1997; 97US-0051480.
 PR 12-SEP-1997; 97US-0058598.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Carter KC, Endress GA, Feng P, Rosen CA, Ruben SM;
 PI WPI; 1999-105683/09.
 DR N-PSDB; AAX22119.
 DR
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, immune deficiency diseases or blood
 PT disorders
 PS
 PS Claim 11; Page 146; 179pp; English.
 CC
 CC The invention relates to nucleic acid sequences (AAX22111 to AAX22134)
 CC encoding human secreted proteins (AAV01135 to AAV01158). The secreted
 CC protein gene sequences are deposited with the ATCC under deposit number
 CC ATCC 209118. Host cells comprising recombinant vectors containing the
 CC nucleic acid sequences are used for the recombinant production of the
 CC secreted proteins. The polynucleotide and amino acid sequences are useful
 CC for are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Pathological conditions can
 CC be also diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new
 CC polynucleotides. Specific uses are described for each of the
 CC polynucleotides, based on which tissues they are most highly expressed
 CC in, and include developing products for the diagnosis or treatment of
 CC cancer, tumours, developmental abnormalities and foetal deficiencies,
 CC autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders,
 CC schizophrenia, immunological disorders, immune deficiency diseases
 CC (AIDS), mood disorders, respiratory disorders, arthritis, asthma,
 CC haematopoietic disorders, neural disorders, skeletal disorders,
 CC osteoporosis, metabolic disorders, cardiovascular disorders, endocrine
 CC disorders or gastrointestinal disorders. The polypeptides are also useful
 CC for identifying their binding partners. The present sequence represents a
 CC human secreted protein (see descriptor line for gene number and clone
 CC identification).
 CC
 CC Sequence 45 AA;
 SQ
 QY Query Match 41.7%; Score 5; DB 20; Length 45;
 Db Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TPVAP 6
 Db 33 tpvap 37
 XX
 XX
 XX
 DE Secreted protein encoded by gene 9 clone HSIDY06.
 XX
 XX
 XX
 DE Secreted protein encoded by gene 9 clone HSIDY06.
 XX
 XX
 KM Human; secreted protein; gene therapy; protein therapy; tissue; cancer;
 KM tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS;
 KM developmental abnormality; foetal deficiency; Alzheimer's disease;
 KM cognitive disorder; schizophrenia; immunological disorder; mood disorder;
 KM immune deficiency disease; respiratory disorder; arthritis; skeletal;
 KM haematopoietic disorder; neural; osteoporosis; metabolic disorders;
 KM cardiovascular; endocrine; gastrointestinal; asthma; diagnosis.
 XX
 XX Homo sapiens.
 OS

XX 28-JUL-2000; 2000WO-US20538.
 PF
 XX
 PR 30-JUL-1999; 99US-0146634.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Resnick MA, Inga A;
 XX
 DR WPI; 2001-123321/13.
 XX
 PT New isolated mutated human p53 polypeptides for inducing toxicity in a
 PT cell, treating cancer and identifying compounds that mimic toxic or
 PT supertransactivating mutations -
 XX
 PS Claim 6; Page -: 144pp; English.
 XX
 CC The present invention provides a number of peptides derived from the
 CC human p53 protein and containing specific mutations. These are useful for
 CC isolating supertransactivating and toxic p53 mutants, and for inhibiting
 CC cell growth and treating cancer. The present sequence is a peptide
 CC derived from the wild-type human p53 protein shown in AAB72878.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from that given in Genbank acc. no. X02469 (see AAB72878).
 CC
 XX
 SQ Sequence 11 AA;

Query Match 41.7%; Score 5; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPT 7
 |||||
 Db 3 pvapt 7

RESULT 22

AAB79982
 ID AAB79982 standard; peptide: 25 AA.

XX
 AC AAB79982;

DT 01-MAY-1996 (first entry)

XX Signal transduction regulatory tyrosine kinase SH3 binding peptide.

DE
 XX
 KW Signal transduction; src-family thymidine kinase; lipid kinase;
 KW tyrosine kinase; adaptor; inhibition; regulation; immunodeficiency;
 KW allergy; inflammation; cancer; autoimmune disease; Epstein-Barr virus;
 KW immunoproliferative disease; bovine leukaemia virus; EBV; BLV;
 KW chronic fatigue syndrome; infectious mononucleosis.

XX Homo sapiens.

OS
 XX
 PN WO9524915-A1.

XX 21-SEP-1995.

PD
 XX 17-MAR-1995; 95WO-US03438.

PF
 XX 17-MAR-1994; 94US-0215116.

PR
 XX (NAJF-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

PI Cambier JC, Clark MR, Pleiman CM;

XX WPI; 1995-336809/43.

PT Regulation of signal transduction pathways, esp. involving
 PT src-family thymidine kinase - useful for treatment of allergic and
 PT inflammatory responses
 XX

PS Claim 10; Page 101; 131pp; English.

XX
 CC AAB79982-83 are signal transduction regulatory ARH1 peptides. They
 CC bind the SH3 domain of src family tyrosine kinases. ARH1 regulatory
 CC peptides are capable of regulating the activity of tyrosine kinases,
 CC lipid kinases, thymidine kinases and adaptor molecules. They can be
 CC used in a method to regulate signal transduction in such cells as
 CC B cells, T cells, macrophages, dendritic cells and pluripotent stem
 CC cells. The method allows regulation and treatment of allergic and
 CC inflammatory responses, autoimmune disease, immunodeficiency and
 CC immunoproliferative diseases, cancer and disease caused by
 CC Epstein-Barr and bovine leukaemia viruses.
 CC
 XX

SQ Sequence 25 AA;

Query Match 41.7%; Score 5; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPVAP 6
 |||||
 Db 16 tpvap 20

RESULT 23

AAB78130
 ID AAB78130 standard; Protein: 27 AA.

XX
 AC AAB78130;

DT 13-APR-1999 (first entry)

XX Human secreted protein encoded by gene 5 clone HRPB036.

DE
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

OS
 XX
 FH Key Location/Qualifiers

FT Misc-difference 27 /label= unknown

PN WO9856804-A1.

XX 17-DEC-1998.

PD 11-JUN-1998; 98WO-US12125.

PF 02-OCT-1997; 97US-0061060.

PR 13-JUN-1997; 97US-0049547.

PR 13-JUN-1997; 97US-0049548.

PR 13-JUN-1997; 97US-0049549.

PR 13-JUN-1997; 97US-0049550.

PR 13-JUN-1997; 97US-0049606.

PR 13-JUN-1997; 97US-0049607.

PR 13-JUN-1997; 97US-0049608.

PR 13-JUN-1997; 97US-0049609.

PR 13-JUN-1997; 97US-0049610.

PR 13-JUN-1997; 97US-0049611.

PR 13-JUN-1997; 97US-0050566.

PR 13-JUN-1997; 97US-0050901.

PR 13-JUN-1997; 97US-0052989.

PR 08-JUL-1997; 97US-0051919.

PR 18-AUG-1997; 97US-0055984.

PR 12-SEP-1997; 97US-0058665.

CC overall electrical charge in neutral media to ensure that the
CC lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents
CC examples of peptide epitopes used to generate the lipopeptides. These are
CC used in therapeutic or prophylactic compositions and vaccines to induce
CC specific immune responses against human immunodeficiency, hepatitis B or
CC papilloma viruses, p53 of melanoma or the malaria parasite.

XX Sequence 9 AA;

Query Match 41.7%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVK 11
|||||
DB 3 tqevk 7

RESULT 17

AAY40367
ID AAY40367 standard; Peptide; 9 AA.

XX AC AAY40367;

DT 19-NOV-1999 (first entry)

DE Amino acid sequence of a HIV-1 epitope.

KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
KM CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
KW vaccine; tumor; infection; immune response; cytokine profile;
KM acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
KW autoimmune disease.

XX OS Human immunodeficiency virus type 1.

PN FR2774687-A1.

XX 13-AUG-1999.

XX PF 06-FEB-1998; 98FR-0001439.

XX PR 06-FEB-1998; 98FR-0001439.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (INSP) INST PASTEUR LILLE.

XX PI Thlam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loinig E;

XX WPI: 1999-510734/43.

PT New lipopeptide comprising C-terminal interferon-gamma fragment with
PT attached lipophilic groups, used as interferon mimic, e.g. for treating
PT cancer or virus infection

PS Disclosure: Page 41; 53pp; French.

XX AAY40123-Y40379 represent epitopes that are able to activate cytotoxic
CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
CC B epitopes recognized by corresponding antibodies. The epitopes may be
CC used in the composition of the invention. The specification describes a
CC lipopeptide that has a peptide part derived from mammalian interferon
CC gamma (IFN γ) and one or more lipophilic parts comprising a linear or
CC branched, (unsaturated 4-20C hydrocarbon) chain or a steroid. The
CC lipopeptide mimics the activity of IFN γ . Compositions comprising the
CC lipopeptide are used to treat or prevent any condition that responds
CC to IFN γ , and as adjuvant for vaccines (particularly those directed
CC against tumors, viral or parasitic infections), to stimulate or
CC (re)orient the immune response between types 1 and 2 cytokine profiles.
CC Particular applications are treatment of infections (particularly
CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers

CC (particularly of kidney, cutaneous T cells or ovary, chronic
CC myelogenous leukemia or mesothelioma), allergy; and autoimmune
CC diseases.

XX Sequence 9 AA;

Query Match 41.7%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TOEVK 11
|||||
DB 3 tqevk 7

RESULT 18

AAY26859
ID AAY26859 standard; peptide; 9 AA.

XX AC AAY26859;

DT 14-SEP-1999 (first entry)

DE HIV-derived lipopeptide epitope #129 for mixed micelles.

KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
KM cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTLV; HBV;
KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
KM melanoma; Plasmodium falciparum; malaria.

XX OS Synthetic.

XX OS Human immunodeficiency virus type 1.

PN FR2771640-A1.

XX 04-JUN-1999.

XX PF 03-DEC-1997; 97FR-0015246.

XX PR 03-DEC-1997; 97FR-0015246.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (INSP) INST PASTEUR LILLE.

XX PI Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;

XX PI Tartar A, Wieruszski JM;

XX WPI: 1999-349509/30.

PT Immunogenic lipopeptide micelles - comprising lipopeptides
PT containing cytotoxic and helper T-lymphocyte epitopes

PS Disclosure: Page 36; 60pp; French.

XX The invention relates to the generation of mixed micelles or
CC microaggregates for inducing an immune response comprise: (a) a first
CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
CC and at least one lipid unit; and (b) a second lipopeptide comprising at
CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
CC different from that of the first lipopeptide. This peptide represents
CC an example of a lipopeptide epitope used in the invention and is derived
CC from a human immunodeficiency virus type 1 (HIV-1) protein. The
CC immunogenic lipopeptide micelles are used in vaccines, especially
CC against HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma
CC or Plasmodium falciparum malaria.

XX Sequence 9 AA;

Query Match 41.7%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;

PI Braun B, Johnson AD;
 XX MPI: 1999-263994/22.
 DR N-PSDB: AAX36552.
 PT Nucleic acid encoding Rbtl polypeptides of Candida albicans
 PS Claim 28; Fig 3b; 82pp; English.
 XX This sequence is the Candida albicans Rbtl protein of the invention.
 CC The Rbtl gene and its fragments are useful for detecting or quantifying
 CC C. albicans nucleic acid in hybridization or amplification methods; as
 CC therapeutic agents; as indicators of TUP1 gene function (and thus of
 CC pathogenic potential); as a polypeptide processing signal or template for
 CC various functional domains of Rbtl. Plasmids containing the Rbtl gene can
 CC be used as vaccines. Rbtl is used to detect or quantify specific
 CC antibodies against Rbtl, while antibodies against Rbtl can be used to
 CC detect Rbtl in standard immunoassays. Rbtl can also be used for drug
 CC screening, rational drug design and identification of proteins that
 CC interact physically with Rbtl. Cells that express Rbtl can be used to
 CC screen for agents that control virulence in C. albicans. Antibodies
 CC against Rbtl may be used to purify Rbtl and to raise anti-idiotypic
 CC antibodies. Modulation of Rbtl function, specifically by disrupting the
 CC corresponding gene, is used to inhibit virulence of C. albicans. The Rbtl
 CC gene and protein allow diagnosis of infection without the need for
 CC culturing and microscopic examination. The presence of Rbtl indicates
 CC lack of TUP1 activity and/or filamentous growth, and also the degree of
 CC virulence and/or resistance/susceptibility to particular antibiotics, for
 CC prognosis or selection of appropriate treatments.
 XX Sequence 750 AA;
 SQ
 Query Match 50.0%; Score 6; DB 20; Length 750;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STPVAP 6
 DB 650 stpvap 655
 RESULT 13
 AAW98275
 ID AAW98275 standard; Protein; 1230 AA.
 XX
 AC AAW98275;
 XX
 DT 31-MAR-1999 (first entry)
 XX
 DE H. pylori GHP0 690 protein.
 XX
 KM GHP0 protein; Helicobacter infection; gastroduodenal disease; gastritis;
 KM peptic ulcer disease.
 XX
 OS Helicobacter pylori.
 XX
 PN W09843478-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 01-APR-1998; 98WO-US06371.
 XX
 PR 29-JUL-1997; 97US-0902615.
 PR 01-APR-1997; 97US-0833457.
 PR 24-JUN-1997; 97US-0881227.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (INMR) MERIEUX ORAYAX PASTEUR MERIEUX SERUMS.
 XX
 PI Al-Garawi A, Kleantous H, Miller C, Oomen RP, Tomb J;
 XX MPI: 1998-542293/46.

DR N-PSDB: AAX13994.
 XX
 PT New isolated Helicobacter polynucleotides - used to develop products
 PT for the diagnosis, prevention and treatment of Helicobacter
 PT infections and gastrointestinal diseases
 PS Claim 8; Page 301-306; 2054pp; English.
 XX
 CC This sequence represents a Helicobacter pylori GHP0 protein of the
 CC invention. The polypeptides can be used for preventing or treating
 CC Helicobacter infections, and gastroduodenal diseases associated with
 CC these infections, including acute, chronic, and atrophic gastritis, and
 CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
 CC used for the production of antibodies. The products can also be used for
 CC detection and diagnosis.
 XX
 SQ Sequence 1230 AA;
 QY 7 TQEVK 12
 DB 173 tqevk 178
 RESULT 14
 AAY21365
 ID AAY21365 standard; Protein; 7 AA.
 XX
 AC AAY21365;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human HUPF-I mutant protein fragment 17.
 XX
 KW Human; beta-amyloid precursor protein; beta-Ap; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 02-APR-1998; 98WO-1B00705.
 XX
 PR 10-APR-1997; 97US-0043163.
 XX
 PA (UYUT-) RIJKSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 DR MPI: 1998-609901/51.
 DR N-PSDB: AAX75768.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type

PI	Griffals R;
XX	
DR	WPI: 1999-371125/31.
XX	
PT	Genome sequence of Chlamydia trachomatis
PS	Disclosure: Page 1323-1324, 1755pp; English.
XX	
CC	AAV36754-v37949 are encoded by open reading frames (ORFs) of the genome
CC	of Chlamydia trachomatis (see AA01425). The polypeptides can be used as
CC	vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC	can also be used to control growth of the microorganism. Chlamydia
CC	trachomatis is responsible for a large number of diseases, e.g. eye
CC	diseases such as conventional trachoma, nongonococcal trachoma,
CC	paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC	nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC	perithelitis, Bartholinitis; pneumonia in breast feeding infants;
CC	and venereal lymphogranulomatosis. The polypeptides of the invention
CC	may be of use in treating these diseases.
XX	
SO	Sequence 157 AA;
XX	
QY	1 STPVAP 6
DB	14 stpvap 19
XX	
RESULT 11	
AA041666	
ID	AA041666 standard; Protein: 343 AA.
XX	
AA041666	
DT	08-FEB-2001 (first entry)
XX	
DE	Human ORFX ORF1430 polypeptide sequence SEQ ID NO:2860.
XX	
KW	Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
KW	vulnerary; antiparasitic; antiparkinsonian; neuroprotective;
KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW	antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KW	antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW	cholesterol ester storage; systemic lupus erythematosus; infection;
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW	thrombosis; contraceptive.
XX	
OS	Homo sapiens.
XX	
PN	WO200058473-A2.
XX	
PD	05-OCT-2000.
XX	
PE	31-MAR-2000; 2000WO-US08621.
XX	
PR	31-MAR-1999; 99US-0127607.
PR	02-APR-1999; 99US-0127636.
PR	05-APR-1999; 99US-0127728.
PR	30-MAR-2000; 2000US-0340763.
XX	
PA	(CURA-) CURAGEN CORP.
XX	

```

PI ShImkets RA, Leach M;
XX
XX WPI: 2000-602362/57.
DR
DR N-PSDB; AAC75875.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
PS
PS Claim 11: Page 2100-2101; 5507pp; English.
XX
XX AAC77446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORF open reading frames 1 to 3161. The ORF
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antiproliferic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiallergic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antihypoid; and antihaemetic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORF-associated disorder. The
CC pathological conditions associated with an ORF-associated disorder. The
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCIP), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 343 AA;
SQ

Query Match 50.0%; Score 6; DB 21; Length 343;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 TPVAPT 7
Db 289 lPvapt 294
|||||

RESULT 12
ID AAY05477 standard; Protein; 750 AA.
XX
XX AAY05477;
AC
XX
XX 07-JUL-1999 (first entry)
DT
XX
XX C. albicans Rbcl protein sequence.
DE
XX
XX Rbcl; detection; Tup1 gene function; pathogenic potential; vaccine;
KW virulence inhibitor; infection; diagnosis; filamentous growth;
XX antibiotic resistance.
XX
XX Candida albicans.
OS
XX
XX MO9918115-A1.
PN
XX
XX 15-APR-1999.
PD
XX
XX 02-OCT-1998; 98WO-US20655.
PF
XX
XX 01-OCT-1998; 98US-0165239.
PR
XX 02-OCT-1997; 97US-0061058.
PR
XX 18-DEC-1997; 97US-0068065.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX

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Db      1 pcfewkk 7
|||||
RESULT  8
AAK54615
ID      AAK54615 standard; Protein; 6 AA.
XX
AC      AAK54615;
XX
DT      16-JUN-1994 (first entry)
XX
DE      Listeria p60 peptide epitope.
XX
KW      Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX
OS      Synthetic.
XX
PN      DEA318450-A.
XX
PD      16-DEC-1993.
XX
PF      03-JUN-1993; 93DE-4318450.
XX
PR      11-JUN-1992; 92DE-4219111.
PR      25-NOV-1992; 92DE-4239567.
XX
PA      (MERE ) MERCK PATENT GMBH.
XX
PI      Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
PI      Hofmann G, Bubert A, Goebel W, Koehler S;
XX
DR      WPI; 1993-406956/51.
XX
PT      New primers for PCR detection of Listeria - including individual
PT      species, also new peptide(s) for raising antibodies for
PT      immunochemical detection
XX
PS      Disclosure; Page 3; 19pp; German.
XX
CC      The sequence is that of a Listeria p60 peptide epitope which
CC      which may be used in the prodn. of antibodies for the detection
CC      of Listeria by immunoassay (partic. ELISA). It may be used as
CC      part of a method that allows determination of individual Listeria
CC      species, esp. L. monocytogenes.
XX
SQ      Sequence 6 AA;

Query Match      50.0%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 PVAPRQ 8
DB      1 pvpapcq 6
|||||

RESULT  9
AAK45159
ID      AAK45159 standard; Protein; 20 AA.
XX
AC      AAK45159;
XX
DT      16-JUN-1994 (first entry)
XX
DE      Listeria p60 peptide epitope.
XX
KW      Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers

```

```

FT      Region      1..7
FT      /note= "opt. 0-7 amino acid residues"
FT      Region      14..20
FT      /note= "opt. 0-7 amino acid residues"
XX
PN      DEA318450-A.
XX
PD      16-DEC-1993.
XX
PF      03-JUN-1993; 93DE-4318450.
XX
PR      11-JUN-1992; 92DE-4219111.
PR      25-NOV-1992; 92DE-4239567.
XX
PA      (MERE ) MERCK PATENT GMBH.
XX
PI      Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
PI      Hofmann G, Bubert A, Goebel W, Koehler S;
XX
DR      WPI; 1993-406956/51.
XX
PT      New primers for PCR detection of Listeria - including individual
PT      species, also new peptide(s) for raising antibodies for
PT      immunochemical detection
XX
PS      Claim 3; Page 4; 19pp; German.
XX
CC      The sequence is that of a Listeria p60 peptide epitope which
CC      which may be used in the prodn. of antibodies for the detection
CC      of Listeria by immunoassay (partic. ELISA). It may be used as
CC      part of a method that allows determination of individual Listeria
CC      species, esp. L. monocytogenes.
XX
SQ      Sequence 20 AA;

Query Match      50.0%; Score 6; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 PVAPRQ 8
DB      8 pvpapcq 13
|||||

RESULT  10
AAK37718
ID      AAK37718 standard; Protein; 157 AA.
XX
AC      AAK37718;
XX
DT      07-OCT-1999 (first entry)
XX
DE      Amino acid sequence of a Chlamydia trachomatis protein.
XX
KW      Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW      paratrachoma; inclusion conjunctivitis; genital disease; perithelpatitis;
KW      nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW      Bartholinitis; pneumopathy; venereal lymphogranulomatosis.
XX
OS      Chlamydia trachomatis.
XX
PN      WO9928475-A2.
XX
PD      10-JUN-1999.
XX
PF      27-NOV-1998; 98WO-IB01939.
XX
PR      04-NOV-1998; 98US-0107077.
PR      28-NOV-1997; 97ER-0015041.
PR      17-DEC-1997; 97ER-0016034.
XX
PA      (GEST ) GENSET.

```


PF 03-JUN-1993: 93DE-4318450.
 XX
 PR 11-JUN-1992: 92DE-4219111.
 PR 25-NOV-1992: 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of *Listeria* - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PS Disclosure; Fig 2; 19pp; German.
 XX
 CC The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 CC
 SQ Sequence 10 AA:
 XX
 OY 3 PVAPTOEVKK 12
 DB 1 pvaptoevkk 10

Query Match 83.3%; Score 10; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 AAR45168
 ID AAR45168 standard; Protein; 9 AA.
 AC AAR45168;
 DT 16-JUN-1994 (first entry)
 XX
 DE *Listeria* p60 peptide epitope.
 XX
 KM *Listeria* monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 PN DE4318450-A.
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993: 93DE-4318450.
 XX
 PR 11-JUN-1992: 92DE-4219111.
 PR 25-NOV-1992: 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of *Listeria* - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PS Disclosure; Fig 2; 19pp; German.
 XX
 CC The sequence is that of a *Listeria* p60 peptide epitope which

CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 CC
 SQ Sequence 9 AA:
 XX
 OY 1 STVPAPRQ 8
 DB 2 stvpaprq 9

Query Match 66.7%; Score 8; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 AAR73903
 ID AAR73903 standard; peptide; 7 AA.
 AC AAR73903;
 DT 05-DEC-1995 (first entry)
 XX
 DE *Listeria* monocytogenes protein p60 precursor peptide 151-157.
 XX
 KM *Listeria* monocytogenes; protein p60 precursor; vaccine;
 KM meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KM immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KM viral; peptide 151-157.
 XX
 OS *Listeria* monocytogenes.
 XX
 PN W09509232-A.
 PD 06-APR-1995.
 XX
 PF 28-SEP-1994: 94NO-CN00516.
 PR 28-SEP-1993: 93US-0127499.
 XX
 PA (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 PI Sharma LR, Van Alstyne D;
 XX
 DR WPI; 1995-147431/19.
 XX
 PT New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 PS Claim 35; Page 76; 98pp; English.
 XX
 CC AAR73913 is the *Listeria* monocytogenes protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 CC
 SQ Sequence 7 AA:
 XX
 OY 6 PTOEVKK 12

Query Match 58.3%; Score 7; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

961	4	33.3	114	14	AAR53361	N-terminally trunc
962	4	33.3	114	20	AAV49136	Consensus sequence
963	4	33.3	114	20	AAV34698	Chlamydia pneumoni
964	4	33.3	114	20	AAM95454	N-terminally trunc
965	4	33.3	114	21	AAV71550	Humanised antibody
966	4	33.3	114	21	AAG03726	Human secreted pro
967	4	33.3	114	21	AAV50974	Human FVIII heavy
968	4	33.3	114	21	AAV75983	Murine skin cell p
969	4	33.3	114	21	AAV76033	Murine skin cell p
970	4	33.3	114	22	AAB55922	Skin cell protein,
971	4	33.3	114	22	AAB55972	Skin cell protein,
972	4	33.3	115	18	AAW12437	Op-1 based morphon
973	4	33.3	115	20	AAV42461	Rat granulysin prepr
974	4	33.3	115	20	AAV39287	Human phospholipase
975	4	33.3	115	20	AAV12133	Human 5' EST seque
976	4	33.3	115	20	AAM97653	Wheat SUG1 polypep
977	4	33.3	115	20	AAM84095	Human Kabat subgro
978	4	33.3	115	21	AAB53629	Human colon cancer
979	4	33.3	115	21	AAB12169	Humanised HBV pre-
980	4	33.3	115	21	AAB12172	Humanised HBV pre-
981	4	33.3	115	21	AAG58270	Arabidopsis thailia
982	4	33.3	115	21	AAG00036	Human secreted pro
983	4	33.3	115	21	AAG00051	Human secreted pro
984	4	33.3	116	13	AAR25726	Humanised VH regio
985	4	33.3	116	14	AAR53362	N-terminally trunc
986	4	33.3	116	16	AAR66310	Human immunoglobul
987	4	33.3	116	16	AAR78728	Rmf gene product d
988	4	33.3	116	17	AAR92218	Humanised LL2 Mab
989	4	33.3	116	17	AAR92219	Humanised heavy cha
990	4	33.3	116	18	AAW27698	Variable heavy cha
991	4	33.3	116	18	AAW22418	Reshaped human AUK
992	4	33.3	116	19	AAW37812	Humanized anti-Tac
993	4	33.3	116	19	AAM58514	Protein SFO ID NO:
994	4	33.3	116	20	AAM95453	N-terminally trunc
995	4	33.3	116	21	AAB56080	Human secreted pro
996	4	33.3	116	21	AAB18036	Eucalyptus grandis
997	4	33.3	116	21	AAB18113	Eucalyptus grandis
998	4	33.3	116	21	AAG18487	Zea mays protein f
999	4	33.3	116	21	AAG00050	Human secreted pro
1000	4	33.3	116	21	AAV50971	Human FVIII antibo

ALIGNMENTS

RESULT 1

AA45172 standard; Protein; 12 AA.

AC AAR45172:

DT 16-JUN-1994 (first entry)

DE Listeria p60 peptide epitope.

XX Listeria monocytogenes; antibodies; immunoassay; conjugate.

OS Synthetic.

PN DE4318450-A.

PD 16-DEC-1993.

PF 03-JUN-1993; 93DE-4318450.

PR 11-JUN-1992; 92DE-4219111.

PR 25-NOV-1992; 92DE-4239567.

PA (MERE) MERCK PATENT GMBH.

PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;

PI Hofmann G, Bubert A, Goebel W, Koehler S;

XX

DR WPI; 1993-406956/51.

XX New primers for PCR detection of Listeria - including individual

PT species; also new peptide(s) for raising antibodies for

PT Immunochemical detection

XX Disclosure; Fig 2; 19pp; German.

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CC which may be used in the prodn. of antibodies for the detection

CC of Listeria by immunoassay (partic. ELISA). It may be used as

CC part of a method that allows determination of individual Listeria

CC species, esp. L. monocytogenes.

XX

SO Sequence 12 AA:

Query Match 100.0%; Score 12; DB 14; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAPTOEVKK 12

DB 1 stvpaptoevkk 12

RESULT 2

AA45172 standard; peptide; 21 AA.

AC AAR73891;

XX

DT 05-DEC-1995 (first entry)

DE Listeria monocytogenes protein P60 precursor peptide 144-164.

XX

DE Listeria monocytogenes; protein P60 precursor; vaccine;

KW meningitis related homologous antigenic sequence; MRHAS; RV-1;

KW immunoassay; diagnosis; treatment; prophylactic; bacterial;

XX viral; peptide 144-164.

XX Listeria monocytogenes.

OS

PN W09509232-A.

XX

PD 06-APR-1995.

XX

PF 28-SEP-1994; 94WO-CA00516.

XX

PR 28-SEP-1993; 93US-0127499.

XX

PA (SHAR/) SHARMA L.R.

PA (VALS/) VAN ALSTYNE D.

PI Sharma LR, Van Alstyne D;

DR WPI; 1995-147431/19.

XX

PT New peptide(s) and corresp. antibodies for the treatment of

PT meningitis - the peptide(s) corresp. to homologous antigenic

PT sites on bacterial and viral agents and on chemokine(s), used for

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PS Claim 34; Page 74; 98pp; English.

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CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a

CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The

CC claimed MRHAS peptides may be used in immunoassays to diagnose the

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CC peptides may also be used as vaccines against meningitis.

669	4	33.3	73	22	AAB70025	Human CD4 D4 domai	742	4	33.3	89	21	AAG54248	Arbidopsiis thalia
670	4	33.3	73	22	AAB70026	Human CD4 D4 domai	743	4	33.3	89	21	AAG01533	Human secreted pro
671	4	33.3	73	22	AAB70027	Human CD4 D4 domai	744	4	33.3	89	21	AAG01562	Human secreted pro
672	4	33.3	73	22	AAB70028	Human CD4 D4 domai	745	4	33.3	90	21	AAG26155	zee mays protein f
673	4	33.3	73	22	AAB70029	Human CD4 D4 domai	746	4	33.3	90	21	AAV32306	Corn acid triacylg
674	4	33.3	73	22	AAB50534	Mouse C-CAM1 cytop	747	4	33.3	91	20	AAV11416	Human 5' EST secre
675	4	33.3	74	20	AAV14475	Fragment of human	748	4	33.3	91	21	AAB42378	Human ORFX ORF2142
676	4	33.3	74	20	AAV03781	S. aureus polypept	749	4	33.3	91	21	AAG27140	zee mays protein f
677	4	33.3	74	21	AAB56214	Human secreted pro	750	4	33.3	92	20	AAV60469	Human normal blad
678	4	33.3	74	21	AAG37064	Arbidopsiis thalia	751	4	33.3	92	21	AAB40314	Human ORFX ORF78 p
679	4	33.3	74	21	AAG55678	Arbidopsiis thalia	752	4	33.3	92	21	AAG22778	Arbidopsiis thalia
680	4	33.3	74	21	AAG60223	Arbidopsiis thalia	753	4	33.3	92	21	AAG26934	zee mays protein f
681	4	33.3	74	22	AAB50533	Human C-CAM1 cytop	754	4	33.3	92	21	AAG33234	zee mays protein f
682	4	33.3	75	18	AAW28231	Staphylococcus aur	755	4	33.3	92	21	AAG33943	Arbidopsiis thalia
683	4	33.3	75	20	AAV30854	Human secreted pro	756	4	33.3	92	21	AAG36731	Arbidopsiis thalia
684	4	33.3	75	20	AAV35810	Chlamydia pneumoni	757	4	33.3	92	21	AAG54495	zee mays protein f
685	4	33.3	75	20	AAV12951	Amino acid sequenc	758	4	33.3	93	21	AAV22860	SEQ ID NO. 56 from
686	4	33.3	75	21	AAV18074	Arbidopsiis thalia	759	4	33.3	93	19	AAW75090	Human secreted pro
687	4	33.3	76	20	AAV35859	Chlamydia pneumoni	760	4	33.3	93	21	AAG04405	Arbidopsiis thalia
688	4	33.3	76	20	AAV12175	Human 5' EST secre	761	4	33.3	93	21	AAG33473	Arbidopsiis thalia
689	4	33.3	76	21	AAG55739	Arbidopsiis thalia	762	4	33.3	93	21	AAG54247	Arbidopsiis thalia
690	4	33.3	76	21	AAV01671	Human secreted pro	763	4	33.3	93	21	AAG03293	Human secreted pro
691	4	33.3	76	22	AAB65860	Murine TANGO 281 c	764	4	33.3	94	15	AAV47117	Complete sequence
692	4	33.3	77	19	AAV86001	S. pneumoniae deri	765	4	33.3	94	19	AAV22861	SEQ ID NO. 57 from
693	4	33.3	77	21	AAV87219	Human secreted pro	766	4	33.3	94	19	AAV75151	Human secreted pro
694	4	33.3	78	21	AAB52108	Human secreted pro	767	4	33.3	94	19	AAV75152	Human secreted pro
695	4	33.3	78	21	AAV64691	Human 5' EST relat	768	4	33.3	94	21	AAB51698	Human secreted pro
696	4	33.3	78	22	AAB87389	Human gene 48 enco	769	4	33.3	94	21	AAG00054	Human secreted pro
697	4	33.3	78	22	AAB87412	Human gene 48 enco	770	4	33.3	94	21	AAG00065	Human secreted pro
698	4	33.3	79	19	AAV22863	SEQ ID NO. 59 from	771	4	33.3	94	22	AAB64488	Human secreted pro
699	4	33.3	79	19	AAV22864	SEQ ID NO. 60 from	772	4	33.3	94	22	AAW20297	H. pylori cytoplas
700	4	33.3	79	20	AAV73910	Human prostate tum	773	4	33.3	95	20	AAV74161	Human prostate tum
701	4	33.3	79	20	AAB54421	Human pancreatic c	774	4	33.3	95	20	AAV60052	Human endometrium
702	4	33.3	80	18	AAV11223	S. pneumoniae indo	775	4	33.3	95	21	AAG14413	Arbidopsiis thalia
703	4	33.3	80	18	AAW27747	Staphylococcus aur	776	4	33.3	95	21	AAG57203	Arbidopsiis thalia
704	4	33.3	80	21	AAG06014	Arbidopsiis thalia	777	4	33.3	95	21	AAG59156	Arbidopsiis thalia
705	4	33.3	80	21	AAG00040	Human secreted pro	778	4	33.3	95	21	AAG00038	Human secreted pro
706	4	33.3	81	20	AAG00067	Human secreted pro	779	4	33.3	95	21	AAV91621	Human secreted pro
707	4	33.3	81	20	AAV60234	Human endometrium	780	4	33.3	96	20	AAV67917	Human secreted pro
708	4	33.3	81	20	AAV28654	Human secreted pro	781	4	33.3	96	21	AAB32768	Eucalyptus grandis
709	4	33.3	81	20	AAV89956	Antigen from Clust	782	4	33.3	96	21	AAG06013	Arbidopsiis thalia
710	4	33.3	81	21	AAV73395	Human secreted pro	783	4	33.3	96	21	AAG12504	zee mays protein f
711	4	33.3	82	21	AAB63188	Human secreted pro	784	4	33.3	96	21	AAG15817	Arbidopsiis thalia
712	4	33.3	82	21	AAB18950	Peptide derived fr	785	4	33.3	96	21	AAG25016	Arbidopsiis thalia
713	4	33.3	82	21	AAG21847	Human 5' EST relat	786	4	33.3	96	21	AAG00039	Human secreted pro
714	4	33.3	82	21	AAV64976	Human 5' EST relat	787	4	33.3	96	21	AAV56644	Partial peptide fr
715	4	33.3	84	19	AAW42039	Mouse prococtistat	788	4	33.3	96	21	AAV56645	Partial peptide fr
716	4	33.3	84	21	AAB03948	Human mesenchymal	789	4	33.3	96	21	AAV56647	Partial peptide fr
717	4	33.3	85	12	AAR14008	HIV-1 hxb2 gag 262	790	4	33.3	96	21	AAV56649	Partial peptide fr
718	4	33.3	85	12	AAR14458	HIV-1 hxb2 gag 262	791	4	33.3	97	14	AAR53359	Osteogenic protein
719	4	33.3	85	21	AAG02769	Human secreted pro	792	4	33.3	97	14	AAR53387	Murine osteogenic
720	4	33.3	85	21	AAV91606	Human secreted pro	793	4	33.3	97	17	AAV57475	Human HV3 VH. Hom
721	4	33.3	86	19	AAV38421	Proteolipid protel	794	4	33.3	97	17	AAV92078	Human HV3 VH. Hom
722	4	33.3	86	20	AAV73904	Human prostate tum	795	4	33.3	97	19	AAB38643	Streptococcus pneu
723	4	33.3	86	20	AAV73929	Human prostate tum	796	4	33.3	97	20	AAV72248	C. elegans CED-6 p
724	4	33.3	86	21	AAG01952	Human secreted pro	797	4	33.3	97	20	AAW89696	Human osteogenic p
725	4	33.3	86	22	AAB35252	HIV-1 p24 protein	798	4	33.3	97	20	AAV95444	Conserved 6 cystei
726	4	33.3	87	17	AAR93003	Homologous sequenc	799	4	33.3	97	21	AAG33072	Arbidopsiis thalia
727	4	33.3	87	17	AAR92991	Homologous sequenc	800	4	33.3	97	21	AAV48926	Arbidopsiis thalia
728	4	33.3	87	21	AAG26156	zee mays protein f	801	4	33.3	97	21	AAG00068	Human secreted pro
729	4	33.3	87	21	AAG44140	Arbidopsiis thalia	802	4	33.3	97	21	AAW90944	Comamonas testoste
730	4	33.3	87	21	AAV76169	Human secreted pro	803	4	33.3	97	21	AAV65401	Human 5' EST relat
731	4	33.3	88	13	AAR22576	Heavy chain VH6.1	804	4	33.3	97	22	AAB65852	Human TANGO 281 cy
732	4	33.3	88	21	AAG04407	Arbidopsiis thalia	805	4	33.3	98	10	AAV95681	Human osteogenic p
733	4	33.3	88	21	AAG33200	zee mays protein f	806	4	33.3	98	14	AAV33701	SP2 Igs VH segment
734	4	33.3	88	21	AAG35339	zee mays protein f	807	4	33.3	98	14	AAR34272	Mutated human VH1
735	4	33.3	89	21	AAG34249	Arbidopsiis thalia	808	4	33.3	98	15	AAR54800	Spt-1reactive Igm h
736	4	33.3	89	14	AAR34271	Dp-74 VH1 gene hea	809	4	33.3	98	16	AAR72068	Dp10 VH region. H
737	4	33.3	89	19	AAW41088	Human matrix metal	810	4	33.3	98	16	AAR72069	HV1263 2 VH-1 H cha
738	4	33.3	89	19	AAW41233	Alpha-V-beta-5 ant	811	4	33.3	98	19	AAV72070	OFH1.2 VH-1 H cha
739	4	33.3	89	20	AAV12949	Amino acid sequenc	812	4	33.3	98	19	AAW54008	Human Anti-CD4 ant
740	4	33.3	89	21	AAB41518	Human ORFX ORF1282	813	4	33.3	98	21	AAB40596	Human ORFX ORF460
741	4	33.3	89	21	AAG04406	Arbidopsiis thalia	814	4	33.3	98	21	AAV50949	Human anti-factor

523	4	33.3	38	15	AAR58457	TSAR binding domain
524	4	33.3	38	20	AAV42830	Erythropoietin receptor
525	4	33.3	38	20	AAV42835	Non-EPOR-binding c
526	4	33.3	38	21	AAG55741	Arabidopsis thaliana
527	4	33.3	39	16	AAR66436	PCOLUS 4-18 (476-49
528	4	33.3	39	16	AAR66410	PCOLUS 4-18 (476-49
529	4	33.3	39	18	AAW19025	HIV envelope glycop
530	4	33.3	39	20	AAV05347	HIV-1 C1UVCAC pepti
531	4	33.3	39	20	AAV05340	HIV-1 C5 region of
532	4	33.3	39	22	AAB59899	Human endothelial
533	4	33.3	40	21	AAB05912	Bovine endothelial
534	4	33.3	40	21	AAB05913	SEQ ID NO. 65 from
535	4	33.3	41	19	AAV22869	A. thaliana D22AT3
536	4	33.3	41	20	AAV42648	Human secreted pro
537	4	33.3	41	20	AAV07893	Peptide 147 from t
538	4	33.3	42	9	AAP80686	SP410-BAL Immuno
539	4	33.3	42	18	AAW19055	GelA TMP-2 binding
540	4	33.3	42	19	AAW59179	Human CHD1 KRAB do
541	4	33.3	42	20	AAV29924	Human 5' EST seque
542	4	33.3	42	20	AAV12163	Human 5' EST seque
543	4	33.3	43	20	AAV12848	Flanking sequence
544	4	33.3	43	20	AAW91057	Flanking sequence
545	4	33.3	43	20	AAW91059	Flanking sequence
546	4	33.3	43	20	AAW91063	Dynamin 41.2 ZELAN
547	4	33.3	43	20	AAW82294	Beta-catenin flank
548	4	33.3	43	21	AAB27071	Beta-catenin flank
549	4	33.3	43	21	AAB27072	Beta-catenin flank
550	4	33.3	43	21	AAB27077	Cytosolic tail p
551	4	33.3	43	21	AAV76821	Arabidopsis thaliana
552	4	33.3	44	21	AAG21848	Non-immunogenic am
553	4	33.3	45	10	AAP90818	Human gene 39 enco
554	4	33.3	45	22	AAB87380	Fusion Immunoglobul
555	4	33.3	46	19	AAW79183	Fragment of human
556	4	33.3	47	20	AAV36545	Human IL-18 bindin
557	4	33.3	47	21	AAV83984	Exon trap L75917.
558	4	33.3	49	19	AAW46754	Human secreted pro
559	4	33.3	49	20	AAV25728	Human secreted pro
560	4	33.3	49	21	AAB56202	HIV gp120-C5. Syn
561	4	33.3	50	16	AAR71628	Enhanced CCK-B/gas
562	4	33.3	50	18	AAW29113	Transactivation do
563	4	33.3	51	16	AAR77798	Enhanced CCK-B/gas
564	4	33.3	51	18	AAR77799	Human prostate can
565	4	33.3	51	20	AAV36715	Fragment of human
566	4	33.3	51	21	AAV36715	Arabidopsis thaliana
567	4	33.3	51	21	AAG19538	Arabidopsis thaliana
568	4	33.3	51	21	AAG24626	Arabidopsis thaliana
569	4	33.3	51	21	AAG34541	Arabidopsis thaliana
570	4	33.3	51	21	AAG34541	Arabidopsis thaliana
571	4	33.3	51	21	AAG46118	Arabidopsis thaliana
572	4	33.3	51	21	AAG46118	Hepatitis GB virus
573	4	33.3	51	21	AAB09225	Amino acids of the
574	4	33.3	52	10	AAP91361	White shrimp multi
575	4	33.3	52	21	AAB22970	Membrane-bound pro
576	4	33.3	52	21	AAB22971	Human PRO819 (UNO4
577	4	33.3	52	21	AAV66682	Human PRO819 prote
578	4	33.3	52	22	AAB65205	Human angiotensin
579	4	33.3	52	22	AAB50985	SEQ ID NO. 94 from
580	4	33.3	53	19	AAV22898	Amino acid sequenc
581	4	33.3	53	17	AAW05836	Mouse M-Serrate-1
582	4	33.3	54	17	AAW05836	SEQ ID NO. 63 from
583	4	33.3	54	19	AAV22867	SEQ ID NO. 64 from
584	4	33.3	54	19	AAV22867	Breast and ovarian
585	4	33.3	54	21	AAV50995	Human secreted pro
586	4	33.3	54	21	AAV50997	Mouse Serrate prot
587	4	33.3	54	21	AAV50995	Sequence of immuno
588	4	33.3	55	8	AAV70360	SEQ ID NO. 62 from
589	4	33.3	55	19	AAV22866	SEQ ID NO. 61 from
590	4	33.3	55	19	AAV22865	Relv envelope glyco
591	4	33.3	55	20	AAV26920	Clone selected aft
592	4	33.3	56	20	AAV02478	Human pancreatic c
593	4	33.3	56	21	AAB54442	Human secreted pro
594	4	33.3	56	21	AAB54442	
595	4	33.3	56	21	AAB28299	

377	4	33.3	15	21	AAB14221	HIV US4 gp120 clea
378	4	33.3	15	21	AAB14223	Mutant HIV cleavag
379	4	33.3	16	18	AAB25388	PLC gamma SH3 doma
380	4	33.3	16	18	AAM09989	HTIV-1 envelope pr
381	4	33.3	16	18	AAM15570	PRNA358. Feline 1
382	4	33.3	16	19	AAM76907	Fusion Immunoglob
383	4	33.3	16	19	AAM50206	Peptide from a Krl
384	4	33.3	16	19	AAM50205	Peptide from a Krl
385	4	33.3	16	19	AAM37117	HTIV-1 envelope an
386	4	33.3	16	20	AAY00795	HTIV1 envelope pep
387	4	33.3	16	22	AAB29975	White shrimp p62 p
388	4	33.3	16	22	AAB68802	Escherichia coli k
389	4	33.3	18	11	AAR02317	Peptide derived fr
390	4	33.3	18	19	AAM79190	Synthetic peptide
391	4	33.3	18	20	AAM94621	Src homology 3 dom
392	4	33.3	19	11	AAR01999	Peptide derived fr
393	4	33.3	19	11	AAR00940	Peptide derived fr
394	4	33.3	19	14	AAR37695	Retroviral gag pep
395	4	33.3	19	16	AAR76724	gp120 epitope from
396	4	33.3	19	17	AAM02223	CD4:gamma chain fu
397	4	33.3	19	17	AAM02221	CD4:zeta chain fus
398	4	33.3	19	18	AAM33957	Vasopressin type 2
399	4	33.3	19	19	AAM35391	Bifidobacterium lo
400	4	33.3	20	12	AAR15532	Immunopeptide deri
401	4	33.3	20	14	AAR37689	Synthetic epitope.
402	4	33.3	20	16	AAR68794	Cytotoxic T lympho
403	4	33.3	20	17	AAR08052	HIV peptide #37.
404	4	33.3	20	19	AAM76943	Fusion Immunoglob
405	4	33.3	20	19	AAM76875	Fusion Immunoglob
406	4	33.3	20	20	AAM82295	Dynamin 41.20 ZELA
407	4	33.3	20	21	AAB03854	Peptide T0120 used
408	4	33.3	20	21	AAY93365	Amino acid sequenc
409	4	33.3	20	21	AAY67262	Protein tyrosine p
410	4	33.3	20	21	AAY66445	H1A-A2-binding HIV
411	4	33.3	20	22	AAB49391	Simian immunodef
412	4	33.3	21	14	AAR31614	Peptide ligand for
413	4	33.3	21	14	AAR34228	HTIV-I gp46 extern
414	4	33.3	21	16	AAR72664	Cladosporium herba
415	4	33.3	21	17	AAR97131	Conantokin-T (Con-
416	4	33.3	21	17	AAR94517	Glut insulin sensi
417	4	33.3	21	18	AAM42769	Peptide of the spe
418	4	33.3	21	19	AAM49947	Conantokin peptide
419	4	33.3	21	19	AAM48174	Conantokin peptide
420	4	33.3	21	19	AAM40272	K. oxyloca R-speci
421	4	33.3	21	20	AAY43600	Peptide fragment o
422	4	33.3	21	20	AAM86146	Conantokin-T (Con-
423	4	33.3	21	22	AAB89251	HIV gp120 protein
424	4	33.3	21	22	AAB89252	HIV gp120 protein
425	4	33.3	21	22	AAB89253	HIV gp120 protein
426	4	33.3	21	22	AAB89254	HIV gp120 protein
427	4	33.3	22	11	AAY17925	Synthetic peptide
428	4	33.3	22	14	AAR43929	Platelet derived g
429	4	33.3	22	14	AAR30539	HIV discriminatory
430	4	33.3	22	14	AAR31965	BCH-13x. Syntheti
431	4	33.3	22	14	AAR41293	Peptide fragment F
432	4	33.3	22	19	AAM67033	Peptide with N-ter
433	4	33.3	22	20	AAY04034	HIV-1 p24 peptide
434	4	33.3	22	21	AAB12539	HIV-1 nucleoprotei
435	4	33.3	23	13	AAR25941	N-terminal peptide
436	4	33.3	23	14	AAR45164	Listeria p60 pepit
437	4	33.3	23	14	AAR41294	Peptide fragment F
438	4	33.3	23	15	AAR41332	HIV gp120 epitope.
439	4	33.3	23	15	AAR63849	HIV-1 gp120-40 epi
440	4	33.3	23	16	AAR74046	Rice carbonic-anhy
441	4	33.3	23	19	AAM50207	Peptide from a Krl
442	4	33.3	23	19	AAM48108	HIV gp120 residues
443	4	33.3	23	20	AAT72500	E. coli beta'-subu
444	4	33.3	23	20	AAM82310	Transport peptide
445	4	33.3	24	8	AAP71151	Anti-HIV peptide 6
446	4	33.3	24	9	AAP80750	Sequence of peptid
447	4	33.3	24	14	AAR33838	Cluster peptide PC
448	4	33.3	24	16	AAR66432	PCUS 4-18 (476-49
449	4	33.3	24	19	AAM54933	HIV gp120 envelope
450	4	33.3	24	20	AAY05354	HIV-1 CLUVAC pepit
451	4	33.3	24	21	AAB22976	White shrimp p62 p
452	4	33.3	25	7	AAP60708	HIV virus p18 prot
453	4	33.3	25	11	AAR02316	Peptide derived fr
454	4	33.3	25	13	AAR27336	Peptide cortesp. t
455	4	33.3	25	19	AAM82523	HIV-1 p24 epitope
456	4	33.3	25	19	AAM82524	HIV-1 p24 epitope
457	4	33.3	25	19	AAM82525	HIV-1 p24 epitope
458	4	33.3	25	19	AAM81958	Human ENDO-II vari
459	4	33.3	26	12	AAR11413	Hepatitis A virus
460	4	33.3	26	13	AAR24867	Sequence of peptid
461	4	33.3	26	14	AAR30538	HIV discriminatory
462	4	33.3	26	14	AAR30755	HIV discriminatory
463	4	33.3	26	14	AAR41301	Peptide fragment F
464	4	33.3	26	14	AAR44111	HIV gp160 epitope.
465	4	33.3	26	19	AAM76909	Fusion Immunoglob
466	4	33.3	26	19	AAM50208	Peptide from a Krl
467	4	33.3	26	21	AAB22977	White shrimp p62 p
468	4	33.3	27	10	AAP90819	Non-immunogenic am
469	4	33.3	27	14	AAR30757	HIV discriminatory
470	4	33.3	27	19	AAM79184	HIV gp120 C5 regio
471	4	33.3	27	20	AAY38474	Human secreted pro
472	4	33.3	28	15	AAR49685	Sequence of crypt
473	4	33.3	28	19	AAY21018	Human glial fibril
474	4	33.3	29	21	AAB33288	Pinus radiata tran
475	4	33.3	29	21	AAY68639	Amino acid sequenc
476	4	33.3	29	22	AAB49392	Simian immunodef
477	4	33.3	29	22	AAB49393	Simian immunodef
478	4	33.3	29	22	AAB49394	Simian immunodef
479	4	33.3	30	12	AAR15700	Human tumour-assoc
480	4	33.3	30	13	AAR27045	Human heavy chain
481	4	33.3	30	16	AAR85163	Human ONS-M21 anti
482	4	33.3	30	16	AAR70657	GLUT4 intracellular
483	4	33.3	30	17	AAR70658	GLUT4 intracellular
484	4	33.3	30	17	AAR96290	Heavy chain framew
485	4	33.3	30	19	AAM76911	Fusion Immunoglob
486	4	33.3	30	19	AAM79211	Fremework 1 region
487	4	33.3	31	17	AAR91189	gp120 HTIV-III pep
488	4	33.3	31	18	AAM24744	Finger 2 domain of
489	4	33.3	31	18	AAM19937	Fibronectin fragme
490	4	33.3	31	19	AAM54936	HIV gp120 envelope
491	4	33.3	31	20	AAY48370	Human prostate can
492	4	33.3	31	20	AAM82455	Tomato Cu/Zn SOD e
493	4	33.3	31	20	AAM82988	Human fibronectin
494	4	33.3	31	21	AAY77377	HIV-1 group O env
495	4	33.3	31	21	AAY77378	HIV-1 group O env
496	4	33.3	32	10	AAP91490	C-terminal portion
497	4	33.3	32	18	AAM26676	Bacteriocin-like-2
498	4	33.3	32	21	AAY98799	WT1 derived immuno
499	4	33.3	33	16	AAR69686	Hepatitis C virus
500	4	33.3	33	17	AAR89558	Hepatitis C virus
501	4	33.3	34	19	AAY22870	SEQ ID NO. 66 from
502	4	33.3	34	19	AAM48443	Human p53 proline-
503	4	33.3	34	20	AAT74105	Human prostate tum
504	4	33.3	34	21	AAB53925	Human colon cancer
505	4	33.3	35	19	AAM70114	Peptide produced b
506	4	33.3	35	21	AAB38462	Fingerprint of human
507	4	33.3	35	21	AAB67806	Peptide #206 for d
508	4	33.3	35	21	AAB67808	Peptide #208 for d
509	4	33.3	35	21	AAT67809	Peptide #209 for d
510	4	33.3	37	18	AAM40369	Human breast cance
511	4	33.3	37	18	AAM30366	Fingerprint #2 of bon
512	4	33.3	37	20	AAY25880	Human secreted pro
513	4	33.3	37	21	AAR44604	Human secreted pro
514	4	33.3	37	21	AAB09516	Human OP-1 finger.
515	4	33.3	37	21	AAB09559	Op-1 mutant protei
516	4	33.3	37	21	AAB09562	Human OP-1 mutant
517	4	33.3	37	21	AAB09563	Human OP-1 mutant
518	4	33.3	37	21	AAB09565	Human OP-1 mutant
519	4	33.3	37	21	AAB09566	Human OP-1 mutant
520	4	33.3	37	21	AAB09573	Human OP-1 mutant
521	4	33.3	37	21	AAT84032	Human OP-1 mutant
522	4	33.3	38	14	AAR41075	Amino acid sequenc
						HIV-1 gp120 C-term

231	5	41.7	802	19	AAW64379	Mycobacterium anti	304	4	33.3	8	14	AAW43520	Sm B/B' epitope 16
232	5	41.7	802	20	AAW32063	Mycobacterium tube	305	4	33.3	8	17	AAW97521	Antigenic peptide,
233	5	41.7	802	20	AAW39224	M. tuberculosis fu	306	4	33.3	8	20	AAW41615	Mammalian ion chan
234	5	41.7	802	20	AAW39176	M. tuberculosis fu	307	4	33.3	8	21	AAW77393	HIV-1 group O env
235	5	41.7	802	20	AAW39081	M. tuberculosis fus	308	4	33.3	9	14	AAW44262	Residues 68-76 of
236	5	41.7	802	20	AAW39033	M. tuberculosis fu	309	4	33.3	9	14	AAW54620	Listeria p60 pepti
237	5	41.7	835	19	AAW96206	Invasin protein..	310	4	33.3	9	14	AAW42578	HIV envelope neutr
238	5	41.7	867	19	AAW98564	H. pylori GHPO 175	311	4	33.3	9	15	AAW57292	Bovine EK tryptic
239	5	41.7	870	21	AAW10948	L. mexicana casein	312	4	33.3	9	15	AAW59259	Peptide fragment (
240	5	41.7	933	20	AAW21621	Ligand binding dom	313	4	33.3	9	19	AAW79187	M38 murine monoclo
241	5	41.7	933	21	AAW97297	Human progesterone	314	4	33.3	9	19	AAW78866	Prostate specific
242	5	41.7	939	21	AAW53192	Macaca mulatta rha	315	4	33.3	9	20	AAW10315	T cell epitope/MHC
243	5	41.7	954	18	AAW19752	Yeast inhibitor of	316	4	33.3	9	20	AAW10297	T cell epitope/MHC
244	5	41.7	986	18	AAW13670	C-proteinase encod	317	4	33.3	9	21	AAW94619	Src homology 3 dom
245	5	41.7	999	22	AAW59817	TudD protein #8,	318	4	33.3	9	21	AAW45556	Human B99-1 HLA A3
246	5	41.7	1006	21	AAW53126	Arabidopsis thalia	319	4	33.3	9	21	AAW45557	Human B99-1 HLA A3
247	5	41.7	1013	19	AAW61539	Human cardiac/brai	320	4	33.3	9	21	AAW33678	MHC class I associ
248	5	41.7	1013	19	AAW40224	Human tollloid-like	321	4	33.3	9	21	AAW98674	WT1 derived immuno
249	5	41.7	1021	18	AAW23281	Alloreactive assoc	322	4	33.3	9	21	AAW98680	WT1 derived immuno
250	5	41.7	1031	19	AAW53572	Human myosin light	323	4	33.3	9	21	AAW98722	WT1 derived immuno
251	5	41.7	1030	19	AAW41378	Human protein p164	324	4	33.3	9	21	AAW98727	WT1 derived immuno
252	5	41.7	1036	21	AAW31888	Arabidopsis thalia	325	4	33.3	9	21	AAW98780	WT1 derived immuno
253	5	41.7	1053	21	AAW98357	Human Prol190 (UNQ	326	4	33.3	9	22	AAW76154	Tumour associated
254	5	41.7	1053	22	AAW66106	Protein of the inv	327	4	33.3	10	17	AAW49590	Human leucocyte an
255	5	41.7	1070	21	AAW31887	Arabidopsis thalia	328	4	33.3	10	17	AAW49591	Human leucocyte an
256	5	41.7	1085	12	AAW11604	P450 17-alpha/P450	329	4	33.3	10	17	AAW49592	Human leucocyte an
257	5	41.7	1096	21	AAW48592	Arabidopsis thalia	330	4	33.3	10	17	AAW96505	Hepatitis C virus
258	5	41.7	1130	21	AAW48591	Arabidopsis thalia	331	4	33.3	10	17	AAW97522	Antigenic peptide,
259	5	41.7	1187	16	AAW6451	AF-4 protein (enco	332	4	33.3	10	18	AAW40675	Peptide which bind
260	5	41.7	1210	16	AAW66450	AF-4 protein (enco	333	4	33.3	10	18	AAW42720	Antigenic decapept
261	5	41.7	1245	18	AAW29029	Bacillus thuringie	334	4	33.3	10	18	AAW42721	Antigenic decapept
262	5	41.7	1245	18	AAW16657	Bacillus thuringie	335	4	33.3	10	19	AAW76876	Fusion immunoglob
263	5	41.7	1245	19	AAW13872	6E03a toxin, Bac	336	4	33.3	10	19	AAW76878	Fusion immunoglob
264	5	41.7	1245	19	AAW73105	B. t. toxin protein	337	4	33.3	10	19	AAW63551	Beta (1 -> 4)-N-ac
265	5	41.7	1245	21	AAW13894	Bacillus thuringie	338	4	33.3	10	22	AAW75991	Human kallikrein (
266	5	41.7	1245	22	AAW59884	6E03 protein, Bac	339	4	33.3	10	22	AAW76201	Tumour associated
267	5	41.7	1252	16	AAW80530	B. sphaericus SLP	340	4	33.3	10	22	AAW76202	Tumour associated
268	5	41.7	1253	13	AAW28337	SEV4 structural po	341	4	33.3	11	10	AAW93053	HIV env protein an
269	5	41.7	1268	21	AAW36836	Human insulin rece	342	4	33.3	11	14	AAW44263	Residues 68-78 of
270	5	41.7	1276	21	AAW31886	Arabidopsis thalia	343	4	33.3	11	14	AAW54627	Listeria innocua p
271	5	41.7	1297	21	AAW36840	Human insulin rece	344	4	33.3	11	14	AAW41809	M13TMD1 mutated fr
272	5	41.7	1300	21	AAW36838	Rat insulin recept	345	4	33.3	11	17	AAW97523	Antigenic peptide,
273	5	41.7	1313	14	AAW36781	A3 maize ACCase.	346	4	33.3	11	17	AAW50203	Peptide from a krl
274	5	41.7	1336	21	AAW48590	Arabidopsis thalia	347	4	33.3	11	21	AAW32972	White shrimp p62 p
275	5	41.7	1409	21	AAW53125	Arabidopsis thalia	348	4	33.3	11	21	AAW09549	Peptide encoded by
276	5	41.7	1420	21	AAW53124	Arabidopsis thalia	349	4	33.3	11	21	AAW02815	BMP mutant chimeri
277	5	41.7	1449	21	AAW23825	Murine DEC 205 rec	350	4	33.3	11	21	AAW92589	Peptide encoded by
278	5	41.7	1484	20	AAW89721	Canine ribosome re	351	4	33.3	11	22	AAW75973	Human kallikrein (
279	5	41.7	1566	16	AAW79643	Immunodominant ant	352	4	33.3	12	16	AAW83319	Kb-binding random
280	5	41.7	1592	22	AAW59827	protein #4 encoded	353	4	33.3	12	16	AAW68778	Cytotoxic T lympho
281	5	41.7	1627	12	AAW12789	M. pneumoniae Pl c	354	4	33.3	12	21	AAW07094	Human peptide-mime
282	5	41.7	1627	15	AAW47911	Mycoplasma pneumon	355	4	33.3	13	17	AAW96827	Human snRNP-associ
283	5	41.7	1627	16	AAW67538	Cytadhesin Pl. My	356	4	33.3	13	19	AAW70128	Peptide produced b
284	5	41.7	1723	17	AAW00645	Mouse DEC-205. Mu	357	4	33.3	13	19	AAW50204	Peptide from a krl
285	5	41.7	1743	19	AAW98879	H. pylori GHPO 175	358	4	33.3	13	21	AAW22973	White shrimp p62 p
286	5	41.7	1780	19	AAW53863	Human gravin polyp	359	4	33.3	14	19	AAW79191	Synthetic peptide
287	5	41.7	1780	21	AAW53863	Human gravin prote	360	4	33.3	14	19	AAW56527	Antigenic HIV-1 pe
288	5	41.7	2001	22	AAW20062	Arabidopsis thalia	361	4	33.3	14	21	AAW22974	White shrimp p62 p
289	5	41.7	2001	22	AAW20063	Arabidopsis thalia	362	4	33.3	14	21	AAW98509	Mouse WPI peptide
290	5	41.7	2237	18	AAW58148	GRNAV-3 polypeptid	363	4	33.3	14	21	AAW98510	Human WPI peptide
291	5	41.7	2247	18	AAW27126	Egulin rhinovirus	364	4	33.3	15	10	AAW90224	Antigenic peptide
292	5	41.7	2325	17	AAW05590	Maize acetyl CoA c	365	4	33.3	15	16	AAW79629	Endocarditis speci
293	5	41.7	2325	19	AAW56736	Maize ACCase enzym	366	4	33.3	15	16	AAW79626	Endocarditis speci
294	5	41.7	2325	21	AAW44687	Maize acetyl CoA c	367	4	33.3	15	18	AAW39011	Peptide resembling
295	5	41.7	2476	20	AAW67738	PLG p105 zona pell	368	4	33.3	15	18	AAW30779	Prostate specific
296	5	41.7	2625	21	AAW23832	Shewanella sp. SCR	369	4	33.3	15	19	AAW78551	SH2 domain binding
297	5	41.7	2785	21	AAW57148	Human down-regulat	370	4	33.3	15	19	AAW58037	Human prostate spe
298	5	41.7	2785	21	AAW09551	Peptide encoded by	371	4	33.3	15	19	AAW58038	Human prostate spe
299	5	41.7	2785	21	AAW09551	BMP mutant chimeri	372	4	33.3	15	19	AAW58039	Human prostate spe
300	5	41.7	2785	21	AAW09551	Peptide encoded by	373	4	33.3	15	19	AAW58040	Human prostate spe
301	5	41.7	2785	21	AAW09551	Human IgG heavy ch	374	4	33.3	15	20	AAW27174	Human S72 peptide
302	5	41.7	2785	21	AAW09551	Conantokin peptide	375	4	33.3	15	20	AAW02215	Mutated human G-a1
303	5	41.7	2785	21	AAW09551	Conantokin peptide	376	4	33.3	15	21	AAW30407	Nuclear localisati

85	5	41.7	240	21	AAV96767	2. mays MADS-box P	158	5	41.7	422	22	AAH66464	protein encoded by
86	5	41.7	242	13	AAAR2390	Antigen ac-1b. E1	159	5	41.7	428	20	AAV13450	Amino acid sequenc
87	5	41.7	243	19	AAW80702	S. pneumoniae caci	160	5	41.7	429	20	AAW73631	Human secreted pro
88	5	41.7	247	21	AAV93998	Human BR43x2, an i	161	5	41.7	434	20	AAW73959	Human tPC3 protein
89	5	41.7	251	21	AAV08987	Arabidopsis thalia	162	5	41.7	442	20	AAW37457	Human tPC3 protein
90	5	41.7	251	21	AAV53861	Arabidopsis thalia	163	5	41.7	445	19	AAW98793	Chlamydia trachoma
91	5	41.7	253	21	AAV05005	Arabidopsis thalia	164	5	41.7	445	19	AAW71558	H. pylori GHPD 125
92	5	41.7	255	20	AAV37385	Amino acid sequenc	165	5	41.7	452	18	AAW20598	Helicobacter poly
93	5	41.7	256	21	AAV04637	Arabidopsis thalia	166	5	41.7	453	18	AAW53867	Gravin polypeptide
94	5	41.7	264	13	AAAR29638	PCPD ORF 3. Chlam	167	5	41.7	453	21	AAH18407	Human gravin PKA r
95	5	41.7	274	21	AAV32589	Arabidopsis thalia	168	5	41.7	461	20	AAH38793	Neisseria gonorrhoe
96	5	41.7	275	21	AAV39342	Arabidopsis thalia	169	5	41.7	461	20	AAH38794	N. gonorrhoeae ant
97	5	41.7	276	20	AAW81577	EDG-1-like G-prote	170	5	41.7	465	21	AAH81676	Streptococcus pneu
98	5	41.7	280	21	AAV04636	Arabidopsis thalia	171	5	41.7	467	14	AAH41890	Bille acid sulphate
99	5	41.7	281	21	AAV05004	Arabidopsis thalia	172	5	41.7	468	18	AAH19722	Mouse p14 (muscle
100	5	41.7	283	21	AAH12148	Hydrophobic domain	173	5	41.7	468	20	AAV24476	Corrected mouse p1
101	5	41.7	283	21	AAV94952	Human secreted pro	174	5	41.7	469	17	AAV97242	SCR phosphotyrosin
102	5	41.7	286	17	AAV03556	Mycobacterium tube	175	5	41.7	473	20	AAH89635	Protein encoded by
103	5	41.7	288	22	AAV79340	Corynebacterium g1	176	5	41.7	486	19	AAW37056	HIV-1 breakthrough
104	5	41.7	292	21	AAV21588	Arabidopsis thalia	177	5	41.7	490	12	AAH15511	Sucrose phosphoryl
105	5	41.7	293	19	AAV75783	Human lymphocyte s	178	5	41.7	491	19	AAV37057	HIV-1 breakthrough
106	5	41.7	293	21	AAH36312	Human neutrokin-e	179	5	41.7	491	21	AAH69278	HIV-1 non-subtype
107	5	41.7	293	21	AAV94000	A transmembrane ac	180	5	41.7	492	21	AAH69268	HIV-1 non-subtype
108	5	41.7	293	21	AAV39341	Arabidopsis thalia	181	5	41.7	492	21	AAH69268	HIV-1 non-subtype
109	5	41.7	293	22	AAV71914	Human tumour necro	182	5	41.7	494	21	AAH69275	HIV-1 non-subtype
110	5	41.7	294	21	AAV21587	Arabidopsis thalia	183	5	41.7	496	21	AAH69277	HIV-1 non-subtype
111	5	41.7	295	21	AAV39340	Arabidopsis thalia	184	5	41.7	497	21	AAH69269	HIV-1 non-subtype
112	5	41.7	296	22	AAV79319	Corynebacterium g1	185	5	41.7	497	21	AAH69272	HIV-1 non-subtype
113	5	41.7	302	21	AAV05003	Arabidopsis thalia	186	5	41.7	498	15	AAW44154	Human neuronal hlc
114	5	41.7	303	21	AAV28099	Arabidopsis thalia	187	5	41.7	498	15	AAH62424	HIV-type virus WVP
115	5	41.7	312	20	AAV93276	Murine WDS12 prote	188	5	41.7	498	15	AAH51691	HIV-type virus WVP
116	5	41.7	312	20	AAV75550	Neisseria gonorrhoe	189	5	41.7	498	18	AAV09027	Neuronal nictotinic
117	5	41.7	323	22	AAH51240	TPA1 protein sequ	190	5	41.7	498	20	AAV93076	HIV isolate 5180 g
118	5	41.7	325	17	AAV03565	Mycobacterium tube	191	5	41.7	498	20	AAV93077	HIV isolate 5180 g
119	5	41.7	325	21	AAV97281	Fibronectin attach	192	5	41.7	500	21	AAH69274	HIV-1 non-subtype
120	5	41.7	327	21	AAV09947	Arabidopsis thalia	193	5	41.7	501	21	AAH32978	Pinus radiata tran
121	5	41.7	328	21	AAV09946	Arabidopsis thalia	194	5	41.7	505	9	AAH80885	Sequence encoded b
122	5	41.7	332	18	AAV32418	Mycobacterium tube	195	5	41.7	505	19	AAV72392	HIV isolate LAV. MA
123	5	41.7	332	18	AAV32350	Mycobacterium tube	196	5	41.7	509	19	AAH80955	Amino acid sequenc
124	5	41.7	332	19	AAV81683	M. tuberculosis im	197	5	41.7	512	19	AAH68473	HIV-1 strain YBF30
125	5	41.7	332	19	AAV64332	Mycobacterium tube	198	5	41.7	515	10	AAH91235	(ENV-80)(GAG-VII)
126	5	41.7	332	20	AAV39083	M. tuberculosis an	199	5	41.7	535	22	AAH49707	Small round struct
127	5	41.7	332	20	AAV38945	M. tuberculosis re	200	5	41.7	537	20	AAV34828	Protein involved i
128	5	41.7	336	21	AAV64021	Arabidopsis thalia	201	5	41.7	559	19	AAV50909	Alteomonas fortis
129	5	41.7	343	21	AAV64020	Arabidopsis thalia	202	5	41.7	561	19	AAV63701	Human hsk1 protein
130	5	41.7	347	19	AAV66197	Maize DIMB0A biosy	203	5	41.7	566	20	AAV49068	Amino acid sequenc
131	5	41.7	351	21	AAV64019	Arabidopsis thalia	204	5	41.7	566	22	AAH31932	Amino acid sequenc
132	5	41.7	357	21	AAV75397	Neisseria gonorrhoe	205	5	41.7	583	20	AAV55919	Pseudomonas fluore
133	5	41.7	359	16	AAV72715	hisc gene product	206	5	41.7	605	16	AAV79625	Endocarditis speci
134	5	41.7	367	21	AAV05434	Arabidopsis thalia	207	5	41.7	612	19	AAV98516	H. pylori GHPD 130
135	5	41.7	368	21	AAV05433	Arabidopsis thalia	208	5	41.7	649	20	AAV90005	Expressed antigen
136	5	41.7	370	13	AAV26183	MS2-Pg3D protein.	209	5	41.7	651	19	AAV53875	Gravin polypeptide
137	5	41.7	371	20	AAV29193	Amino acid sequenc	210	5	41.7	651	21	AAH18410	Human gravin PKA r
138	5	41.7	375	21	AAV09945	Arabidopsis thalia	211	5	41.7	652	20	AAV39225	M. tuberculosis fu
139	5	41.7	381	20	AAV35327	Amino acid sequenc	212	5	41.7	652	20	AAV39082	M. tuberculosis fus
140	5	41.7	382	20	AAV44865	Human tPC3 telomer	213	5	41.7	655	14	AAH31041	smr polypeptide.
141	5	41.7	384	20	AAV06411	Human EDG-7 recept	214	5	41.7	662	20	AAV31940	Human rad17 cell c
142	5	41.7	384	20	AAV06412	Human EDG-7 recept	215	5	41.7	663	20	AAV31941	Human rad17 cell c
143	5	41.7	384	21	AAV69500	A human G-protein	216	5	41.7	669	20	AAV31939	Human rad17 cell c
144	5	41.7	388	21	AAV08082	Human eg6g protein	217	5	41.7	670	17	AAV97869	Testis-associated
145	5	41.7	388	20	AAV04998	Mycobacterium spec	218	5	41.7	670	20	AAV31937	Human rad17 cell c
146	5	41.7	396	21	AAV3868	Gravin polypeptide	219	5	41.7	671	17	AAH85290	Streptococcus faec
147	5	41.7	396	21	AAH18408	Human gravin PKA r	220	5	41.7	691	14	AAH38735	Beta-galactosidase
148	5	41.7	399	18	AAV05432	Arabidopsis thalia	221	5	41.7	707	21	AAV95065	Candida albicans p
149	5	41.7	399	18	AAV33417	Human integrin reg	222	5	41.7	714	18	AAH35316	M. catarrhalis R1
150	5	41.7	399	20	AAV26927	Human integrin reg	223	5	41.7	717	10	AAH91933	BI antigen. Toxop
151	5	41.7	402	20	AAV24475	Mouse p14. Mus sp	224	5	41.7	730	9	AAH80618	Human Bone Morphog
152	5	41.7	404	20	AAV98621	H. pylori GHPD 245	225	5	41.7	730	18	AAH13669	C-proteinase encod
153	5	41.7	410	21	AAV818329	Arabidopsis thalia	226	5	41.7	739	18	AAV25790	Gene 036 product d
154	5	41.7	421	20	AAV39368	SBHMSBI cytokine s	227	5	41.7	752	20	AAV00939	Desulfurococcus M1
155	5	41.7	421	21	AAH12445	Human WSBI protein	228	5	41.7	757	19	AAV75919	C-proteinase sequ
156	5	41.7	421	21	AAH18328	Arabidopsis thalia	229	5	41.7	788	19	AAV70963	Human Ras signal11
157	5	41.7	421	21	AAV53885	A suppressor of cy	230	5	41.7	802	19	AAH81746	M. tuberculosis fu

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:35:42 ; Search time 56.84 Seconds
(without alignments)
12.799 Million cell updates/sec

Title: US-09-372-036-30

Perfect score: 12

Sequence: 1 STPVAPTQEVKK 12

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	12	14	AA45172
2	12	100.0	21	16	AA73891
3	12	100.0	478	14	AA45178
4	12	100.0	484	16	AA73913
5	10	83.3	10	14	AA45173
6	8	66.7	9	14	AA45168
7	7	58.3	7	16	AA73903
8	6	50.0	6	14	AA54615
9	6	50.0	20	14	AA45159
10	6	50.0	157	20	AA73778
11	6	50.0	343	21	AA41666

12	6	50.0	750	20	AA705477	C. albicans Rb1 P
13	6	50.0	1230	19	AA988275	H. pylori GHP0 690
14	5	41.7	7	19	AA721365	Human HUPF-1 mutan
15	5	41.7	9	19	AA70120	Peptide produced b
16	5	41.7	9	20	AA753518	HIV-1 p24 protein
17	5	41.7	9	20	AA740367	Amino acid sequenc
18	5	41.7	9	20	AA726859	HIV-derived lipope
19	5	41.7	11	14	AA54624	Listeria innocua p
20	5	41.7	11	14	AA70126	Peptide produced b
21	5	41.7	11	22	AA72848	Human p53 A767 mut
22	5	41.7	25	16	AA72982	Signal transductio
23	5	41.7	27	20	AA78130	Human secreted pro
24	5	41.7	45	20	AA701143	Secreted protein e
25	5	41.7	48	21	AA733087	Pinus radiata tran
26	5	41.7	87	20	AA727569	Human secreted pro
27	5	41.7	98	21	AA54394	Arabidopsis thalia
28	5	41.7	101	21	AA782898	CUB domain from BM
29	5	41.7	102	22	AA72875	Human p53 A767/V12
30	5	41.7	107	19	AA75784	Human lymphocyte s
31	5	41.7	110	21	AA712211	Arabidopsis thalia
32	5	41.7	110	21	AA759955	Arabidopsis thalia
33	5	41.7	112	21	AA754393	Arabidopsis thalia
34	5	41.7	114	19	AA711113	H. pylori ORF np6e
35	5	41.7	114	21	AA712210	Arabidopsis thalia
36	5	41.7	114	21	AA759954	Arabidopsis thalia
37	5	41.7	121	21	AA754455	zeta mays protein f
38	5	41.7	125	21	AA740264	Human ORF28 p
39	5	41.7	125	21	AA754454	zeta mays protein f
40	5	41.7	130	19	AA77657	Staphylococcus aur
41	5	41.7	132	20	AA735155	Chlamydia pneumoni
42	5	41.7	134	21	AA759953	Arabidopsis thalia
43	5	41.7	135	20	AA736760	Amino acid sequenc
44	5	41.7	142	21	AA708989	Arabidopsis thalia
45	5	41.7	142	21	AA753843	Arabidopsis thalia
46	5	41.7	148	21	AA708988	Arabidopsis thalia
47	5	41.7	148	21	AA753842	Arabidopsis thalia
48	5	41.7	151	21	AA743699	Human cancer assoc
49	5	41.7	152	21	AA754453	zeta mays protein f
50	5	41.7	158	21	AA712578	zeta mays protein f
51	5	41.7	160	21	AA710791	M. avium Innazine
52	5	41.7	168	22	AA79120	Corynebacterium g1
53	5	41.7	168	22	AA79813	Corynebacterium g1
54	5	41.7	174	20	AA789904	Antigen from clust
55	5	41.7	179	21	AA755986	Arabidopsis thalia
56	5	41.7	179	21	AA759942	Arabidopsis thalia
57	5	41.7	180	21	AA755985	Arabidopsis thalia
58	5	41.7	180	21	AA753941	Arabidopsis thalia
59	5	41.7	181	21	AA725268	Arabidopsis thalia
60	5	41.7	181	21	AA708966	Arabidopsis thalia
61	5	41.7	184	21	AA710820	Arabidopsis thalia
62	5	41.7	184	22	AA780053	Corynebacterium g1
63	5	41.7	185	20	AA734781	Chlamydia pneumoni
64	5	41.7	185	21	AA754822	Arabidopsis thalia
65	5	41.7	192	16	AA769639	Hepatitis C virus
66	5	41.7	192	17	AA789510	Hepatitis C virus
67	5	41.7	193	14	AA733986	HCT27 El protein.
68	5	41.7	193	21	AA708865	Arabidopsis thalia
69	5	41.7	193	21	AA710819	Arabidopsis thalia
70	5	41.7	196	21	AA755984	Arabidopsis thalia
71	5	41.7	196	21	AA759940	Arabidopsis thalia
72	5	41.7	201	20	AA789834	Protein encoded by
73	5	41.7	202	21	AA709042	Arabidopsis thalia
74	5	41.7	202	21	AA738651	Arabidopsis thalia
75	5	41.7	205	21	AA708864	Arabidopsis thalia
76	5	41.7	205	21	AA710818	Arabidopsis thalia
77	5	41.7	214	21	AA750386	Human uncoupling p
78	5	41.7	216	22	AA753229	Human secreted pro
79	5	41.7	217	21	AA704638	Arabidopsis thalia
80	5	41.7	219	20	AA730653	Human secreted pro
81	5	41.7	221	20	AA760589	Human normal blad
82	5	41.7	226	21	AA732101	Human secreted pro
83	5	41.7	231	20	AA704036	HIV-1 (BH10 clone)
84	5	41.7	238	21	AA713699	Chlamydia sp. prot

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	217	QTAPK	221						

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Job time: 55 sec

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,517
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-339-517-2

Query Match 45.5%; Score 5; DB 1; Length 296;
Best local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QTAAP 7
DB 217 QTAAP 221

RESULT 49
US-08-438-863-5
Sequence 5; Application US/08438863
Patent No. 5849585
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Ronghao Li
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,863
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-863-5

Query Match 45.5%; Score 5; DB 2; Length 296;
Best local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QTAAP 7
DB 217 QTAAP 221

RESULT 50
US-08-438-862-5
Sequence 5; Application US/08438862
Patent No. 6033660
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,862
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-862-5

Query Match 45.5%; Score 5; DB 3; Length 296;
Best local Similarity 100.0%; Pred. No. 92;

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,436
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-436-5

Query Match 45.5%; Score 5; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 217 QTAPE 221

RESULT 46
US-08-428-927-2

Sequence 2, Application US/08428927
Patent No. 5756456
GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,927
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-428-927-2

Query Match 45.5%; Score 5; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QTAPE 7
Db 217 QTAPE 221

RESULT 47

US-08-428-298-2
Sequence 2, Application US/08428298
Patent No. 5763213
GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,298
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-428-298-2

Query Match 45.5%; Score 5; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QTAPE 7
Db 217 QTAPE 221

RESULT 48

US-08-339-517-2
Sequence 2, Application US/08339517
Patent No. 5770567
GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)

SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-23

Query Match 45.5%; Score 5; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APPAP 9
|||||
DB 266 APPAP 270

RESULT 43

US-08-428-926-2
; Sequence 2, Application US/08428926
; Patent No. 5667780

GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
APPLICANT: Osheroiff, Phyllis L.
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,926
FILING DATE: 25-APR-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-428-926-2

Query Match 45.5%; Score 5; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QYAPK 7
|||||
DB 217 QYAPK 221

RESULT 44
US-08-435-434-5
; Sequence 5, Application US/08435434

Patent No. 5714385
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,434
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-434-5

Query Match 45.5%; Score 5; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QYAPK 7
|||||
DB 217 QYAPK 221

RESULT 45
US-08-435-436-5
; Sequence 5, Application US/08435436
; Patent No. 5721139

GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)

APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-246-361A-23

Query Match 45.5%; Score 5; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
Db 266 APKAP 270

RESULT 41
US-08-463-772-23
Sequence 23, Application US/08463772
Patent No. 6065501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-772-23

Query Match 45.5%; Score 5; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
Db 266 APKAP 270

RESULT 42
PCT-US93-05000-23
Sequence 23, Application PC/7US9305000
GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 23:

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSH91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCR-US93-05000-6

Query Match 45.5%; Score 5; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
DB 265 APKAP 269

RESULT 38
US-08-464-517-23
Sequence 23, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-23

Query Match 45.5%; Score 5; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
DB 266 APKAP 270

RESULT 39
US-08-246-361A-6
Sequence 6, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-246-361A-6

Query Match 45.5%; Score 5; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
DB 266 APKAP 270

RESULT 40
US-08-246-361A-23
Sequence 23, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:

QY 4 TAPKA 8
|||||
Db 92 TAPKA 96

RESULT 35
US-08-464-517-6
; Sequence 6, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIT-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-517-6

Query Match 45.5%; Score 5; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
Db 254 APKAP 258

RESULT 36
US-08-463-772-6
; Sequence 6, Application US/08463772
; Patent No. 6066501
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,772
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIT-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-772-6

Query Match 45.5%; Score 5; DB 3; Length 280;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
Db 254 APKAP 258

RESULT 37
PCT-US93-05000-6
; Sequence 6, Application PC/TUS9305000
; GENERAL INFORMATION:
; APPLICANT: MITOTIX
; TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05000
; FILING DATE: 19930525
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,178
; FILING DATE: 26-MAY-1992

LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-849-420-6

Query Match 45.5%; Score 5; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
|||||
DB 92 TAPKA 96

RESULT 32

US-09-253-854-6
Sequence 6, Application US/09253854
Patent No. 6132717

GENERAL INFORMATION:

APPLICANT: van de Ven, Willem Jan Marie;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van Duljnhoven, Johannes Lambertus Petrus;
APPLICANT: Robbreck, Antonius Johannes Maria; and
APPLICANT: Konling, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity: A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
ZIP: 11753

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,854

CLASSIFICATION:

FILING DATE: Unassigned
ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II/CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-253-854-6

Query Match 45.5%; Score 5; DB 4; Length 278;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
|||||

DB 92 TAPKA 96

RESULT 33

US-09-135-658-4
Sequence 4, Application US/09135658
Patent No. 5972683

GENERAL INFORMATION:

APPLICANT: TSAI, Ying-Chieh
TITLE OF INVENTION: MUTANT TYPE SUBTILISIN YAB AND ITS APPLICATION
FILE REFERENCE: 6653-011-999
CURRENT APPLICATION NUMBER: US/09/135,658
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 86112766
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 4
LENGTH: 279
TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-135-658-4

Query Match 45.5%; Score 5; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
|||||
DB 92 TAPKA 96

RESULT 34

5472855-6
Patent No. 5472855

APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/287,964
FILING DATE: 22-SEP-1994
Prior Application Data:
APPLICATION NUMBER: 90,902
FILING DATE: 12-JUL-1993

APPLICATION NUMBER: 823,039
FILING DATE: 14-JAN-1992
APPLICATION NUMBER: 35,652
FILING DATE: 06-APR-1987
APPLICATION NUMBER: 334,081
FILING DATE: 04-APR-1989

APPLICATION NUMBER: 127,134
FILING DATE: 01-DEC-1987
APPLICATION NUMBER: 846,627
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 858,594
FILING DATE: 30-APR-1986

APPLICATION NUMBER: 614,612
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984

APPLICATION NUMBER: 614,491
FILING DATE: 29-MAY-1984
SEQ ID NO: 6:
LENGTH: 279

5472855-6

Query Match 45.5%; Score 5; DB 6; Length 279;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C11363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4396
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02058-7

Query Match 45.5%; Score 5; DB 5; Length 190;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OQOTA 5
DB 41 OQOTA 45

RESULT 30
US-08-865-203-6
Sequence 6, Application US/08865203
Patent No. 5935815
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van Duljnhoven, Johannes Lambertus Petrus
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Konig, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity: A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.24

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,203
FILING DATE: 29-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-865-203-6

Query Match 45.5%; Score 5; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
DB 92 TAPKA 96

RESULT 31
US-07-849-420-6
Sequence 6, Application US/07849420
Patent No. 5989856
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van Duljnhoven, Johannes Lambertus Petrus
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Konig, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity: A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,420
FILING DATE: 19920624
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Moran, Thomas F.
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 2805/41413
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9550
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-797-7

Query Match 45.5%; Score 5; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 000TA 5
11111
DB 41 000TA 45

RESULT 27

US-08-701-005A-5
Sequence 5, Application US/08/01005A
Patent No. 5877019
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Almin
TITLE OF INVENTION: Animal 2-5A-Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5877019
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, F199, Ernst & Kurtz
STREET: 555 - 13th Street, N.W., Suite 701 E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,005A
FILING DATE: 21-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,304
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1255-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: E. coli
US-08-701-005A-5

Query Match 45.5%; Score 5; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 000TA 5
11111
DB 41 000TA 45

RESULT 28

US-08-479-895-5
Sequence 5, Application US/08/479895
Patent No. 5972678
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Almin
TITLE OF INVENTION: Animal 2-5A-Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5972678
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,895
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-895-5

Query Match 45.5%; Score 5; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 000TA 5
11111
DB 41 000TA 45

RESULT 29

PCT-US95-02058-7
Sequence 7, Application PC/TUS9502058
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

Patent No. 5861300
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,771
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-771-7

Query Match 45.5%; Score 5; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQTA 5
|||||
Db 41 QOQTA 45

RESULT 25
US-08-434-998-7
Sequence 7, Application US/08434998
Patent No. 5866781
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,998
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-998-7

Query Match 45.5%; Score 5; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQTA 5
|||||
Db 41 QOQTA 45

RESULT 26
US-08-487-797-7
Sequence 7, Application US/08487797
Patent No. 5866787
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Holland & Knight
STREET: One E. Broward Boulevard, #1300
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,797
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16(C)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/468-7811
TELEFAX: 305/463-2030
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid

NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-710-749-27

Query Match 45.5%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TAPKA 8
|||||
DB 99 TAPKA 103

RESULT 22
US-08-905-223-464
Sequence 464, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 464:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: sig-peptide
LOCATION: -79...-1
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.
OTHER INFORMATION: seq SFLGSAPTPIQA/LT

US-08-905-223-464

Query Match 45.5%; Score 5; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTAPK 7
|||||
DB 8 QTAPK 12

RESULT 23
US-08-462-481-5
Sequence 5, Application US/08462481
Patent No. 5840577
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Almin
TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5840577
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,481
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL1363-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-481-5

Query Match 45.5%; Score 5; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTA 5
|||||
DB 41 QOOTA 45

RESULT 24
US-08-436-771-7
Sequence 7, Application US/08436771

OY 7 KAPTE 11
|||||
Db 49 KAPTE 53

RESULT 19
US-08-241-853-18
; Sequence 18, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauder & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ. ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-241-853-18

Query Match 45.5%; Score 5; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 APKAP 9
|||||
Db 1 APKAP 5
RESULT 20
US-08-850-917-18
; Sequence 18, Application US/08850917
; Patent No. 585045
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauder & Jackson
; STREET: 411 Hackensack Avenue

CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,917
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,853
; FILING DATE: 12-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ. ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-850-917-18

Query Match 45.5%; Score 5; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
|||||
Db 1 APKAP 5

RESULT 21
US-08-710-749-27
; Sequence 27, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Biles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,197A
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UALB-03293
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-053-197A-46

Query Match 45.5%; Score 5; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTA 5
11111
DB 35 QOOTA 39

RESULT 17
US-08-102-385G-15
Sequence 15, Application US/08102385G
Patent No. 5962294
GENERAL INFORMATION:
APPLICANT: Paulson, James C.
APPLICANT: Wen, Xiaohong
APPLICANT: Livingston, Brian Duane
APPLICANT: Gillespie, William
APPLICANT: Kelm, Sorge
APPLICANT: Burlingame, Alma L.
APPLICANT: Medzhiradzsky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Stalyltransferases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, 38th Floor
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,385G
FILING DATE: 04-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925369
FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310)788-5000

TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-385G-15

Query Match 45.5%; Score 5; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KAPTE 11
11111
DB 33 KAPTE 37

RESULT 18
US-08-102-385G-29
Sequence 29, Application US/08102385G
Patent No. 5962294
GENERAL INFORMATION:
APPLICANT: Paulson, James C.
APPLICANT: Wen, Xiaohong
APPLICANT: Livingston, Brian Duane
APPLICANT: Gillespie, William
APPLICANT: Kelm, Sorge
APPLICANT: Burlingame, Alma L.
APPLICANT: Medzhiradzsky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Stalyltransferases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, 38th Floor
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,385G
FILING DATE: 04-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925369
FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310)788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-385G-29

Query Match 45.5%; Score 5; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria innocua
US-08-456-670B-36

Query Match 45.5%; Score 5; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOTAP 6
11111
DB 8 QOTAP 12

RESULT 15
US-08-456-670B-23
Sequence 23, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWELTER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUEBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL XAA AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 19-25
OTHER INFORMATION: /note= "SOME OR ALL XAA AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-23

Query Match 45.5%; Score 5; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOTAP 6
11111
DB 14 QOTAP 18

RESULT 16
US-09-053-197A-46
Sequence 46, Application US/09053197A
Patent No. 6022952
GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Patent No. 5656452
GENERAL INFORMATION:
APPLICANT: Rao, Anjana
APPLICANT: Hogan, Patrick Gerald
APPLICANT: McCaffrey, Patricia
APPLICANT: Jain, Jugnu
TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE
TITLE OF INVENTION: DNA-BINDING PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,006C
FILING DATE: October 29, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,052
FILING DATE: February 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 04590/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 890
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-145-006C-5

Query Match 54.5%; Score 6; DB 1; Length 890;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 000TAP 6
111111
DB 695 000TAP 700

RESULT 13
PCT-US94-00545-5
Sequence 5, Application PC/TUS9400545
GENERAL INFORMATION:
APPLICANT: Rao, Anjana
APPLICANT: Hogan, Patrick Gerald
APPLICANT: McCaffrey, Patricia
APPLICANT: Jain, Jugnu
TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE
TITLE OF INVENTION: DNA-BINDING PROTEIN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00545
FILING DATE: 18-JAN-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,006
FILING DATE: October 29, 1993
APPLICATION NUMBER: 08/017,052
FILING DATE: February 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 04590/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 890
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-00545-5

Query Match 54.5%; Score 6; DB 5; Length 890;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 000TAP 6
111111
DB 695 000TAP 700

RESULT 14
US-08-456-670B-36
Sequence 36, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORGANISM SOURCE: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note- "SOME OR ALL Xaa AMINO ACIDS
FEATURE:
NAME/KEY: Modified-site
LOCATION: 17-23
OTHER INFORMATION: /note- "SOME OR ALL Xaa AMINO ACIDS
US-08-456-670B-20

Query Match 81.8%; Score 9; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQTAPKAPT 10
Db 8 QQTAPKAPT 16

RESULT 10
US-08-127-499A-34
Sequence 34, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-34

Query Match 63.6%; Score 7; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQTAPKA 8
Db 1 QQTAPKA 7

RESULT 11
US-08-482-847-34
Sequence 34, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-34

Query Match 63.6%; Score 7; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQTAPKA 8
Db 1 QQTAPKA 7

RESULT 12
US-08-145-006C-5
Sequence 5, Application US/08145006C

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-26

Query Match 100.0%; Score 11; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 000TAPKAPTE 11
|||||
Db 291 000TAPKAPTE 301

RESULT 8
US-08-482-847-26
Sequence 26, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-26

Query Match 100.0%; Score 11; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 000TAPKAPTE 11
|||||
Db 291 000TAPKAPTE 301

RESULT 9
US-08-456-670B-20
Sequence 20, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302

APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-39

Query Match 100.0%; Score 11; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
Db 222 000TAPKAPTE 232

RESULT 6
US-08-456-670B-40
Sequence 40 Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BURGER, CHRISTA

APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-40

Query Match 100.0%; Score 11; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
Db 291 000TAPKAPTE 301

RESULT 7
US-08-127-499A-26
Sequence 26 Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
HOMOLOGOUS ANTIGENIC SEQUENCES

APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-456-670B-42

Query Match 100.0%; Score 11; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOOTAPKAPTE 11
DB 2 QOOTAPKAPTE 12

RESULT 3
US-08-127-499A-33
Sequence 33, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-33

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOOTAPKAPTE 11
DB 7 QOOTAPKAPTE 17

RESULT 4
US-08-482-847-33
Sequence 33, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-33

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOOTAPKAPTE 11
DB 7 QOOTAPKAPTE 17

RESULT 5
US-08-456-670B-39
Sequence 39, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED

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977 4 36.4 1457 2 US-08-087-244A-1 Sequence 1, Appl1
978 4 36.4 1457 2 US-08-991-258A-3 Sequence 3, Appl1
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980 4 36.4 1457 3 US-08-665-259-27 Sequence 27, Appl
981 4 36.4 1457 3 US-08-762-500-27 Sequence 27, Appl
982 4 36.4 1457 3 US-08-991-953A-3 Sequence 3, Appl1
983 4 36.4 1501 2 US-08-447-664-3 Sequence 3, Appl1
984 4 36.4 1501 2 US-08-716-679-3 Sequence 3, Appl1
985 4 36.4 1535 3 US-08-755-587-185 Sequence 185, App
986 4 36.4 1580 2 US-08-804-227C-11 Sequence 11, Appl
987 4 36.4 1580 2 US-08-804-198-5 Sequence 5, Appl
988 4 36.4 1596 3 US-08-356-952-3 Sequence 3, Appl1
989 4 36.4 1612 1 US-08-169-927-2 Sequence 2, Appl1
990 4 36.4 1620 1 US-08-542-363-2 Sequence 2, Appl1
991 4 36.4 1620 1 US-09-100-089-2 Sequence 2, Appl1
992 4 36.4 1663 2 US-08-793-126-1 Sequence 1, Appl1
993 4 36.4 1663 4 US-09-132-371-1 Sequence 1, Appl1
994 4 36.4 1663 4 US-09-142-334-22 Sequence 22, Appl
995 4 36.4 1664 2 US-08-642-846-2 Sequence 2, Appl1
996 4 36.4 1720 2 US-08-477-451-12 Sequence 12, Appl
997 4 36.4 1754 1 US-07-745-206A-13 Sequence 13, Appl
998 4 36.4 1848 4 US-08-311-363-13 Sequence 6, Appl1
999 4 36.4 1848 4 US-08-286-791-6 Sequence 6, Appl1
1000 4 36.4 1848 5 PCT-US95-10661A-6
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ALIGNMENTS

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RESULT 1
US-08-456-670B-29
: Sequence 29, Application US/08456670B
: Patent No. 5932415
: GENERAL INFORMATION:
: APPLICANT: SCHUBERT, PETER
: APPLICANT: NEUMANN, SIEGFRIED
: APPLICANT: PAMELZIK, MARTINA
: APPLICANT: LINXWEILER, WINFRIED
: APPLICANT: BURGER, CHRISTA
: APPLICANT: HOFMANN, GOTTFRIED
: APPLICANT: HUBERT, ANDREAS
: APPLICANT: GOEBEL, WERNER
: APPLICANT: KOHLER, STEFAN
: TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
: STREET: 2200 CLARENDON BLVD., SUITE 1400
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: US
: ZIP: 22201
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/456,670B
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/412,227
: FILING DATE: 27-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/075,248
: FILING DATE: 11-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4239567.4
: FILING DATE: 25-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4219111.4
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: FILING DATE: 11-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: HAMLET-KING, DIANA
: REGISTRATION NUMBER: 33,302
: REFERENCE/DOCKET NUMBER: MERCK 1694D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-243-6333
: TELEFAX: 703-243-6410
: TELEX: 64191
: INFORMATION FOR SEQ ID NO: 29:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Listeria monocytogenes
: STRAIN: EGD
: US-08-456-670B-29
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Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QOOTAPKAPTE 11
Db 1 QOOTAPKAPTE 11
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RESULT 2
US-08-456-670B-42
: Sequence 42, Application US/08456670B
: Patent No. 5932415
: GENERAL INFORMATION:
: APPLICANT: SCHUBERT, PETER
: APPLICANT: NEUMANN, SIEGFRIED
: APPLICANT: PAMELZIK, MARTINA
: APPLICANT: LINXWEILER, WINFRIED
: APPLICANT: BURGER, CHRISTA
: APPLICANT: HOFMANN, GOTTFRIED
: APPLICANT: HUBERT, ANDREAS
: APPLICANT: GOEBEL, WERNER
: APPLICANT: KOHLER, STEFAN
: TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
: STREET: 2200 CLARENDON BLVD., SUITE 1400
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: US
: ZIP: 22201
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/456,670B
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/412,227
: FILING DATE: 27-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/075,248
: FILING DATE: 11-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4239567.4
: FILING DATE: 25-NOV-1992
: PRIOR APPLICATION DATA:
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833	4	36.4	851	4	US-09-364-970-2	Sequence 2, Appl1	906	4	36.4	921	1	US-08-646-715-2	Sequence 2, Appl1
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836	4	36.4	852	1	US-08-81-890-13	Sequence 13, Appl	909	4	36.4	941	2	US-08-343-760A-2	Sequence 2, Appl1
837	4	36.4	852	1	US-08-471-033-36	Sequence 36, Appl	910	4	36.4	942	1	US-08-141-324-14	Sequence 14, Appl
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842	4	36.4	852	2	US-08-408-519-5	Sequence 5, Appl1	915	4	36.4	979	2	US-09-058-263-6	Sequence 6, Appl1
843	4	36.4	852	2	US-08-469-334-36	Sequence 36, Appl	916	4	36.4	979	2	US-09-059-099-6	Sequence 6, Appl1
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845	4	36.4	852	3	PCT-US95-03552-5	Sequence 5, Appl1	918	4	36.4	979	5	PCT-US95-06530-6	Sequence 6, Appl1
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847	4	36.4	855	3	US-08-085-291-2	Sequence 2, Appl1	920	4	36.4	984	1	US-08-714-481-2	Sequence 2, Appl1
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849	4	36.4	858	1	US-07-712-284-2	Sequence 2, Appl1	922	4	36.4	989	4	US-09-110-517-4	Sequence 4, Appl1
850	4	36.4	858	2	US-08-583-562B-2	Sequence 2, Appl1	923	4	36.4	992	1	US-08-127-499A-1	Sequence 1, Appl1
851	4	36.4	858	5	PCT-US92-04227-2	Sequence 2, Appl1	924	4	36.4	992	1	US-08-482-847-1	Sequence 1, Appl1
852	4	36.4	859	2	US-08-395-580-2	Sequence 2, Appl1	925	4	36.4	995	5	PCT-US95-04910-14	Sequence 14, Appl1
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854	4	36.4	860	5	PCT-US95-08493-19	Sequence 19, Appl	927	4	36.4	1018	1	US-08-408-093-6	Sequence 6, Appl1
855	4	36.4	866	1	US-08-405-392-17	Sequence 17, Appl	928	4	36.4	1018	1	US-08-408-420A-6	Sequence 6, Appl1
856	4	36.4	866	3	US-08-487-691-17	Sequence 17, Appl	929	4	36.4	1018	1	US-08-714-901-6	Sequence 6, Appl1
857	4	36.4	868	1	US-08-374-834-1	Sequence 1, Appl1	930	4	36.4	1018	1	US-08-452-052-2	Sequence 2, Appl1
858	4	36.4	868	2	US-08-644-271-1	Sequence 1, Appl1	931	4	36.4	1018	3	US-08-040-741-6	Sequence 6, Appl1
859	4	36.4	868	5	PCT-US95-08493-21	Sequence 21, Appl	932	4	36.4	1025	2	US-08-530-792D-23	Sequence 23, Appl
860	4	36.4	869	1	US-08-188-582-32	Sequence 32, Appl	933	4	36.4	1026	2	US-08-542-003-6	Sequence 6, Appl1
861	4	36.4	869	1	US-08-646-715-32	Sequence 32, Appl	934	4	36.4	1026	2	US-08-322-760A-6	Sequence 6, Appl1
862	4	36.4	869	1	US-08-374-834-16	Sequence 16, Appl	935	4	36.4	1026	2	US-08-530-792D-22	Sequence 22, Appl
863	4	36.4	869	2	US-08-644-271-29	Sequence 29, Appl	936	4	36.4	1063	1	US-08-093-453B-3	Sequence 3, Appl1
864	4	36.4	872	1	US-08-766-014-2	Sequence 2, Appl1	937	4	36.4	1063	1	US-08-127-499A-8	Sequence 8, Appl1
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866	4	36.4	881	4	US-09-073-898-32	Sequence 32, Appl	939	4	36.4	1078	3	US-08-480-474-11	Sequence 11, Appl
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868	4	36.4	884	2	US-08-471-044-5	Sequence 5, Appl1	941	4	36.4	1141	1	US-08-131-365B-54	Sequence 54, Appl
869	4	36.4	884	2	US-08-463-483A-5	Sequence 5, Appl1	942	4	36.4	1141	1	US-08-363-300-2	Sequence 2, Appl1
870	4	36.4	884	2	US-08-471-046A-5	Sequence 5, Appl1	943	4	36.4	1141	2	US-08-668-122-54	Sequence 54, Appl
871	4	36.4	884	2	US-08-470-566B-5	Sequence 5, Appl1	944	4	36.4	1164	2	US-08-589-736-1	Sequence 1, Appl
872	4	36.4	884	2	US-08-469-334-5	Sequence 5, Appl1	945	4	36.4	1240	2	US-08-680-326-37	Sequence 37, Appl
873	4	36.4	884	3	US-09-300-529-5	Sequence 5, Appl1	946	4	36.4	1248	2	US-08-348-353-17	Sequence 17, Appl
874	4	36.4	885	2	US-08-310-912A-2	Sequence 2, Appl1	947	4	36.4	1248	2	US-08-465-965-17	Sequence 17, Appl
875	4	36.4	885	5	US-08-841-089-2	Sequence 2, Appl1	948	4	36.4	1248	3	US-08-465-966-17	Sequence 17, Appl
876	4	36.4	885	5	PCT-US95-04570-2	Sequence 2, Appl1	949	4	36.4	1257	4	US-09-220-641-3	Sequence 3, Appl1
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878	4	36.4	894	2	US-08-867-941-15	Sequence 15, Appl	951	4	36.4	1285	4	US-08-974-549A-600	Sequence 600, App
879	4	36.4	898	1	US-08-465-995A-2	Sequence 2, Appl1	952	4	36.4	1285	3	US-08-762-428A-6	Sequence 6, Appl1
880	4	36.4	898	1	US-08-465-995A-4	Sequence 4, Appl1	953	4	36.4	1324	2	US-08-811-897A-56	Sequence 56, Appl
881	4	36.4	898	2	US-08-465-994C-2	Sequence 2, Appl1	954	4	36.4	1336	2	US-08-551-355-6	Sequence 6, Appl1
882	4	36.4	898	2	US-08-465-994C-4	Sequence 4, Appl1	955	4	36.4	1336	5	PCT-US93-12687-6	Sequence 6, Appl1
883	4	36.4	898	2	US-08-966-145-2	Sequence 2, Appl1	956	4	36.4	1338	1	US-08-471-033-50	Sequence 50, Appl
884	4	36.4	898	2	US-08-966-145-4	Sequence 4, Appl1	957	4	36.4	1338	2	US-08-471-044-50	Sequence 50, Appl
885	4	36.4	898	2	US-08-867-941-11	Sequence 11, Appl	958	4	36.4	1338	2	US-08-463-483A-50	Sequence 50, Appl
886	4	36.4	903	2	US-08-853-310-2	Sequence 2, Appl1	959	4	36.4	1338	2	US-08-471-046A-50	Sequence 50, Appl
887	4	36.4	905	1	US-08-405-392-2	Sequence 2, Appl1	960	4	36.4	1338	2	US-08-470-566B-50	Sequence 50, Appl
888	4	36.4	905	3	US-08-487-691-2	Sequence 2, Appl1	961	4	36.4	1338	2	US-08-469-334-50	Sequence 50, Appl
889	4	36.4	905	4	US-08-666-221B-4	Sequence 4, Appl1	962	4	36.4	1338	3	US-09-300-529-50	Sequence 50, Appl
890	4	36.4	905	4	US-08-666-221B-10	Sequence 10, Appl	963	4	36.4	1346	1	US-08-471-033-23	Sequence 23, Appl
891	4	36.4	907	3	US-08-783-774-2	Sequence 7, Appl1	964	4	36.4	1346	2	US-08-471-044-23	Sequence 23, Appl
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895	4	36.4	908	3	US-08-604-298-1	Sequence 1, Appl1	968	4	36.4	1346	2	US-08-469-334-23	Sequence 23, Appl
896	4	36.4	908	4	US-08-855-146-2	Sequence 2, Appl1	969	4	36.4	1346	2	US-09-300-529-23	Sequence 23, Appl
897	4	36.4	909	5	US-08-310-912A-142	Sequence 142, App	970	4	36.4	1358	2	US-08-570-311-27	Sequence 27, Appl
898	4	36.4	909	5	PCT-US95-04589-142	Sequence 142, App	971	4	36.4	1439	2	US-08-449-644-4	Sequence 2, Appl1
899	4	36.4	913	3	US-08-911-853-17	Sequence 17, Appl	972	4	36.4	1439	2	US-08-087-244A-2	Sequence 2, Appl1
900	4	36.4	913	4	US-09-479-408-17	Sequence 17, Appl	973	4	36.4	1443	2	US-08-670-707A-39	Sequence 39, Appl
901	4	36.4	918	2	US-08-843-530B-35	Sequence 35, Appl	974	4	36.4	1443	4	US-09-037-601-39	Sequence 39, Appl
902	4	36.4	920	1	US-08-101-593-2	Sequence 2, Appl1	975	4	36.4	1457	2	US-08-652-971-3	Sequence 3, Appl1
903	4	36.4	920	1	US-08-101-593-4	Sequence 4, Appl1	976	4	36.4	1457	2	US-08-449-644-1	Sequence 1, Appl1

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687	4	36.4	600	3	US-08-904-871-2	Sequence 2, Appl1	760	4	36.4	733	4	US-08-464-700-2	Sequence 1, Appl1
688	4	36.4	605	1	US-08-462-884A-3	Sequence 3, Appl1	761	4	36.4	734	4	US-09-000-016-4	Sequence 4, Appl1
689	4	36.4	605	1	US-08-461-881B-3	Sequence 3, Appl1	762	4	36.4	737	1	US-08-185-432-2	Sequence 2, Appl1
690	4	36.4	605	2	US-08-869-402-2	Sequence 2, Appl1	763	4	36.4	737	1	US-08-185-432-2	Sequence 4, Appl1
691	4	36.4	605	2	US-08-687-956A-1	Sequence 1, Appl1	764	4	36.4	739	1	US-07-803-622E-2	Sequence 2, Appl1
692	4	36.4	605	2	US-09-123-960-3	Sequence 3, Appl1	765	4	36.4	739	1	US-08-836-943-2	Sequence 2, Appl1
693	4	36.4	607	2	US-08-752-307B-12	Sequence 12, Appl1	766	4	36.4	754	3	US-08-646-273-30	Sequence 30, Appl1
694	4	36.4	610	1	US-08-365-470-3	Sequence 3, Appl1	767	4	36.4	755	3	US-09-071-101-2	Sequence 2, Appl1
695	4	36.4	610	2	US-08-455-073A-2	Sequence 2, Appl1	768	4	36.4	755	3	US-09-369-618-2	Sequence 2, Appl1
696	4	36.4	610	3	US-09-209-668-19	Sequence 19, Appl1	769	4	36.4	755	3	US-09-369-617-2	Sequence 2, Appl1
697	4	36.4	610	6	5217870-2	Patent No. 5217870	770	4	36.4	758	1	US-08-289-911-2	Sequence 2, Appl1
698	4	36.4	614	1	US-07-732-962A-2	Sequence 2, Appl1	771	4	36.4	760	1	US-08-195-152-2	Sequence 2, Appl1
699	4	36.4	614	1	US-08-652-207A-2	Sequence 2, Appl1	772	4	36.4	761	4	US-09-046-894-35	Sequence 35, Appl1
700	4	36.4	614	2	US-08-370-156-2	Sequence 2, Appl1	773	4	36.4	763	2	US-08-677-862-2	Sequence 2, Appl1
701	4	36.4	614	3	US-08-446-100-19	Sequence 19, Appl1	774	4	36.4	763	2	US-09-252-571-2	Sequence 2, Appl1
702	4	36.4	614	3	US-08-446-100-20	Sequence 20, Appl1	775	4	36.4	763	3	US-09-434-065-2	Sequence 2, Appl1
703	4	36.4	614	3	US-08-446-100-21	Sequence 21, Appl1	776	4	36.4	763	4	US-08-789-275-4	Sequence 4, Appl1
704	4	36.4	614	3	US-08-446-100-22	Sequence 22, Appl1	777	4	36.4	763	4	US-08-789-275-5	Sequence 5, Appl1
705	4	36.4	614	3	US-08-446-100-23	Sequence 23, Appl1	778	4	36.4	768	2	US-08-232-617A-5	Sequence 5, Appl1
706	4	36.4	614	3	US-08-446-100-25	Sequence 25, Appl1	779	4	36.4	770	1	US-08-445-135-2	Sequence 2, Appl1
707	4	36.4	614	3	US-08-814-095-2	Sequence 2, Appl1	780	4	36.4	776	4	US-08-961-083-86	Sequence 86, Appl1
708	4	36.4	616	5	PCT-US92-06106-2	Sequence 2, Appl1	781	4	36.4	777	4	US-08-764-870-13	Sequence 13, Appl1
709	4	36.4	616	1	US-08-385-370-2	Sequence 2, Appl1	782	4	36.4	782	1	US-07-725-083-2	Sequence 2, Appl1
710	4	36.4	616	1	US-08-385-370-4	Sequence 4, Appl1	783	4	36.4	782	4	US-08-669-286-10	Sequence 10, Appl1
711	4	36.4	617	2	US-08-370-156-6	Sequence 6, Appl1	784	4	36.4	782	4	US-09-469-253-10	Sequence 10, Appl1
712	4	36.4	617	3	US-08-814-095-6	Sequence 6, Appl1	785	4	36.4	791	4	US-08-861-745B-1	Sequence 1, Appl1
713	4	36.4	622	1	US-08-426-819A-35	Sequence 35, Appl1	786	4	36.4	792	2	US-08-678-039A-40	Sequence 40, Appl1
714	4	36.4	624	2	US-08-879-561-3	Sequence 3, Appl1	787	4	36.4	792	2	US-08-190-802A-64	Sequence 64, Appl1
715	4	36.4	624	2	US-08-879-561-9	Sequence 9, Appl1	788	4	36.4	798	1	US-08-190-802A-68	Sequence 68, Appl1
716	4	36.4	628	3	US-08-776-271-2	Sequence 2, Appl1	789	4	36.4	799	2	US-08-308-818-8	Sequence 2, Appl1
717	4	36.4	628	4	US-09-215-035-2	Sequence 2, Appl1	790	4	36.4	805	4	US-08-989-299-2	Sequence 2, Appl1
718	4	36.4	629	3	US-08-556-419-23	Sequence 23, Appl1	791	4	36.4	811	2	US-08-933-750C-45	Sequence 45, Appl1
719	4	36.4	630	2	US-08-797-366-3	Sequence 3, Appl1	792	4	36.4	811	4	US-09-234-613-45	Sequence 45, Appl1
720	4	36.4	630	2	US-08-956-268-3	Sequence 3, Appl1	793	4	36.4	814	1	US-08-318-831-2	Sequence 2, Appl1
721	4	36.4	635	4	US-08-857-076-101	Sequence 101, Appl1	794	4	36.4	816	1	US-07-731-157A-4	Sequence 4, Appl1
722	4	36.4	638	2	US-08-426-125-4	Sequence 4, Appl1	795	4	36.4	816	1	US-08-229-444B-2	Sequence 2, Appl1
723	4	36.4	638	2	US-08-455-355-4	Sequence 4, Appl1	796	4	36.4	816	2	US-08-267-803B-9	Sequence 9, Appl1
724	4	36.4	639	1	US-08-466-390-2	Sequence 2, Appl1	797	4	36.4	816	2	US-08-541-180-4	Sequence 4, Appl1
725	4	36.4	639	1	US-08-470-950-2	Sequence 2, Appl1	798	4	36.4	816	4	US-09-041-886-17	Sequence 17, Appl1
726	4	36.4	639	1	US-08-467-781-2	Sequence 2, Appl1	799	4	36.4	820	4	US-09-173-914-2	Sequence 2, Appl1
727	4	36.4	639	1	US-08-195-487-2	Sequence 2, Appl1	800	4	36.4	821	1	US-07-935-311A-4	Sequence 4, Appl1
728	4	36.4	639	2	US-08-483-924-2	Sequence 2, Appl1	801	4	36.4	821	1	US-08-368-079-4	Sequence 4, Appl1
729	4	36.4	639	5	PCT-US93-06160-2	Sequence 2, Appl1	802	4	36.4	821	5	PCT-US93-07996-4	Sequence 4, Appl1
730	4	36.4	640	4	US-09-177-349-4	Sequence 4, Appl1	803	4	36.4	823	3	US-09-000-0163-2	Sequence 2, Appl1
731	4	36.4	642	2	US-08-245-511-48	Sequence 48, Appl1	804	4	36.4	828	3	US-08-481-435-2	Sequence 2, Appl1
732	4	36.4	642	2	US-08-600-993A-48	Sequence 48, Appl1	805	4	36.4	830	1	US-07-977-834-6	Sequence 6, Appl1
733	4	36.4	645	1	US-07-779-172A-3	Sequence 3, Appl1	806	4	36.4	830	1	US-08-458-819-6	Sequence 6, Appl1
734	4	36.4	649	4	US-09-183-706-43	Sequence 43, Appl1	807	4	36.4	830	5	PCT-US91-07035-6	Sequence 6, Appl1
735	4	36.4	649	4	US-09-188-930-305	Sequence 305, Appl1	808	4	36.4	834	1	US-08-471-033-21	Sequence 21, Appl1
736	4	36.4	655	1	US-07-736-178C-2	Sequence 2, Appl1	809	4	36.4	834	2	US-08-471-044A-21	Sequence 21, Appl1
737	4	36.4	657	3	US-08-893-852A-3	Sequence 3, Appl1	810	4	36.4	834	2	US-08-463-883A-21	Sequence 21, Appl1
738	4	36.4	657	3	US-07-705-490-14	Sequence 14, Appl1	811	4	36.4	834	2	US-08-471-046A-21	Sequence 21, Appl1
739	4	36.4	657	4	US-08-821-818-3	Sequence 3, Appl1	812	4	36.4	834	2	US-08-470-566B-21	Sequence 21, Appl1
740	4	36.4	657	4	US-07-751-891B-14	Sequence 14, Appl1	813	4	36.4	834	2	US-08-469-334-21	Sequence 21, Appl1
741	4	36.4	664	1	US-08-421-661-6	Sequence 6, Appl1	814	4	36.4	834	3	US-09-300-529-21	Sequence 21, Appl1
742	4	36.4	664	3	US-08-669-408B-2	Sequence 2, Appl1	815	4	36.4	837	1	US-07-923-976-2	Sequence 2, Appl1
743	4	36.4	666	1	US-08-318-831-3	Sequence 3, Appl1	816	4	36.4	845	3	US-08-804-439A-94	Sequence 94, Appl1
744	4	36.4	668	1	US-08-205-018-2	Sequence 2, Appl1	817	4	36.4	845	3	US-08-720-229-94	Sequence 94, Appl1
745	4	36.4	669	2	US-07-861-800-2	Sequence 2, Appl1	818	4	36.4	846	3	US-08-885-291-55	Sequence 55, Appl1
746	4	36.4	694	2	US-08-895-522-4	Sequence 4, Appl1	819	4	36.4	846	3	US-09-107-847-2	Sequence 2, Appl1
747	4	36.4	694	2	US-09-195-391-4	Sequence 4, Appl1	820	4	36.4	849	1	US-08-405-392-18	Sequence 18, Appl1
748	4	36.4	694	3	US-08-559-397A-31	Sequence 31, Appl1	821	4	36.4	849	3	US-08-804-439A-17	Sequence 17, Appl1
749	4	36.4	699	1	US-08-348-006B-7	Sequence 7, Appl1	822	4	36.4	849	3	US-08-487-691-18	Sequence 18, Appl1
750	4	36.4	699	2	US-08-800-825A-7	Sequence 7, Appl1	823	4	36.4	849	3	US-08-720-229-17	Sequence 17, Appl1
751	4	36.4	699	4	US-09-158-657-7	Sequence 7, Appl1	824	4	36.4	850	3	US-08-481-135-10	Sequence 10, Appl1
752	4	36.4	699	4	PCT-US94-07297-39	Sequence 39, Appl1	825	4	36.4	851	2	US-08-369-996-2	Sequence 2, Appl1
753	4	36.4	700	3	US-08-931-952-2	Sequence 2, Appl1	826	4	36.4	851	2	US-08-852-091-2	Sequence 2, Appl1
754	4	36.4	700	3	US-08-272-247-2	Sequence 2, Appl1	827	4	36.4	851	3	US-08-820-754-2	Sequence 2, Appl1
755	4	36.4	700	5	PCT-US95-08560-2	Sequence 2, Appl1	828	4	36.4	851	3	US-08-956-652-2	Sequence 2, Appl1
756	4	36.4	709	4	US-08-646-273-23	Sequence 23, Appl1	829	4	36.4	851	3	US-08-956-669-2	Sequence 2, Appl1
757	4	36.4	715	3	US-08-425-843-7	Sequence 7, Appl1	830	4	36.4	851	3	US-09-012-710-2	Sequence 2, Appl1

539	4	36.4	428	1	US-08-332-576-2	Sequence 2, Appl1	612	4	36.4	500	2	US-08-987-519-1	Sequence 1, Appl1
540	4	36.4	428	2	US-08-551-687-1	Sequence 1, Appl1	613	4	36.4	500	2	PCT-US95-05471-77	Sequence 77, Appl1
541	4	36.4	428	5	PCT-US95-13672-2	Sequence 2, Appl1	614	4	36.4	501	2	US-08-966-650-4	Sequence 4, Appl1
542	4	36.4	431	3	US-08-807-342B-5	Sequence 5, Appl1	615	4	36.4	503	3	US-09-010-998-2	Sequence 2, Appl1
543	4	36.4	431	4	US-09-188-930-341	Sequence 341, App	616	4	36.4	506	2	US-08-849-460A-5	Sequence 3, Appl1
544	4	36.4	431	4	US-09-381-681-3	Sequence 3, Appl1	617	4	36.4	507	1	US-08-305-505-3	Sequence 5, Appl1
545	4	36.4	432	1	US-08-522-166-8	Sequence 8, Appl1	618	4	36.4	507	6	US-08-833-096-2	Sequence 2, Appl1
546	4	36.4	432	1	US-08-488-382A-8	Sequence 8, Appl1	619	4	36.4	509	2	US-08-559-505-2	Sequence 2, Appl1
547	4	36.4	432	2	US-08-480-912-8	Sequence 8, Appl1	620	4	36.4	509	2	US-08-749-907-2	Sequence 2, Appl1
548	4	36.4	432	5	PCT-US95-04910-13	Sequence 13, Appl1	621	4	36.4	509	2	US-08-890-960-4	Sequence 4, Appl1
549	4	36.4	433	1	US-07-672-483-4	Sequence 4, Appl1	622	4	36.4	509	2	US-08-890-960-4	Sequence 4, Appl1
550	4	36.4	433	3	US-08-941-533-6	Sequence 6, Appl1	623	4	36.4	509	3	US-08-890-960-4	Sequence 4, Appl1
551	4	36.4	434	3	US-08-337-602-3	Sequence 3, Appl1	624	4	36.4	509	3	US-08-822-324-8	Sequence 8, Appl1
552	4	36.4	434	3	US-08-558-135-3	Sequence 3, Appl1	625	4	36.4	509	4	US-09-023-894-4	Sequence 4, Appl1
553	4	36.4	437	1	US-08-136-119-2	Sequence 2, Appl1	626	4	36.4	509	4	US-08-857-076-46	Sequence 46, Appl1
554	4	36.4	437	2	US-08-481-814A-7	Sequence 7, Appl1	627	4	36.4	509	4	US-09-023-894-4	Sequence 4, Appl1
555	4	36.4	438	1	US-07-923-095-2	Sequence 2, Appl1	628	4	36.4	509	5	PCT-US95-07721-4	Sequence 4, Appl1
556	4	36.4	438	1	US-08-229-511-2	Sequence 2, Appl1	629	4	36.4	517	1	US-08-132-649-2	Sequence 2, Appl1
557	4	36.4	438	1	US-08-314-979-2	Sequence 2, Appl1	630	4	36.4	517	1	US-08-764-343-4	Sequence 4, Appl1
558	4	36.4	438	1	US-08-436-716-2	Sequence 2, Appl1	631	4	36.4	517	3	US-08-767-579-2	Sequence 2, Appl1
559	4	36.4	440	1	US-07-930-686-12	Sequence 12, Appl1	632	4	36.4	520	1	US-08-261-832A-10	Sequence 10, Appl1
560	4	36.4	440	2	US-08-460-998-12	Sequence 12, Appl1	633	4	36.4	520	4	US-09-000-016-7	Sequence 7, Appl1
561	4	36.4	441	4	US-08-244-603A-1	Sequence 1, Appl1	634	4	36.4	520	5	PCT-US95-07744A-10	Sequence 10, Appl1
562	4	36.4	441	4	US-09-191-136-31	Sequence 31, Appl1	635	4	36.4	525	4	US-08-984-618-17	Sequence 17, Appl1
563	4	36.4	443	1	US-08-476-008-69	Sequence 69, Appl1	636	4	36.4	529	1	US-07-779-890-2	Sequence 2, Appl1
564	4	36.4	443	1	US-08-306-063-69	Sequence 69, Appl1	637	4	36.4	529	1	US-07-779-890-2	Sequence 2, Appl1
565	4	36.4	443	1	US-08-833-485-69	Sequence 69, Appl1	638	4	36.4	529	5	PCT-US93-05640-2	Sequence 2, Appl1
566	4	36.4	443	1	US-09-137-440-69	Sequence 69, Appl1	639	4	36.4	537	1	US-08-173-508-2	Sequence 2, Appl1
567	4	36.4	445	1	US-08-447-925-6	Sequence 6, Appl1	640	4	36.4	537	1	US-08-472-028A-2	Sequence 2, Appl1
568	4	36.4	445	1	US-08-353-400-33	Sequence 33, Appl1	641	4	36.4	537	2	US-08-265-310-2	Sequence 2, Appl1
569	4	36.4	447	3	US-09-109-204-3	Sequence 3, Appl1	642	4	36.4	537	2	US-08-808-931-2	Sequence 2, Appl1
570	4	36.4	447	6	US-09-109-204-3	Sequence 3, Appl1	643	4	36.4	537	3	US-08-808-931-2	Sequence 2, Appl1
571	4	36.4	448	4	US-08-952-127-21	Sequence 21, Appl1	644	4	36.4	537	3	US-09-050-603A-2	Sequence 2, Appl1
572	4	36.4	453	4	US-08-961-083-38	Sequence 38, Appl1	645	4	36.4	537	3	US-09-102-420B-2	Sequence 2, Appl1
573	4	36.4	454	1	US-07-930-686-10	Sequence 10, Appl1	646	4	36.4	537	3	US-08-951-742-2	Sequence 2, Appl1
574	4	36.4	454	2	US-08-460-998-10	Sequence 10, Appl1	647	4	36.4	537	4	US-09-071-296-2	Sequence 2, Appl1
575	4	36.4	455	2	US-08-272-255-14	Sequence 14, Appl1	648	4	36.4	538	2	US-08-729-214-24	Sequence 24, Appl1
576	4	36.4	455	5	PCT-US95-08565-14	Sequence 14, Appl1	649	4	36.4	538	3	US-09-028-994-24	Sequence 24, Appl1
577	4	36.4	455	1	US-08-403-545-5	Sequence 5, Appl1	650	4	36.4	539	3	US-09-264-737-1	Sequence 1, Appl1
578	4	36.4	459	4	US-08-404-381-5	Sequence 5, Appl1	651	4	36.4	540	4	US-08-991-677-8	Sequence 8, Appl1
579	4	36.4	461	1	US-08-672-571A-3	Sequence 3, Appl1	652	4	36.4	545	1	US-08-133-347-2	Sequence 2, Appl1
580	4	36.4	464	1	US-08-353-400-36	Sequence 36, Appl1	653	4	36.4	548	4	US-08-687-590-31	Sequence 31, Appl1
581	4	36.4	469	1	US-08-551-687-6	Sequence 6, Appl1	654	4	36.4	549	5	PCT-US93-05701-2	Sequence 2, Appl1
582	4	36.4	469	2	US-08-551-687-6	Sequence 6, Appl1	655	4	36.4	550	3	US-08-807-342B-4	Sequence 4, Appl1
583	4	36.4	471	3	US-08-911-853-4	Sequence 4, Appl1	656	4	36.4	554	4	US-08-180-371-2	Sequence 2, Appl1
584	4	36.4	471	4	US-09-479-409-4	Sequence 4, Appl1	657	4	36.4	557	4	US-09-027-064-2	Sequence 2, Appl1
585	4	36.4	472	4	US-09-088-425-1	Sequence 1, Appl1	658	4	36.4	559	1	US-08-424-788-3	Sequence 3, Appl1
586	4	36.4	478	5	PCT-US95-08493-15	Sequence 15, Appl1	659	4	36.4	559	2	US-08-756-317-10	Sequence 10, Appl1
587	4	36.4	480	2	US-08-570-227A-2	Sequence 2, Appl1	660	4	36.4	562	2	US-08-687-702-1	Sequence 1, Appl1
588	4	36.4	480	4	US-09-077-991-2	Sequence 2, Appl1	661	4	36.4	566	3	US-09-264-737-2	Sequence 2, Appl1
589	4	36.4	485	1	US-07-881-075-1	Sequence 1, Appl1	662	4	36.4	567	3	US-08-646-273-19	Sequence 19, Appl1
590	4	36.4	485	1	US-08-120-827-1	Sequence 1, Appl1	663	4	36.4	568	1	US-07-803-632E-4	Sequence 4, Appl1
591	4	36.4	485	1	US-08-453-956-15	Sequence 15, Appl1	664	4	36.4	568	1	US-08-262-424-7	Sequence 7, Appl1
592	4	36.4	485	1	US-08-478-675-1	Sequence 1, Appl1	665	4	36.4	568	2	US-08-493-197-7	Sequence 7, Appl1
593	4	36.4	485	1	US-08-086-631-15	Sequence 15, Appl1	666	4	36.4	568	2	US-08-717-587A-4	Sequence 4, Appl1
594	4	36.4	485	2	US-08-452-930-15	Sequence 15, Appl1	667	4	36.4	568	3	US-08-883-610A-4	Sequence 4, Appl1
595	4	36.4	485	5	PCT-US93-08174-15	Sequence 15, Appl1	668	4	36.4	568	5	US-08-936-094A-4	Sequence 4, Appl1
596	4	36.4	489	1	US-08-318-831-4	Sequence 4, Appl1	669	4	36.4	568	5	PCT-US95-07844-7	Sequence 7, Appl1
597	4	36.4	489	1	PCT-US93-11110-1	Sequence 1, Appl1	670	4	36.4	575	1	US-08-424-788-2	Sequence 2, Appl1
598	4	36.4	489	6	5221789-1	Patent No. 5221789	671	4	36.4	575	1	US-08-110-663-4	Sequence 4, Appl1
599	4	36.4	490	1	US-08-672-571A-1	Sequence 1, Appl1	672	4	36.4	575	2	US-08-477-166-4	Sequence 4, Appl1
600	4	36.4	490	2	US-08-687-916-24	Sequence 24, Appl1	673	4	36.4	575	2	US-08-472-097-4	Sequence 4, Appl1
601	4	36.4	490	4	US-09-138-614-24	Sequence 24, Appl1	674	4	36.4	575	5	PCT-US93-11638-4	Sequence 4, Appl1
602	4	36.4	491	2	US-08-687-916-23	Sequence 23, Appl1	675	4	36.4	584	1	US-08-426-819A-36	Sequence 36, Appl1
603	4	36.4	491	4	US-09-138-614-23	Sequence 23, Appl1	676	4	36.4	590	3	US-08-893-852A-4	Sequence 4, Appl1
604	4	36.4	493	4	US-08-378-313-13	Sequence 13, Appl1	677	4	36.4	590	4	US-08-821-818-2	Sequence 2, Appl1
605	4	36.4	493	4	US-08-378-313-21	Sequence 21, Appl1	678	4	36.4	591	2	US-08-889-402-1	Sequence 1, Appl1
606	4	36.4	493	4	US-08-378-313-28	Sequence 28, Appl1	679	4	36.4	594	3	US-08-581-186C-14	Sequence 14, Appl1
607	4	36.4	494	4	US-08-378-313-23	Sequence 23, Appl1	680	4	36.4	597	1	US-08-462-884A-1	Sequence 1, Appl1
608	4	36.4	494	4	US-08-378-313-29	Sequence 23, Appl1	681	4	36.4	597	1	US-08-461-881B-1	Sequence 1, Appl1
609	4	36.4	495	2	US-08-687-916-22	Sequence 22, Appl1	682	4	36.4	597	2	US-09-123-960-1	Sequence 1, Appl1
610	4	36.4	495	4	US-09-138-614-22	Sequence 22, Appl1	683	4	36.4	599	1	US-08-442-542-18	Sequence 18, Appl1
611	4	36.4	500	1	US-08-260-582-77	Sequence 77, Appl1	684	4	36.4	599	3	US-08-765-469-18	Sequence 18, Appl1

393	4	36.4	296	1	US-07-745-382-14	Sequence 14, Appl	466	4	36.4	352	2	US-09-076-193-3	Sequence 3, Appl1
394	4	36.4	296	1	US-07-921-848-14	Sequence 14, Appl	467	4	36.4	352	2	US-09-076-193-5	Sequence 7, Appl1
395	4	36.4	296	1	US-08-115-680-4	Sequence 4, Appl1	468	4	36.4	352	2	US-09-076-193-7	Sequence 11, Appl
396	4	36.4	296	1	US-07-941-372-4	Sequence 14, Appl	469	4	36.4	352	5	PCT-US94-05286-11	Sequence 2, Appl1
397	4	36.4	296	1	US-08-105-301A-14	Sequence 14, Appl	470	4	36.4	353	3	US-08-978-889A-2	Sequence 1, Appl1
398	4	36.4	296	4	US-08-810-436-14	Sequence 14, Appl	471	4	36.4	353	4	US-09-336-601-1	Sequence 1, Appl1
399	4	36.4	296	4	PCT-US93-08247-4	Sequence 4, Appl1	472	4	36.4	353	4	US-09-301-665-4	Sequence 4, Appl1
400	4	36.4	296	5	PCT-US94-14179-14	Sequence 14, Appl	473	4	36.4	354	1	US-08-626-994A-1	Sequence 1, Appl1
401	4	36.4	297	4	US-08-580-545B-6	Sequence 6, Appl1	474	4	36.4	354	4	US-08-957-442-1	Sequence 1, Appl1
402	4	36.4	297	4	US-09-262-653A-6	Sequence 6, Appl1	475	4	36.4	354	5	PCT-US96-10618-2	Sequence 2, Appl1
403	4	36.4	298	4	US-08-961-083-24	Sequence 24, Appl	476	4	36.4	355	2	US-08-515-251A-2	Sequence 2, Appl1
404	4	36.4	299	2	US-08-773-608A-2	Sequence 2, Appl1	477	4	36.4	356	3	US-08-945-056-6	Sequence 8, Appl1
405	4	36.4	302	3	US-08-303-861-20	Sequence 20, Appl	478	4	36.4	356	3	US-08-945-056-8	Sequence 4, Appl1
406	4	36.4	308	1	US-08-499-568-2	Sequence 2, Appl1	479	4	36.4	357	2	US-08-515-251A-4	Sequence 4, Appl1
407	4	36.4	308	1	US-08-793-958-2	Sequence 2, Appl1	480	4	36.4	359	2	US-08-139-609-1	Sequence 1, Appl1
408	4	36.4	309	4	US-09-342-084-2	Sequence 2, Appl1	481	4	36.4	375	1	US-08-027-986-1	Sequence 1, Appl1
409	4	36.4	315	5	PCT-US94-03796-2	Sequence 2, Appl1	482	4	36.4	375	1	US-08-027-986-2	Sequence 1, Appl1
410	4	36.4	317	1	US-07-688-299-1	Sequence 1, Appl1	483	4	36.4	375	2	US-08-525-596B-14	Sequence 14, Appl
411	4	36.4	317	1	US-07-980-517A-1	Sequence 1, Appl1	484	4	36.4	375	2	US-08-765-875-5	Sequence 5, Appl1
412	4	36.4	318	1	US-07-688-299-3	Sequence 3, Appl1	485	4	36.4	375	3	US-08-795-671-5	Sequence 5, Appl1
413	4	36.4	319	2	US-07-688-299-13	Sequence 13, Appl	486	4	36.4	375	3	US-09-177-860A-14	Sequence 14, Appl
414	4	36.4	322	4	US-08-347-335A-3	Sequence 3, Appl	487	4	36.4	377	1	US-08-891-898B-2	Sequence 2, Appl1
415	4	36.4	324	2	US-09-188-930-141	Sequence 141, App	488	4	36.4	377	1	US-08-525-697-2	Sequence 2, Appl1
416	4	36.4	334	2	US-08-579-940-7	Sequence 7, Appl1	489	4	36.4	379	4	US-09-191-136-32	Sequence 32, Appl
417	4	36.4	335	2	US-09-018-576-3	Sequence 3, Appl1	490	4	36.4	379	4	US-09-426-557-2	Sequence 2, Appl1
418	4	36.4	335	2	US-09-018-576-12	Sequence 12, Appl	491	4	36.4	379	4	US-09-426-557-4	Sequence 4, Appl1
419	4	36.4	335	3	US-09-248-137-3	Sequence 3, Appl	492	4	36.4	379	4	US-09-426-557-6	Sequence 6, Appl1
420	4	36.4	335	3	US-09-248-137-12	Sequence 12, Appl	493	4	36.4	379	4	US-09-426-557-8	Sequence 8, Appl1
421	4	36.4	330	2	US-08-838-543-3	Sequence 3, Appl1	494	4	36.4	380	4	US-08-924-345-2	Sequence 4, Appl1
422	4	36.4	331	3	US-08-445-515-59	Sequence 59, Appl	495	4	36.4	382	2	US-08-455-968E-5	Sequence 5, Appl1
423	4	36.4	335	4	US-09-387-699-2	Sequence 2, Appl1	496	4	36.4	382	2	US-08-360-606B-30	Sequence 30, Appl
424	4	36.4	336	4	US-08-235-836C-54	Sequence 54, Appl	497	4	36.4	382	2	US-08-823-116-139	Sequence 139, App
425	4	36.4	338	2	US-08-602-359A-40	Sequence 40, Appl	498	4	36.4	383	6	5470718-5	Patent No. 5470718
426	4	36.4	339	1	US-08-626-994A-3	Sequence 3, Appl1	499	4	36.4	384	2	US-08-637-559B-375	Sequence 375, App
427	4	36.4	339	3	US-08-957-742-3	Sequence 3, Appl1	500	4	36.4	384	3	US-08-871-335A-375	Sequence 375, App
428	4	36.4	339	4	US-09-330-117B-4	Sequence 4, Appl1	501	4	36.4	388	1	US-08-499-568-11	Sequence 11, Appl
429	4	36.4	339	4	US-09-330-117B-10	Sequence 10, Appl	502	4	36.4	388	2	US-08-793-958-11	Sequence 11, Appl
430	4	36.4	339	4	US-09-330-117B-12	Sequence 12, Appl	503	4	36.4	391	2	US-08-244-951A-10	Sequence 10, Appl
431	4	36.4	339	4	US-09-330-117B-14	Sequence 14, Appl	504	4	36.4	391	2	US-08-389-011-13	Sequence 13, Appl
432	4	36.4	339	4	US-09-330-117B-16	Sequence 16, Appl	505	4	36.4	391	3	US-08-403-017A-23	Sequence 23, Appl
433	4	36.4	340	2	US-08-446-875-16	Sequence 16, Appl	506	4	36.4	391	4	US-09-348-952A-23	Sequence 23, Appl
434	4	36.4	340	4	US-08-960-780-34	Sequence 34, Appl	507	4	36.4	393	6	5182195-10	Patent No. 5182195
435	4	36.4	340	4	US-09-073-898-34	Sequence 34, Appl	508	4	36.4	394	1	US-08-499-568-4	Sequence 4, Appl1
436	4	36.4	344	1	US-08-180-209B-58	Sequence 58, Appl	509	4	36.4	394	2	US-08-793-958-4	Sequence 4, Appl1
437	4	36.4	344	2	US-08-755-728-3	Sequence 3, Appl1	510	4	36.4	406	1	US-07-973-431B-1	Sequence 1, Appl1
438	4	36.4	344	2	US-08-974-655-3	Sequence 3, Appl1	511	4	36.4	407	2	US-08-765-875-2	Sequence 2, Appl1
439	4	36.4	344	5	US-09-283-011-13	Sequence 3, Appl1	512	4	36.4	407	2	US-08-765-875-6	Sequence 6, Appl1
440	4	36.4	344	5	PCT-US94-02629-58	Sequence 58, Appl	513	4	36.4	407	3	US-08-776-585-3	Sequence 3, Appl1
441	4	36.4	346	2	US-08-401-068-8	Sequence 8, Appl1	514	4	36.4	407	3	US-08-795-671-2	Sequence 2, Appl1
442	4	36.4	346	2	US-08-846-338-8	Sequence 8, Appl1	515	4	36.4	408	2	US-08-683-007A-2	Sequence 2, Appl1
443	4	36.4	346	2	US-08-687-702-36	Sequence 36, Appl	516	4	36.4	409	2	US-08-609-740A-5	Sequence 5, Appl1
444	4	36.4	346	3	US-08-411-768B-2	Sequence 2, Appl1	517	4	36.4	412	3	US-08-465-885C-14	Sequence 14, Appl
445	4	36.4	347	2	US-09-016-000-1	Sequence 1, Appl1	518	4	36.4	412	4	US-08-652-446-14	Sequence 14, Appl
446	4	36.4	347	4	US-08-960-780-25	Sequence 25, Appl	519	4	36.4	412	2	US-09-027-064-4	Sequence 4, Appl1
447	4	36.4	347	4	US-09-073-898-25	Sequence 25, Appl	520	4	36.4	412	2	US-08-461-379A-14	Sequence 14, Appl
448	4	36.4	348	4	US-09-060-780-21	Sequence 21, Appl	521	4	36.4	412	2	US-08-462-390B-14	Sequence 14, Appl
449	4	36.4	348	4	US-08-960-780-42	Sequence 42, Appl	522	4	36.4	412	3	US-08-463-074B-14	Sequence 14, Appl
450	4	36.4	348	4	US-09-073-898-21	Sequence 21, Appl	523	4	36.4	412	3	US-08-465-885C-14	Sequence 14, Appl
451	4	36.4	348	4	US-09-073-898-42	Sequence 42, Appl	524	4	36.4	412	4	US-08-652-446-14	Sequence 14, Appl
452	4	36.4	351	1	US-08-159-969-2	Sequence 42, Appl	525	4	36.4	412	4	US-09-027-064-4	Sequence 4, Appl1
453	4	36.4	351	2	US-08-726-306A-17	Sequence 17, Appl	526	4	36.4	413	3	US-08-669-108B-10	Sequence 10, Appl
454	4	36.4	352	2	US-08-137-627-4	Sequence 4, Appl1	527	4	36.4	415	2	US-08-576-626A-52	Sequence 52, Appl
455	4	36.4	359	2	US-08-865-348-4	Sequence 4, Appl1	528	4	36.4	417	4	US-09-276-400-5	Sequence 5, Appl1
456	4	36.4	359	2	US-08-865-348-4	Sequence 4, Appl1	529	4	36.4	419	3	US-09-155-200-4	Sequence 4, Appl1
457	4	36.4	359	4	US-08-809-103B-2	Sequence 2, Appl1	530	4	36.4	422	1	US-08-132-649-4	Sequence 4, Appl1
458	4	36.4	359	4	US-08-809-103B-6	Sequence 6, Appl1	531	4	36.4	422	1	US-08-767-579-4	Sequence 4, Appl1
459	4	36.4	359	4	US-08-809-103B-8	Sequence 8, Appl1	532	4	36.4	424	1	US-08-419-614-2	Sequence 2, Appl1
460	4	36.4	361	2	US-08-209-521-5	Sequence 5, Appl1	533	4	36.4	424	2	US-08-871-268A-23	Sequence 23, Appl
461	4	36.4	361	3	US-09-034-985-2	Sequence 3, Appl1	534	4	36.4	424	3	US-08-871-267B-31	Sequence 31, Appl
462	4	36.4	361	4	US-08-961-810-1	Sequence 1, Appl1	535	4	36.4	425	4	US-08-960-780-27	Sequence 27, Appl
463	4	36.4	361	4	US-08-352-902D-1	Sequence 1, Appl1	536	4	36.4	425	4	US-09-073-898-27	Sequence 27, Appl
464	4	36.4	362	1	US-08-247-907A-11	Sequence 11, Appl	537	4	36.4	428	1	US-08-969-125-9	Sequence 9, Appl1
465	4	36.4	362	1	US-08-452-772-11	Sequence 11, Appl	538	4	36.4	428	1	US-08-190-802A-29	Sequence 29, Appl

247	4	36.4	111	1	US-08-466-886-33	Sequence 33, Appl	320	4	36.4	188	2	US-08-933-750C-8	Sequence 8, Appl
248	4	36.4	111	2	US-08-852-091-18	Sequence 18, Appl	321	4	36.4	188	4	US-09-234-613-8	Sequence 8, Appl
249	4	36.4	111	2	US-08-665-202-36	Sequence 36, Appl	322	4	36.4	189	2	US-08-861-266-7	Sequence 7, Appl
250	4	36.4	111	2	US-08-665-202-40	Sequence 40, Appl	323	4	36.4	189	2	US-09-134-556-7	Sequence 7, Appl
251	4	36.4	111	2	US-08-665-202-41	Sequence 41, Appl	324	4	36.4	189	3	US-09-293-273-7	Sequence 7, Appl
252	4	36.4	111	2	US-08-665-202-42	Sequence 42, Appl	325	4	36.4	189	3	US-08-646-273-14	Sequence 14, Appl
253	4	36.4	111	2	US-08-665-202-43	Sequence 43, Appl	326	4	36.4	193	3	US-09-041-889-5	Sequence 5, Appl
254	4	36.4	111	4	US-08-983-607-21	Sequence 21, Appl	327	4	36.4	193	3	US-08-837-058-5	Sequence 5, Appl
255	4	36.4	111	4	US-08-983-607-23	Sequence 23, Appl	328	4	36.4	196	2	US-08-829-110-5	Sequence 5, Appl
256	4	36.4	111	4	US-08-983-607-35	Sequence 35, Appl	329	4	36.4	196	2	US-08-748-483-3	Sequence 3, Appl
257	4	36.4	111	4	US-08-469-617-33	Sequence 33, Appl	330	4	36.4	199	3	US-08-737-248-9	Sequence 9, Appl
258	4	36.4	111	5	PCT-US95-08950-6	Sequence 6, Appl	331	4	36.4	201	1	US-08-292-945-4	Sequence 4, Appl
259	4	36.4	111	5	PCT-US95-17025-18	Sequence 18, Appl	332	4	36.4	201	1	US-08-252-073A-4	Sequence 4, Appl
260	4	36.4	112	3	US-08-665-202-39	Sequence 39, Appl	333	4	36.4	201	5	PCT-US93-12074-4	Sequence 4, Appl
261	4	36.4	112	3	US-08-666-360-1	Sequence 1, Appl	334	4	36.4	205	2	US-08-912-227-4	Sequence 4, Appl
262	4	36.4	112	4	US-08-983-607-31	Sequence 31, Appl	335	4	36.4	206	4	US-09-107-381-15	Sequence 15, Appl
263	4	36.4	112	4	US-09-240-274-64	Sequence 64, Appl	336	4	36.4	209	4	US-09-266-220-1	Sequence 1, Appl
264	4	36.4	113	1	US-08-211-202-112	Sequence 112, App	337	4	36.4	209	4	US-09-266-220-2	Sequence 2, Appl
265	4	36.4	113	1	US-08-211-202-113	Sequence 113, App	338	4	36.4	214	2	US-08-572-447C-13	Sequence 13, Appl
266	4	36.4	113	1	US-08-211-202-114	Sequence 114, App	339	4	36.4	216	2	US-08-929-418-2	Sequence 2, Appl
267	4	36.4	114	2	US-09-240-274-62	Sequence 62, Appl	340	4	36.4	222	2	US-08-391-743A-2	Sequence 2, Appl
268	4	36.4	118	2	US-08-443-639-13	Sequence 13, Appl	341	4	36.4	226	2	US-08-572-447C-15	Sequence 15, Appl
269	4	36.4	118	3	US-08-577-483-13	Sequence 13, Appl	342	4	36.4	227	4	US-08-944-453-40	Sequence 40, Appl
270	4	36.4	119	2	US-08-588-258B-31	Sequence 31, Appl	343	4	36.4	233	2	US-09-151-611-1	Sequence 1, Appl
271	4	36.4	119	2	US-08-460-505-31	Sequence 31, Appl	344	4	36.4	233	4	US-08-523-894-6	Sequence 6, Appl
272	4	36.4	119	5	PCT-US96-08295-31	Sequence 31, Appl	345	4	36.4	234	4	US-08-487-550-2	Sequence 2, Appl
273	4	36.4	120	1	US-08-211-747-7	Sequence 7, Appl	346	4	36.4	235	2	US-08-378-939-12	Sequence 12, Appl
274	4	36.4	123	1	US-07-869-912-2	Sequence 2, Appl	347	4	36.4	235	4	US-09-049-672A-10	Sequence 10, Appl
275	4	36.4	123	1	US-08-482-728A-7	Sequence 7, Appl	348	4	36.4	235	4	US-09-049-672A-12	Sequence 12, Appl
276	4	36.4	126	1	US-08-202-047-13	Sequence 13, Appl	349	4	36.4	236	3	US-08-487-550-10	Sequence 10, Appl
277	4	36.4	126	1	US-08-202-047-15	Sequence 15, Appl	350	4	36.4	236	4	US-09-049-672A-8	Sequence 8, Appl
278	4	36.4	126	1	US-08-202-047-17	Sequence 17, Appl	351	4	36.4	236	5	PCT-US95-04601-8	Sequence 8, Appl
279	4	36.4	126	1	US-08-202-047-19	Sequence 19, Appl	352	4	36.4	237	2	US-08-464-517-24	Sequence 24, Appl
280	4	36.4	126	3	US-08-964-690-13	Sequence 13, Appl	353	4	36.4	237	2	US-08-246-361A-24	Sequence 24, Appl
281	4	36.4	126	3	US-08-964-690-15	Sequence 15, Appl	354	4	36.4	237	3	US-08-463-772-24	Sequence 24, Appl
282	4	36.4	126	3	US-08-964-690-17	Sequence 17, Appl	355	4	36.4	237	5	PCT-US93-05000-24	Sequence 24, Appl
283	4	36.4	126	3	US-08-964-690-19	Sequence 19, Appl	356	4	36.4	239	2	US-08-114-555A-12	Sequence 12, Appl
284	4	36.4	131	1	US-08-012-543-4	Sequence 4, Appl	357	4	36.4	239	3	US-08-559-397A-17	Sequence 17, Appl
285	4	36.4	131	1	US-08-305-683A-4	Sequence 4, Appl	358	4	36.4	240	4	US-09-049-672A-11	Sequence 11, Appl
286	4	36.4	131	1	US-08-371-121-25	Sequence 25, Appl	359	4	36.4	244	1	US-08-289-659A-3	Sequence 3, Appl
287	4	36.4	131	5	PCT-US93-07645A-4	Sequence 4, Appl	360	4	36.4	244	2	US-08-878-283-3	Sequence 3, Appl
288	4	36.4	132	2	US-08-345-321-4	Sequence 4, Appl	361	4	36.4	247	2	US-08-851-974-1	Sequence 1, Appl
289	4	36.4	132	2	US-08-649-991-95	Sequence 95, Appl	362	4	36.4	247	2	US-08-851-974-4	Sequence 4, Appl
290	4	36.4	133	1	US-08-196-218-32	Sequence 32, Appl	363	4	36.4	247	2	US-09-213-390-1	Sequence 1, Appl
291	4	36.4	133	1	US-08-681-953-32	Sequence 32, Appl	364	4	36.4	247	2	US-09-213-390-4	Sequence 4, Appl
292	4	36.4	133	2	US-08-649-991-110	Sequence 110, App	365	4	36.4	249	2	US-08-685-992-28	Sequence 28, Appl
293	4	36.4	134	2	US-08-850-910A-45	Sequence 45, Appl	366	4	36.4	249	2	US-09-144-925-28	Sequence 28, Appl
294	4	36.4	134	2	US-08-850-910A-48	Sequence 48, Appl	367	4	36.4	258	2	US-08-602-941-3	Sequence 3, Appl
295	4	36.4	138	2	US-08-684-101-2	Sequence 2, Appl	368	4	36.4	258	2	US-08-665-202-5	Sequence 5, Appl
296	4	36.4	138	2	US-09-205-814-2	Sequence 2, Appl	369	4	36.4	258	3	US-08-961-264-3	Sequence 3, Appl
297	4	36.4	147	3	US-09-136-442-3	Sequence 3, Appl	370	4	36.4	258	3	US-08-303-861-18	Sequence 18, Appl
298	4	36.4	148	5	PCT-US95-07135-2	Sequence 2, Appl	371	4	36.4	258	3	US-08-303-861-19	Sequence 19, Appl
299	4	36.4	148	5	US-08-046-583-11	Sequence 11, Appl	372	4	36.4	260	3	US-08-857-213-3	Sequence 3, Appl
300	4	36.4	152	1	US-08-261-677-11	Sequence 11, Appl	373	4	36.4	260	6	5320958-4	Patent No. 5320958
301	4	36.4	152	1	US-08-384-556A-2	Sequence 2, Appl	374	4	36.4	263	2	US-08-767-026-16	Sequence 13, Appl
302	4	36.4	152	1	US-08-384-556A-7	Sequence 7, Appl	375	4	36.4	264	1	US-08-463-115-93	Sequence 93, Appl
303	4	36.4	152	1	US-08-592-936B-17	Sequence 17, Appl	376	4	36.4	264	1	US-08-465-388-99	Sequence 93, Appl
304	4	36.4	152	1	US-08-331-355A-11	Sequence 11, Appl	377	4	36.4	268	1	US-08-446-919A-2	Sequence 2, Appl
305	4	36.4	152	2	US-08-331-355A-13	Sequence 23, Appl	378	4	36.4	270	4	US-09-082-593-10	Sequence 10, Appl
306	4	36.4	152	2	US-09-111-573-17	Sequence 17, Appl	379	4	36.4	270	4	US-09-342-084-8	Sequence 8, Appl
307	4	36.4	152	5	PCT-US94-12364-11	Sequence 11, Appl	380	4	36.4	277	6	5164481-2	Patent No. 5164481
308	4	36.4	152	5	PCT-US94-12364-23	Sequence 23, Appl	381	4	36.4	278	2	US-08-416-603-6	Sequence 6, Appl
309	4	36.4	152	5	PCT-US95-07753-2	Sequence 2, Appl	382	4	36.4	280	1	US-08-409-452-1	Sequence 1, Appl
310	4	36.4	152	5	PCT-US95-07753-7	Sequence 7, Appl	383	4	36.4	280	6	5182210-12	Patent No. 5182210
311	4	36.4	154	4	US-09-404-670-4	Sequence 4, Appl	384	4	36.4	281	3	US-09-320-878-5	Sequence 5, Appl
312	4	36.4	155	4	US-09-315-794-12	Sequence 12, Appl	385	4	36.4	286	3	US-08-891-789B-4	Sequence 4, Appl
313	4	36.4	155	4	US-09-389-341-12	Sequence 12, Appl	386	4	36.4	288	1	US-08-396-650-1	Sequence 1, Appl
314	4	36.4	163	3	US-09-053-197A-26	Sequence 26, Appl	387	4	36.4	288	1	US-08-768-656-1	Sequence 1, Appl
315	4	36.4	163	3	US-08-673-269-2	Sequence 2, Appl	388	4	36.4	291	4	US-09-328-869-2	Sequence 2, Appl
316	4	36.4	178	1	PCT-US93-04365-10	Sequence 10, Appl	389	4	36.4	293	4	US-09-037-113-52	Sequence 52, Appl
317	4	36.4	180	5	PCT-US93-04365-11	Sequence 11, Appl	390	4	36.4	293	4	US-08-260-174-52	Sequence 52, Appl
318	4	36.4	180	5	PCT-US93-04365-11	Sequence 11, Appl	391	4	36.4	294	2	US-08-923-856-3	Sequence 3, Appl
319	4	36.4	181	2	US-08-766-551-1	Sequence 1, Appl	392	4	36.4	294	3	US-09-216-294-3	Sequence 3, Appl

101	4	36.4	12	4	US-09-073-898-61	Sequence 61, Appl	174	4	36.4	69	1	US-08-175-393A-4	Sequence 4, Appl1
102	4	36.4	13	1	US-08-211-747-9	Sequence 29, Appl1	175	4	36.4	74	4	US-09-025-151-19	Sequence 19, Appl
103	4	36.4	13	2	US-08-666-473-29	Sequence 9, Appl	176	4	36.4	75	4	US-08-686-878A-12	Sequence 12, Appl
104	4	36.4	13	2	US-08-934-222-104	Sequence 104, App	177	4	36.4	79	1	US-08-011-398B-19	Sequence 19, Appl
105	4	36.4	13	2	US-08-933-602-104	Sequence 104, App	178	4	36.4	79	1	US-08-464-051-19	Sequence 19, Appl
106	4	36.4	13	2	US-09-207-621-104	Sequence 104, App	179	4	36.4	79	2	US-08-462-498-19	Sequence 19, Appl
107	4	36.4	13	2	US-08-532-818-104	Sequence 104, App	180	4	36.4	79	2	US-08-554-385-18	Sequence 18, Appl
108	4	36.4	13	3	US-09-231-797-104	Sequence 104, App	181	4	36.4	81	3	US-08-436-420-35	Sequence 35, Appl
109	4	36.4	13	3	US-08-934-224-104	Sequence 104, App	182	4	36.4	83	2	US-08-878-546-8	Sequence 8, Appl1
110	4	36.4	13	3	US-08-933-843-104	Sequence 104, App	183	4	36.4	98	1	US-08-211-202-111	Sequence 111, App
111	4	36.4	13	4	US-08-934-223-104	Sequence 104, App	184	4	36.4	98	2	US-08-665-202-37	Sequence 37, Appl
112	4	36.4	13	6	546585-11	Patent No. 546585	185	4	36.4	98	2	US-08-665-202-38	Sequence 38, Appl
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GN CG14554.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Chame M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Crawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003754; AAF56570.1; -.
DR FlyBase: FBgn0039412; CG14554.
SQ SEQUENCE 114 AA; 13638 MW; C649F2D65FDC5CFE CRC64;

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Query Match 45.5%; Score 5; DB 5; Length 114;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOOTA 5
 |||||
 Db 105 QOOTA 109

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OX NCBI_TaxId=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL160493; CAB98023.1; -.
DR EMBL: AL160493; CAB98023.1; -.
FT NON_TER 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 12967 MW; 9DEBDEBEE514C372 CRC64;

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Query Match 45.5%; Score 5; DB 5; Length 117;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOOTA 5
 |||||
 Db 48 QOOTA 52

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RESULT 47
O9RTX9 PRELIMINARY; PRT; 118 AA.
ID O9RTX9;
AC O9RTX9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE HT FAMILY PROTEIN.
DE DR1621.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxId=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R1;
MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Olin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE002005; AAF1181.1; -.
DR HSSP: P49773; IKPF.
DR TIGR: DR1621; -.
DR InterPro: IPR001310; -.
DR Pfam: PF01230; HIT: 1.
DR PRINTS: PRO0332; HISTRIAD.
DR PROSITE: PS00892; HIT: 1.
SQ SEQUENCE 118 AA; 13112 MW; AA6C3A4FC73EF912 CRC64;

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Query Match 45.5%; Score 5; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
 |||||
 Db 40 APRAP 44

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RESULT 48
O9PBW7 PRELIMINARY; PRT; 120 AA.
ID O9PBW7;
AC O9PBW7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE POSSIBLE L7138-8-RELATED PROTEIN (FRAGMENT).
DE GN
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

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RC STRAIN-A3(2); PubMed=8843436;
 RX MEDLINE=97000351; Denapalte D., Eichner A., Cullum J.,
 RA Redenbach M., Kleser H.M., Hopwood D.A.;
 RA Khashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RT Mol. Microbiol. 21:77-96(1996).
 RL EMBL: AL163641; CAB87228.1; -
 DR EMBL: AL163641; CAB87228.1; -
 KM Hypothetical protein.
 SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 45.5%; Score 5; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OQOTA 5
 |||||
 DB 40 OQOTA 44

RESULT 42

O9N3V6 PRELIMINARY; PRT; 110 AA.
 ID O9N3V6;
 AC O9N3V6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHEICAL PROTEIN Y46E12A.D.
 GN Y46E12A.D.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 NCBI_TaxID=6239;
 OK NCBI_TaxID=6239;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN 12;
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024788; AAF0614.1; -
 SQ SEQUENCE 110 AA; 12150 MW; BC5FBF808B497E66 CRC64;

Query Match 45.5%; Score 5; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 DB 20 APKAP 24

RESULT 43

O9ESAB PRELIMINARY; PRT; 111 AA.
 ID O9ESAB;
 AC O9ESAB;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SMDF NEUREGULIN BETA 2 (FRAGMENT).
 GN NRCL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;

RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RC TISSUE=AXOTOMIZED LUMBAR DORSAL ROOT GANGLION/SPINAL CORD;
 RA Carroll S.L., Anderson K.D., Frohner P.W.;
 RT "Structural and Functional Diversity of SMDF Neuregulin Splice
 Variants Expressed in the Adult Rat Nervous System.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF194441; AAG28430.1; -
 FT NON_TER 1 111
 FT NON_TER 1 111
 SQ SEQUENCE 111 AA; 12198 MW; CC8BB870584C9F8C CRC64;

Query Match 45.5%; Score 5; DB 11; Length 111;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QAPK 7
 |||||
 DB 38 QAPK 42

RESULT 44

O95014 PRELIMINARY; PRT; 114 AA.
 ID O95014;
 AC O95014;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE WUGSC:H.DJ0855D21.2 PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 OK NCBI_TaxID=9606;
 RN 11;
 RP SEQUENCE FROM N.A.
 RA Courtney L., Langston Y., Stoneking T., Drone K., Shih K.;
 RT "The sequence of Homo sapiens PAC clone DJ0855D21.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 12;
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 13;
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN 14;
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004908; AAD05196.1; -
 SQ SEQUENCE 114 AA; 12265 MW; 1455C818AE3FB962 CRC64;

Query Match 45.5%; Score 5; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
 |||||
 DB 36 TAPKA 40

RESULT 45

O9VBH2 PRELIMINARY; PRT; 114 AA.
 ID O9VBH2;
 AC O9VBH2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG14554 PROTEIN.

DR PRINTS: PR00835; NOPREGULATRY.
 KW Plasmid.
 SO SEQUENCE 64 AA; 7298 MW; 514D070E518CF78F CRC64;

Query Match 45.5%; Score 5; DB 2; Length 64;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 OQ0TA 5
 |||||
 Db 4 OQ0TA 8

RESULT 38
 O9MAC9 PRELIMINARY; PRT; 82 AA.
 AC O9MAC9;
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-MAR-2001 (TREMUREL. 16, Last annotation update)
 DE HYPOHETICAL 8.9 KDA. PROTEIN (FRAGMENT).
 GN BCI-7.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triflicae;
 OC Hordeum.
 OC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. INGRID; TISSUE-LEAF;
 RA Besser K., Jarosch B., Langen G., Kogel K.H.;
 RT "Identification and expression analysis of genes induced in barley by
 chemical that activate disease resistance."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ250663; CAB71340.1; -
 DR InterPro: IPR000864; -
 DR Pfam: PF00280; potato_inh1b1; 1.
 DR PRINTS: PR00292; POTATOINH1BTR.
 KW Hypothetical protein.
 FT NON_TER 1
 SO SEQUENCE 82 AA; 8862 MW; B13F86F8EB78AE9 CRC64;

Query Match 45.5%; Score 5; DB 10; Length 82;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 13 APKAP 17

RESULT 39
 O9YGP4 PRELIMINARY; PRT; 88 AA.
 AC O9YGP4;
 DT 01-MAY-1999 (TREMUREL. 10, Created)
 DT 01-NOV-1999 (TREMUREL. 12, Last sequence update)
 DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)
 DE WMT-3A HOMOLOG (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA "Assignment of a close homologue of murine homeless-type WMTV
 RT Integration site family member 3a (WMT3A) to chicken chromosome 2."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF109144; AAD19652.2; -

DR InterPro: IPR000970; -
 DR Pfam: PF00110; wnt; 1.
 FT NON_TER 1
 FT NON_TER 88
 SO SEQUENCE 88 AA; 10322 MW; 9124F1CGAFB7F108 CRC64;

Query Match 45.5%; Score 5; DB 13; Length 88;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 KAPTE 11
 |||||
 Db 56 KAPTE 60

RESULT 40
 O38792 PRELIMINARY; PRT; 95 AA.
 AC O38792;
 DT 01-NOV-1996 (TREMUREL. 01, Created)
 DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
 DT 01-AUG-1998 (TREMUREL. 07, Last annotation update)
 DE HYBRID OF A. MAJUS AND A. HISPANICUM PTL2 MRNA.
 GN PTL2.
 OS Antirrhinum sp. (snapdragon).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Lamiales; Scrophulariaceae; Antirrhinum.
 OC NCBI_TaxID=29720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T249 17; TISSUE-STYLAR TISSUE;
 RA Baldwin T.C., Coen E.S., Dickinson H.G.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X71782; CAA50667.1; -
 SO SEQUENCE 95 AA; 9964 MW; 96C39D978C7821BF CRC64;

Query Match 45.5%; Score 5; DB 10; Length 95;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 63 APKAP 67

RESULT 41
 O9L063 PRELIMINARY; PRT; 103 AA.
 AC O9L063;
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
 DE HYPOHETICAL 10.6 KDA. PROTEIN.
 GN SCC105.22C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Brown S.P., Harris D.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA "Assignment of a close homologue of murine homeless-type WMTV
 RT Integration site family member 3a (WMT3A) to chicken chromosome 2."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RT amplification.";
 RL Can. J. Microbiol. 39:402-411(1993).
 CC -1- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
 CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
 CC DEHYDROGENASE TO FERREDOXIN.
 CC -1- PFM: BINDS FOUR NONPARALLEL HEME GROUPS PER MOLECULE.
 CC -1- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
 DR HSSP: P00132; 2CDV.
 KM Electron transport; Sulfate respiration; Heme.
 FT NON_TER 1 1
 FT METAL 13 13 IRON (HEME 1 AXIAL LIGAND) (BY
 FT METAL 16 16 SIMILARITY).
 FT METAL 16 16 IRON (HEME 3 AXIAL LIGAND) (BY
 FT METAL 16 16 SIMILARITY).
 FT NON_TER 23 23
 FT SEQUENCE 23 AA; 2477 MW; 1114D6AC22FAD6B CRC64;

Query Match 45.5%; Score 5; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 DB 2 APKAP 6

RESULT 35

O56859 PRELIMINARY; PRT; 61 AA.
 AC O56859;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ADENYLATE KINASE (FRAGMENT).
 GN ADK.
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 OX NCBI_Taxid=630;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=8081-C;
 RX MEDLINE=97086507; Pubmed=8932701;
 RA Zhang L., Tolvanen P., Skurnik M.;
 RT "The gene cluster directing O-antigen biosynthesis in Yersinia
 RT enterocolitica serotype O:8: Identification of the genes for mannose
 RT and galactose biosynthesis and the gene for the O-antigen
 RT polymerase.";
 RL Microbiology 142:277-288(1996).
 DR EMBL: U46859; AAC60759.1; -.
 DR HSSP: P05082; LAKE.
 FT NON_TER 1 1
 FT SEQUENCE 61 AA; 6941 MW; 68407A9B73F0DD69 CRC64;

Query Match 45.5%; Score 5; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OQTAP 6
 DB 10 OQTAP 14

RESULT 36

O9S1E1 PRELIMINARY; PRT; 64 AA.
 AC O9S1E1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PUTATIVE REPLICATION REGULATORY PROTEIN.

GN YPCP1.03.
 OS Yersinia pestis.
 OG Plasmid pCP1.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 OX NCBI_Taxid=632;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 BIOVAR ORIENTALIS;
 RA Baker S.G., Mungall K.;
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 BIOVAR ORIENTALIS;
 RA Parhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 BIOVAR ORIENTALIS;
 RA Kariyshev A.V., Wren B.W.;
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL109969; CAB53166.1; -.
 DR HSSP: P03051; IROP.
 DR InterPro: IPR000769; -.
 DR Pfam: PF01815; ROP; 1.
 DR PRINTS: PRO0835; ROPREGULATRY.
 DR ProDom: PD012167; -; 1.
 KW Plasmid.
 SQ SEQUENCE 64 AA; 7280 MW; 42D0A3562BA452FF CRC64;

Query Match 45.5%; Score 5; DB 2; Length 64;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOOTA 5
 DB 4 QOOTA 8

RESULT 37

O9JP69 PRELIMINARY; PRT; 64 AA.
 AC O9JP69;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ROM-LIKE PROTEIN.
 GN ROM.
 OS Escherichia coli.
 OG Plasmid pEC156.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=EI585-68;
 RX MEDLINE=99077830; Pubmed=98586694;
 RA Kaczorowski T., Szybalski W.;
 RT "Genomic DNA sequencing by SP6L-6 primer walking using hexamer
 RT ligation.";
 RL Gene 223:83-91(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=EI585-68;
 RA Biedrzycka I., Kaczorowska A., Sektas M., Kaczorowski T.;
 RT "Characterization of pEC156, a ColEI-like plasmid from Escherichia
 RT coli EI585-68 that carries the genes of the EcoVIII restriction-
 RT modification system.";
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF158026; AAF71175.1; -.
 DR InterPro: IPR000769; -.
 DR Pfam: PF01815; ROP; 1.

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarly B., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03497; AAF48411.1; -;
 DR FlyBase: FBgn0030600; h1w; -;
 DR InterPro: IPR000315; -;
 DR InterPro: IPR001298; -;
 DR InterPro: IPR001841; -;
 DR SMART: SM00336; BBOX: 1.
 SO SEQUENCE 2478 AA; 270371 MW; 727D854E6C51B3FA CRC64;

Query Match 54.5%; Score 6; DB 5; Length 2478;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOQTAP 6
 111111
 Db 1736 QOQTAP 1741

RESULT 32
 ID Q9NB71 PRELIMINARY; PRT; 5233 AA.
 AC Q9NB71;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HIGHMIRE
 GN h1w OR CG9041 OR CG9049.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 ON NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON S;
 RX MEDLINE-20296162; PubMed-10839352;
 RA Wen H.I., Dianzon A., Fetter R.D., Bergstrom K., Strauss R.,
 RA Goodman C.S.;
 RT "Highwire regulates synaptic growth in *Drosophila*.";
 RL Neuron 26:313-329(2000).
 DR EMBL: AF262977; AAF76150.1; -;
 DR FlyBase: FBgn0030600; h1w;
 DR InterPro: IPR000315; -;
 DR InterPro: IPR000345; -;
 DR InterPro: IPR000408; -;
 DR InterPro: IPR001298; -;
 DR InterPro: IPR001841; -;
 DR Pfam: PF00415; RCL1: 4.
 DR PRINTS: PR00633; RCGNSATION.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE: PS00626; RCL1_2; UNKNOWN_2.
 DR SMART: SM00336; BBOX: 1.

SO SEQUENCE 5233 AA; 565692 MW; 47141BF02CE07E25 CRC64;

Query Match 54.5%; Score 6; DB 5; Length 5233;
 Best Local Similarity 100.0%; Pred. No. 14e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOQTAP 6
 111111
 Db 4491 QOQTAP 4496

RESULT 33
 ID P81150 PRELIMINARY; PRT; 22 AA.
 AC P81150;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CYTOCHROME C3 (FRAGMENT).
 OS *Desulfovibrio vulgaris*.
 OC Bacteria; Proteobacteria; delta subdivision; *Desulfovibrio*.
 ON NCBI_TaxID=881;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-93272123; PubMed-8388770;
 RA Koch D.Y., Vedvick T.S., McCue A.F., Gevertz D.;
 RT "Rapid comparison of the cytochrome c3 gene from nine strains of
 RT *Desulfovibrio vulgaris* using polymerase chain reaction
 RT amplification.";
 RL Can. J. Microbiol. 39:402-411(1993).
 CC -1- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
 CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
 CC DEHYDROGENASE TO FERREDOXIN.
 CC -1- PTM: BINDS FOUR NONPARALLEL HEME GROUPS PER MOLECULE.
 CC -1- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
 DR HSSP: P00131; 2CTH.
 KM Electron transport; Sulfate respiration; Heme.
 FT NON_TER 1 1
 FT METAL 12 12 IRON (HEME 1 AXIAL LIGAND) (BY
 FT METAL 15 15 SIMILARITY).
 FT IRON (HEME 3 AXIAL LIGAND) (BY
 FT SIMILARITY).
 FT NON_TER 22 22
 SO SEQUENCE 22 AA; 2350 MW; 501C75E1C2225A6C CRC64;

Query Match 45.5%; Score 5; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
 111111
 Db 1 APRAP 5

RESULT 34
 ID P81149 PRELIMINARY; PRT; 23 AA.
 AC P81149;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE CYTOCHROME C3 (FRAGMENT).
 OS *Desulfovibrio vulgaris*.
 OC Bacteria; Proteobacteria; delta subdivision; *Desulfovibrio*.
 ON NCBI_TaxID=881;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-93272123; PubMed-8388770;
 RA Koch D.Y., Vedvick T.S., McCue A.F., Gevertz D.;
 RT "Rapid comparison of the cytochrome c3 gene from nine strains of
 RT *Desulfovibrio vulgaris* using polymerase chain reaction

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RP SEQUENCE FROM N.A.
RA Anderson J.B., Yamashita R.A., Sellers J.R.;
RT "Complete cDNA for an unconventional Myosin (Class VII) in Drosophila
RT melanogaster";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF233269; AAF34810.1; -.
DR FlyBase; FBgn0040299; Myo28B1.
DR InterPro; IPR000048; -.
DR InterPro; IPR000299; -.
DR InterPro; IPR000857; -.
DR InterPro; IPR001609; -.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF00612; IQ; 3.
DR Pfam; PF00784; MYTH4; 2.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PROSITE; PS50057; BAND_41_3; 2.
DR SMART; SM00295; B41; 1.
SO SEQUENCE 2121 AA; 243312 MW; 1D2ED04C8D1DA7 CRC64;

Query Match          54.5%; Score 6; DB 5; Length 2121;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAPT 10
DB 915 APKAPT 920

RESULT 30
O9VL23 PRELIMINARY; PRT; 2129 AA.
AC O9VL23;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CG6976 PROTEIN.
GN MYO28B1 OR CG6976.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Deodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA Jaiswal M., Katush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jettli B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,

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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relbert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
DR EMBL; AE003618; AAF52536.1; -.
DR HSSP; P08799; 1MND.
DR FlyBase; FBgn0040299; Myo28B1.
DR InterPro; IPR000048; -.
DR InterPro; IPR000299; -.
DR InterPro; IPR000857; -.
DR InterPro; IPR001609; -.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF00612; IQ; 3.
DR Pfam; PF00784; MYTH4; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRODOM; PD000355; -.
DR PROSITE; PS50057; BAND_41_3; 2.
DR SMART; SM00295; B41; 1.
SO SEQUENCE 2129 AA; 244144 MW; 1A90EBDC35103481 CRC64;

Query Match          54.5%; Score 6; DB 5; Length 2129;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAPT 10
DB 921 APKAPT 926

RESULT 31
O9VX25 PRELIMINARY; PRT; 2478 AA.
AC O9VX25;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CG9041 PROTEIN.
GN HIW OR CG9041 OR CG9049.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Deodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mel M.-H., Ikegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter R., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Welschbach J.,
 RA Williams S.M., Woodage T., Morley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03831; AAF58849.1; -
 DR FlyBase: FBgn003462; CG1371.
 SQ SEQUENCE 1199 AA; 130890 MW; 043D72C8D2D5E71F CRC64;

Query Match 54.5%; Score 6; DB 5; Length 1199;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPTE 11
 Db 597 PKAPTE 602

RESULT 27
 013617 PRELIMINARY; PRT; 1241 AA.
 AC 013617;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE TAT-BINDING HOMOLOG 7.
 GN P1026.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972 H-;
 RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Halkawa Y., Yamazaki J.,
 RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai K.,
 RA Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Aoki K.,
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB004535; BAA21405.1; -
 DR InterPro: IPR001939; -
 DR InterPro: IPR003593; -
 DR Pfam: PF00004; AAA; 1.

DR PROSITE: PS00674; AAA; 1.
 DR SMART: SM00382; AAA; 1.
 SQ SEQUENCE 1241 AA; 142188 MW; F19BD7AF49BF87E5 CRC64;

Query Match 54.5%; Score 6; DB 3; Length 1241;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPTE 11
 Db 202 PKAPTE 207

RESULT 28
 09NF04 PRELIMINARY; PRT; 1257 AA.
 AC 09NF04;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Y1058C.B PROTEIN.
 GN Y1058C.B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sulston J.E.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99069613; PubMed-9851916;
 RA none;
 RT "Genome sequence of the nematode *C. elegans*: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: AL132879; CAB60860.2; -
 DR InterPro: IPR000619; -
 DR InterPro: IPR000906; -
 DR InterPro: IPR001478; -
 DR Pfam: PF00595; PD2; 3.
 DR Pfam: PF00791; ZU5; 1.
 DR PROSITE: PSS0052; GUANYLATE_KINASE_2; 1.
 DR SMART: SM00872; Gukc; 1.
 SQ SEQUENCE 1257 AA; 139391 MW; 617E729417136819 CRC64;

Query Match 54.5%; Score 6; DB 5; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOQTAP 6
 Db 1022 QOQTAP 1027

RESULT 29
 09NH54 PRELIMINARY; PRT; 2121 AA.
 AC 09NH54;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE MYO28B1 OR CG6976.
 GN MYO28B1 OR CG6976.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Percy C.;
 RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
 CC -1- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
 DR EMBL: 281094; CAB03153.1; -;
 DR InterPro: IPR000629; -;
 DR InterPro: IPR001410; -;
 DR InterPro: IPR001650; -;
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; helicase.C; 1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 DR SMART: SM00490; HELICC; 1.
 DR SMART: SM00490; HELICC; 1.
 KW ATP-binding; Helicase; RNA-binding.
 SQ SEQUENCE 995 AA; 107563 MW; 94A25950B93C93F5 CRC64;

Query Match 54.5%; Score 6; DB 5; Length 995;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAPT 10
 |||||
 DB 889 APKAPT 894

RESULT 24
 ID 088532 PRELIMINARY; PRT: 1052 AA.
 AC 088532;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ZINC FINGER RNA BINDING PROTEIN.
 GN ZFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Mesgher M.J., Schumacher J.M., Lee K., Holdcraft R.W., Egelhoff S.,
 RA Distche C., Braun R.E.;
 RT "Identification of ZFR, an ancient and highly conserved chromosome-
 associated zinc finger RNA binding protein.";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF011059; AAC25762.1; -;
 DR MGD: MGI:1341890; Zfr.
 DR InterPro: IPR000690; -;
 DR InterPro: IPR000822; -;

DR Pfam: PF00096; zf-C2H2; 3.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2; UNKNOWN_3.
 DR SMART: SM00355; Znf_C2H2; 1.
 KW DNA-binding; Zinc-finger.
 SQ SEQUENCE 1052 AA; 114434 MW; 29E2927CC0B60B9D CRC64;

Query Match 54.5%; Score 6; DB 11; Length 1052;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QTPAKA 8
 |||||
 DB 165 QTPAKA 170

RESULT 25
 ID 097169 PRELIMINARY; PRT: 1158 AA.
 AC 097169;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HAIRLESS PROTEIN.
 DE HAIRLESS.
 OS Drosophila hydei (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WILD TYPE; CV: HESS, O.;
 RA Marguart J., Alexief-Damianof C., Preiss A., Maier D.;
 RT "Rapid divergence in the course of Drosophila evolution reveals
 structural important domains of the Notch antagonist Hairless.";
 RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ232783; CAB38221.1; -;
 DR FLYBase: FBgn0019190; DhydVH.
 SQ SEQUENCE 1158 AA; 119635 MW; 0B611D3739CF397F CRC64;

Query Match 54.5%; Score 6; DB 5; Length 1158;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKAP 9
 |||||
 DB 159 TAPKAP 164

RESULT 26
 ID 09V5G1 PRELIMINARY; PRT: 1199 AA.
 AC 09V5G1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG1371 PROTEIN.
 GN CG1371.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RL Science 282:2012-2018(1998).
 DR EMBL: AL132889; CAB81909.1; -.
 DR InterPro: IPR001680; -.
 DR InterPro: IPR001865; -.
 DR InterPro: IPR001899; -.
 DR Pfam: PF00400; WD40; 8.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 SQ SEQUENCE 855 AA; 94259 MW; E4426D383235E008 CRC64;

Query Match 54.5%; Score 6; DB 5; Length 855;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OTAPKA 8
 Db 767 OTAPKA 772

RESULT 21

O9HUA6 PRELIMINARY; PRT; 861 AA.

AC O9HUA6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE PERIPLASMIC GLUCANS BIOSYNTHESIS PROTEIN MDOH.
 GN MDOH OR PA5077.

OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.

OX NCBI_TaxID=287;
 RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20437337; PubMed=10984043;

RA Slover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larby K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reitzer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";

RL Nature 406:959-964(2000).

EMBL: AE004820; AAC08462.1; -.
 DR InterPro: IPR001173; -.

DR P1am: PF00535; Glycosyltransferase_2; 1.
 DR SMART: SM00355; znr_C2H2; 1.

SQ SEQUENCE 861 AA; 96994 MW; 63557B5A83107E7E CRC64;

Query Match 54.5%; Score 6; DB 2; Length 861;
 Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OTAPKA 8
 Db 376 OTAPKA 381

RESULT 22

O9VEM6 PRELIMINARY; PRT; 925 AA.

AC O9VEM6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CG10309 PROTEIN.

GN CG10309.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

EMBL=20196006; PubMed=10731132;

RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balling R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshirel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacible J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

EMBL: AE003713; AAP5301.1; -.

DR HSSP: P08046; 1A1J.

DR FlyBase: FBgn0038418; CG10309.

DR InterPro: IPR000822; -.

DR P1am: PF00096; zif-C2H2; 4.

DR PROSITE: PS00028; ZINC_FINGER_C2H2; 4.

DR SMART: SM00355; znr_C2H2; 1.

DR DNA-binding; Metal-binding; Zinc-finger.

SQ SEQUENCE 925 AA; 100378 MW; E3866DA1BCE2A2AF2 CRC64;

OY 3 OTAPKA 8
 Db 618 OTAPKA 623

RESULT 23

P90897 PRELIMINARY; PRT; 995 AA.

AC P90897;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE F58G11.2 PROTEIN.

GN F58G11.2.

Query Match 54.5%; Score 6; DB 5; Length 925;
 Best Local Similarity 100.0%; Pred. No. 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 17
ID 09P196 PRELIMINARY: PRT: 663 AA.
AC 09P196:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1).
GN FRDA OR CJD409.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCYC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kellley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.M.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL: AL139075; CAB74245.1;
DR InterPro: IPR000464;
DR Pfam: PF00890; FAD_binding_2; 1.
SQ SEQUENCE 663 AA; 73788 MW; 4FE340FEE783E9F9 CRC64;

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Query Match 54.5%; Score 6; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QTAPKA 8
DB 91 QTAPKA 96

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RESULT 18
ID 025586 PRELIMINARY: PRT: 672 AA.
AC 025586:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE PARAMYOSIN-RELATED PROTEIN (FRAGMENT).
OS Onchocerca gibsoni.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6284;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96360163; PubMed=8719949;
RA Zhang D., Miller D.J.;
RT "Characterization of a novel non-muscle myosin-related protein from
RT Onchocerca gibsoni."
RL Int. J. Parasitol. 25:1385-1391(1995).
DR EMBL: U20609; A850272.1;
DR InterPro: IPR000727;
FT NON_TER 1
FT NON_TER 672
SQ SEQUENCE 672 AA; 80074 MW; C610249CEFF0FFED1 CRC64;

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Query Match 54.5%; Score 6; DB 5; Length 672;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 000TAP 6
DB 111111

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DB 240 000TAP 245
RESULT 19
ID 09RKV7 PRELIMINARY: PRT: 689 AA.
AC 09RKV7:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PUTATIVE SERINE/THREONINE PROTEIN KINASE (FRAGMENT).
GN SC961.09.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Oliver K., Harris D.;
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapalte D., Elchner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL132997; CAB61321.1;
KW kinase; Serine/threonine-protein kinase.
FT NON_TER 689
FT NON_TER 689
SQ SEQUENCE 689 AA; 73645 MW; 6CF7BF01BC8556DA CRC64;

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Query Match 54.5%; Score 6; DB 2; Length 689;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TAPKAP 9
DB 659 TAPKAP 664

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RESULT 20
ID 09NEW7 PRELIMINARY: PRT: 855 AA.
AC 09NEW7:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Y11B2G.H PROTEIN.
GN Y11B2G.H.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX Sulston J.E.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9905613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA de Padlos B., Delcher S., Dahlke C., Davenport L.B., Davies P.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei R., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshneff A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gidbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003608; AAF52199.1; -;
 DR FLYBase: FBgn0031667; CG18623.
 DR InterPro: IPR002048; -;
 DR InterPro: IPR002965; -;
 DR PRINTS: PRO1217; PRICHEXTENSN.
 DR PROSITE: PS001018; EF_HAND; UNKNOWN.1.
 SO SEQUENCE 388 AA; 40889 MW; 13903464EBC79CB3 CRC64;

Query Match 54.58; Score 6; DB 5; Length 388;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAPT 10
 |||||
 Db 325 APRAPT 330

RESULT 15
 ID 086584 PRELIMINARY; PRT; 606 AA.
 AC 086584;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 18, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 04, Last annotation update)
 DE PUTATIVE ATP/GTP BINDING PROTEIN (FRAGMENT).
 GN SC2H4.01.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID:1902;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE:97000351; PubMed-8843436;
 RA Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kinashil H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL031514; CAA20595.1; -;
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 606 AA; 63662 MW; 42ADF496AFAF39CCD CRC64;

Query Match 54.58; Score 6; DB 2; Length 606;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKAP 9
 |||||
 Db 4 TAPKAP 9

RESULT 16
 ID 092614 PRELIMINARY; PRT; 612 AA.
 AC 092614;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE DIHYDROLIPOAMIDE ACETYLTRANSFERASE.
 GN PDHB.
 OS Streptomyces seoulensis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID:73044;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99078078; PubMed-9858775;
 RA Youn H., Kwak J., Youn H.D., Hah Y.C., Kang S.O.;
 RT "Lipoamide dehydrogenase from Streptomyces seoulensis: biochemical and
 genetic properties.";
 RL Biochim. Biophys. Acta 1388:405-418(1998).
 RN [2]
 RC SEQUENCE FROM N.A.
 RA Youn H., Kang S.-O.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS LIPOYL-BINDING DOMAIN(S).
 DR EMBL: AF047034; AAD17484.2; -;
 DR HSP; P11961; IEBD.
 DR InterPro: IPR000089; -;
 DR InterPro: IPR000531; -;
 DR InterPro: IPR001078; -;
 DR InterPro: IPR001978; -;
 DR InterPro: IPR002965; -;
 DR InterPro: IPR003016; -;
 DR Pfam: PF00198; 2-oxoacid_dh; 1.
 DR Pfam: PF00364; biotin_lipoyl; 2.
 DR PRINTS: PRO1217; PRICHEXTENSN.
 DR PRODOM: PD001115; -; 1
 DR PROSITE: PS00189; LIPOYL; 2.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN.1.
 KW Lipoyl; transferase.
 SO SEQUENCE 612 AA; 61367 MW; B804109089943056 CRC64;

Query Match 54.58; Score 6; DB 2; Length 612;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOQTAP 6
 |||||
 Db 262 QOQTAP 267

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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Min P., Le T.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U50197; AAA91256.1;
DR HSSP: P23911; IC80;
SQ SEQUENCE 343 AA; 38845 MW; 239065057669E8A0 CRC64;

Query Match 54.5%; Score 6; DB 5; Length 343;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPTE 11
| | | | |
DB 4 PKAPTE 9

RESULT 12
O9FPA4 PRELIMINARY; PRT; 348 AA.
AC O9FPA4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE PUTATIVE HEAT SHOCK FACTOR PROTEIN 1 (HSF 1).
GN P0006C01.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
OC Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Saeki T., Matsunoto T., Yamamoto K.;
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0006C01.";
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AP002744; BAB19067.1;
KW Heat shock
SQ SEQUENCE 348 AA; 37756 MW; 98C61C272160A134 CRC64;

Query Match 54.5%; Score 6; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOQTAP 6
| | | | |
DB 21 QOQTAP 26

RESULT 13
O20966 PRELIMINARY; PRT; 371 AA.
ID O20966

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AC Q20966;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE F58B3.7 PROTEIN.
GN F58B3.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B.;
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: 273427; CA97799.1;
DR InterPro: IPR000467;
DR InterPro: IPR000504;
DR Pfam: PR00076; rrm; 1.
DR Pfam: PF01585; G-patch; 1.
DR SMART: SM00360; RRM; 1.
SQ SEQUENCE 371 AA; 41207 MW; 7789A85A10CCCEC3D CRC64;

Query Match 54.5%; Score 6; DB 5; Length 371;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAPT 10
| | | | |
DB 255 APKAPT 260

RESULT 14
O9VMV9 PRELIMINARY; PRT; 388 AA.
AC O9VMV9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CG18623 PROTEIN.
GN CG18623.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

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Query Match 90.9%; Score 10; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAPKAPTE 11
 |||||
 DB 1 OOTAPKAPTE 10

RESULT 4

O48775 PRELIMINARY; PRT; 86 AA.

AC O48775: 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INVASIVE ASSOCIATED PROTEIN (FRAGMENT).
 GN IAP.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12705/89, TYPE 1;
 RX MEDLINE=96118685; PubMed=7496516;
 RA Rasmussen O.F., Skouboe P., Dons L., Rossen L., Olsen J.E.;
 RT "Listeria monocytogenes exists in at least three evolutionary lines:
 evidence from flagellin, Invasive associated protein and listeriolysin
 O genes.";
 RT O genes.";
 RL Microbiology 141:2053-2061(1995).
 DR EMBL: X85869; CAA59883.1; -.
 FT NON_TER 1
 FT NON_TER 86
 SQ SEQUENCE 86 AA; 8842 MW; AEE753BE7EA6D6F0 CRC64;

Query Match 90.9%; Score 10; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAPKAPTE 11
 |||||
 DB 1 OOTAPKAPTE 10

RESULT 5

O48782 PRELIMINARY; PRT; 86 AA.

AC O48782: 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INVASIVE ASSOCIATED PROTEIN (FRAGMENT).
 GN IAP.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=7785, TYPE 2;
 RX MEDLINE=96118685; PubMed=7496516;
 RA Rasmussen O.F., Skouboe P., Dons L., Rossen L., Olsen J.E.;
 RT "Listeria monocytogenes exists in at least three evolutionary lines:
 evidence from flagellin, Invasive associated protein and listeriolysin
 O genes.";
 RT O genes.";
 RL Microbiology 141:2053-2061(1995).
 DR EMBL: X85877; CAA59889.1; -.
 FT NON_TER 1
 FT NON_TER 86
 SQ SEQUENCE 86 AA; 8784 MW; DBA33D02B0E797B7 CRC64;

Query Match 90.9%; Score 10; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAPKAPTE 11
 |||||
 DB 1 OOTAPKAPTE 10

RESULT 6

O48781 PRELIMINARY; PRT; 88 AA.

AC O48781: 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INVASIVE ASSOCIATED PROTEIN (FRAGMENT).
 GN IAP.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=64.1.1, TYPE 2;
 RX MEDLINE=96118685; PubMed=7496516;
 RA Rasmussen O.F., Skouboe P., Dons L., Rossen L., Olsen J.E.;
 RT "Listeria monocytogenes exists in at least three evolutionary lines:
 evidence from flagellin, Invasive associated protein and listeriolysin
 O genes.";
 RT O genes.";
 RL Microbiology 141:2053-2061(1995).
 DR EMBL: X85875; CAA59887.1; -.
 FT NON_TER 1
 FT NON_TER 88
 SQ SEQUENCE 88 AA; 8999 MW; B61ACB649E465739 CRC64;

Query Match 90.9%; Score 10; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAPKAPTE 11
 |||||
 DB 1 OOTAPKAPTE 10

RESULT 7

O48774 PRELIMINARY; PRT; 117 AA.

AC O48774: 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 10, Last annotation update)
 DE INVASIVE ASSOCIATED PROTEIN (FRAGMENT).
 GN IAP.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12067, TYPE 1;
 RX MEDLINE=96118685; PubMed=7496516;
 RA Rasmussen O.F., Skouboe P., Dons L., Rossen L., Olsen J.E.;
 RT "Listeria monocytogenes exists in at least three evolutionary lines:
 evidence from flagellin, Invasive associated protein and listeriolysin
 O genes.";
 RT O genes.";
 RL Microbiology 141:2053-2061(1995).
 DR EMBL: X85856; CAA59870.1; -.
 FT NON_TER 1
 FT NON_TER 117

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969 4 36.4 137 14 036896 036896 human immun
970 4 36.4 137 14 065517 065517 barman fore
971 4 36.4 137 14 093671 093671 human immun
972 4 36.4 137 14 09E2J0 09E2J0 hepatitis c
973 4 36.4 137 14 09E2I9 09E2I9 hepatitis c
974 4 36.4 138 3 09A376 09A376 schizosacch
975 4 36.4 138 4 09NVS5 09NVS5 homo sapien
976 4 36.4 138 5 09VVP6 09VVP6 drosophila
977 4 36.4 138 10 043217 043217 titicum ae
978 4 36.4 138 10 09ZUS0 09ZUS0 arabidopsis
979 4 36.4 138 10 09LEF6 09LEF6 arabidopsis
980 4 36.4 138 14 09YTH4 09YTH4 human immun
981 4 36.4 138 14 09WS65 09WS65 human immun
982 4 36.4 139 2 09KZ29 09KZ29 streptomyc
983 4 36.4 139 2 09FA78 09FA78 vibrio pela
984 4 36.4 139 2 09FA76 09FA76 vibrio orle
985 4 36.4 139 3 09USJ1 09USJ1 schizosacch
986 4 36.4 139 5 09VM28 09VM28 drosophila
987 4 36.4 139 5 09UCU3 09UCU3 plasmodium
988 4 36.4 139 5 09NJM3 09NJM3 eumesocampa
989 4 36.4 139 5 09NLT1 09NLT1 machiloides
990 4 36.4 139 5 09NLT3 09NLT3 speleonecte
991 4 36.4 139 5 09NLT1 09NLT1 tomocerus s
992 4 36.4 139 5 09GQ22 09GQ22 plasmodium
993 4 36.4 139 10 065818 065818 lycopersico
994 4 36.4 139 10 09LL86 09LL86 solanum tub
995 4 36.4 139 10 09FK03 09FK03 arabidopsis
996 4 36.4 140 1 030082 030082 archaeoglob
997 4 36.4 140 5 025703 025703 plasmodium
998 4 36.4 140 5 018318 018318 chiromomus
999 4 36.4 140 10 065052 065052 picea maria
1000 4 36.4 140 10 09XETO 09XETO glycine max
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ALIGNMENTS

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RESULT 1
ID 003493 PRELIMINARY; PRT; 478 AA.
AC 003493;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094153; PubMed=1459966;
RA Hubert A., Kuhn M., Goebel W., Koehler S.;
RT "Structural and functional properties of the p60 proteins from
RT different Listeria species."
RL J. Bacteriol. 174:8166-8171(1992).
CC -1- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE
CC INVASION OF NONPROFESSIONAL PHAGOCYTTIC CELLS BY LISTERIA.
CC EMBL: M80351; AAA25280.1; -.
DR InterPro: IPR000064; -.
DR InterPro: IPR002482; -.
DR Pfam: PF00877; NRPC_P60; 1.
DR Pfam: PF01476; LysM; 2.
DR SMART: SM00257; LysM; 1.
KW Signal.
FT SIGNAL. 1 27 BY SIMILARITY.
FT CHAIN 28 478 PROTEIN P60.
FT SEQUENCE 478 AA; 49997 MW; D46D050507402344 CRC64;
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Query Match 100.0%; Score 11; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 00OTAPKAPTE 11
Db 291 00OTAPKAPTE 301

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RESULT 2
ID 048784 PRELIMINARY; PRT; 76 AA.
AC 048784;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE INVASIVE ASSOCIATED PROTEIN (FRAGMENT).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=443, TYPE 3;
RA Rasmussen O.F., Skouboe P., Dons L., Rossen L., Olsen J.E.;
RT "Listeria monocytogenes exists in at least three evolutionary lines:
RT evidence from flagellin, invasive associated protein and listeriolysin
RT O genes."
RL Microbiolgy 141:2053-2061(1995).
DR EMBL: X85880; CAA59892.1; -.
FT NON_TER 1 1
FT NON_TER 76 76
SO SEQUENCE 76 AA; 7744 MW; D5AC5B516193652E CRC64;
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Query Match 90.9%; Score 10; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 00TAPKAPTE 11
Db 1 00TAPKAPTE 10

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RESULT 3
ID 057205 PRELIMINARY; PRT; 84 AA.
AC 057205;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE INVASIVE ASSOCIATED PROTEIN (FRAGMENT).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=10165, TYPE 1;
RA Rasmussen O.F., Skouboe P., Dons L., Rossen L., Olsen J.E.;
RT "Listeria monocytogenes exists in at least three evolutionary lines:
RT evidence from flagellin, invasive associated protein and listeriolysin
RT O genes."
RL Microbiology 141:2053-2061(1995).
DR EMBL: X85859; CAA59873.1; -.
DR EMBL: X85857; CAA59871.1; -.
DR EMBL: X85858; CAA59872.1; -.
FT NON_TER 1 1
FT NON_TER 84 84
SO SEQUENCE 84 AA; 8627 MW; 8796F59721315E3C CRC64;
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823	4	36.4	119	5	Q9N6G3	Q9N6G3 trypanosoma	896	4	36.4	128	5	Q9N1Q2	Q9N1Q2 trypanosoma
824	4	36.4	119	10	Q39332	Q39332 brassica na	897	4	36.4	128	5	Q9N2V3	Q9N2V3 caenorhabdi
825	4	36.4	119	10	Q39404	Q39404 brassica ra	898	4	36.4	128	10	Q9FY37	Q9FY37 brassica ol
826	4	36.4	119	10	Q9STW3	Q9STW3 arabidopsis	899	4	36.4	128	13	P98190	P98190 carthartinu
827	4	36.4	119	10	Q9STR1	Q9STR1 arabidopsis	900	4	36.4	128	14	Q9JG52	Q9JG52 tlv-like mi
828	4	36.4	119	10	Q9FJL1	Q9FJL1 arabidopsis	901	4	36.4	129	2	Q57111	Q57111 veillonella
829	4	36.4	119	13	Q9W7A3	Q9W7A3 coturnix co	902	4	36.4	129	5	Q9Y1V5	Q9Y1V5 ephydactia f
830	4	36.4	119	13	Q9PWB2	Q9PWB2 coturnix co	903	4	36.4	129	5	Q9VIR5	Q9VIR5 drosophila
831	4	36.4	119	14	Q37047	Q37047 human immun	904	4	36.4	129	14	Q36883	Q36883 human immun
832	4	36.4	119	14	Q26134	Q26134 human immun	905	4	36.4	130	1	Q9Y9Y3	Q9Y9Y3 pyrococcus
833	4	36.4	119	14	Q9J696	Q9J696 human immun	906	4	36.4	130	2	Q47852	Q47852 erwinia her
834	4	36.4	119	14	Q9J672	Q9J672 human immun	907	4	36.4	130	2	Q45333	Q45333 bruceella ov
835	4	36.4	120	2	P76515	P76515 escherichia	908	4	36.4	130	2	Q56729	Q56729 vibrio sp.
836	4	36.4	120	2	Q9ZNI2	Q9ZNI2 staphylococ	909	4	36.4	130	2	Q66857	Q66857 aquifex aeo
837	4	36.4	120	5	Q9N1Q7	Q9N1Q7 trypanosoma	910	4	36.4	130	2	Q9S347	Q9S347 prevotella
838	4	36.4	120	6	Q77637	Q77637 sus scrofa	911	4	36.4	130	5	Q3U4A0	Q3U4A0 manduca sex
839	4	36.4	120	10	Q9LJW6	Q9LJW6 arabidopsis	912	4	36.4	130	6	Q9TST4	Q9TST4 sus scrofa
840	4	36.4	120	14	Q9J019	Q9J019 human immun	913	4	36.4	130	9	Q92XJ0	Q92XJ0 bacterioph
841	4	36.4	120	14	Q9J018	Q9J018 human immun	914	4	36.4	130	13	Q9PU29	Q9PU29 struthio ca
842	4	36.4	121	2	Q84349	Q84349 chlamydia t	915	4	36.4	131	2	Q9RSV2	Q9RSV2 delinococcus
843	4	36.4	121	2	P74135	P74135 synechocyst	916	4	36.4	131	2	Q85701	Q85701 streptomyce
844	4	36.4	121	2	Q9PRD4	Q9PRD4 ureaplasma	917	4	36.4	131	4	Q9S331	Q9S331 homo sapien
845	4	36.4	121	5	Q9W306	Q9W306 drosophila	918	4	36.4	131	5	Q9N131	Q9N131 plasmidium
846	4	36.4	121	5	Q9W2S2	Q9W2S2 drosophila	919	4	36.4	132	2	Q52174	Q52174 salmonella
847	4	36.4	121	6	Q9TSD5	Q9TSD5 bos taurus	920	4	36.4	132	3	Q9P323	Q9P323 pneumocysti
848	4	36.4	121	8	Q34194	Q34194 crithidia o	921	4	36.4	132	4	Q16609	Q16609 homo sapien
849	4	36.4	121	10	Q41575	Q41575 triticum ae	922	4	36.4	132	5	Q9N1Q3	Q9N1Q3 trypanosoma
850	4	36.4	121	10	Q9M573	Q9M573 perilla fru	923	4	36.4	132	5	Q9N803	Q9N803 leishmania
851	4	36.4	121	13	Q9PWB4	Q9PWB4 coturnix co	924	4	36.4	132	5	Q9GR02	Q9GR02 plasmidium
852	4	36.4	121	13	Q9PWB1	Q9PWB1 coturnix co	925	4	36.4	132	10	Q9LZ45	Q9LZ45 arabidopsis
853	4	36.4	121	14	Q72893	Q72893 human immun	926	4	36.4	132	11	Q60581	Q60581 mus musc
854	4	36.4	121	14	Q9WB17	Q9WB17 human immun	927	4	36.4	132	14	Q36856	Q36856 human immun
855	4	36.4	122	2	Q59657	Q59657 methanosarc	928	4	36.4	132	14	Q97693	Q97693 human immun
856	4	36.4	122	2	Q9S173	Q9S173 streptococc	929	4	36.4	132	14	Q9YFD3	Q9YFD3 human immun
857	4	36.4	122	2	Q9RA82	Q9RA82 streptococc	930	4	36.4	132	14	Q9WL78	Q9WL78 human immun
858	4	36.4	122	2	Q9RA81	Q9RA81 streptococc	931	4	36.4	132	14	Q9WL77	Q9WL77 human immun
859	4	36.4	122	2	Q9R391	Q9R391 streptococc	932	4	36.4	132	14	Q9JHL4	Q9JHL4 chimpanzee
860	4	36.4	122	2	Q9R390	Q9R390 streptococc	933	4	36.4	133	3	Q05666	Q05666 saccharomyc
861	4	36.4	122	5	Q97361	Q97361 phytophthor	934	4	36.4	133	14	Q9YRE8	Q9YRE8 human immun
862	4	36.4	122	5	Q9GXY4	Q9GXY4 leishmania	935	4	36.4	133	14	Q9YTA7	Q9YTA7 human immun
863	4	36.4	122	13	Q9DFN7	Q9DFN7 gilllichthys	936	4	36.4	134	1	Q9YF06	Q9YF06 aeropyrum p
864	4	36.4	123	1	Q9YB08	Q9YB08 aeropyrum p	937	4	36.4	134	2	Q9YF06	Q9YF06 aeropyrum p
865	4	36.4	123	2	Q24882	Q24882 helicobacte	938	4	36.4	134	2	Q9JZ33	Q9JZ33 neisseria m
866	4	36.4	123	2	Q9RXU9	Q9RXU9 delinococcus	939	4	36.4	134	4	Q9NV29	Q9NV29 homo sapien
867	4	36.4	123	4	Q9H7H2	Q9H7H2 homo sapien	940	4	36.4	134	5	Q24959	Q24959 giardia lam
868	4	36.4	123	5	Q9VE70	Q9VE70 drosophila	941	4	36.4	134	5	Q24988	Q24988 giardia lam
869	4	36.4	124	2	Q9R2F1	Q9R2F1 bruceella ab	942	4	36.4	134	5	Q9GX38	Q9GX38 leishmania
870	4	36.4	124	4	Q9H1H0	Q9H1H0 homo sapien	943	4	36.4	134	6	Q9N2E7	Q9N2E7 gorilla gor
871	4	36.4	124	5	Q97359	Q97359 phytophthor	944	4	36.4	134	10	Q9FSP1	Q9FSP1 oryza sativ
872	4	36.4	124	9	Q38372	Q38372 lactococcus	945	4	36.4	134	11	Q70483	Q70483 rattus norv
873	4	36.4	124	11	Q62286	Q62286 mus musc	946	4	36.4	134	14	Q97679	Q97679 human immun
874	4	36.4	124	13	Q9DFD3	Q9DFD3 oncorhynch	947	4	36.4	135	2	Q53977	Q53977 mycobacteri
875	4	36.4	124	14	Q9J4Z3	Q9J4Z3 fowlpox vir	948	4	36.4	135	4	Q9P207	Q9P207 homo sapien
876	4	36.4	125	1	Q9Y973	Q9Y973 aeropyrum p	949	4	36.4	135	4	Q9H524	Q9H524 homo sapien
877	4	36.4	125	10	P72987	P72987 synechocyst	950	4	36.4	135	6	Q9N2E8	Q9N2E8 pan troglod
878	4	36.4	125	10	Q9FRS9	Q9FRS9 arabidopsis	951	4	36.4	135	6	Q9N2E6	Q9N2E6 pongo pygma
879	4	36.4	125	13	Q9W7A4	Q9W7A4 coturnix co	952	4	36.4	135	10	Q43215	Q43215 triticum ae
880	4	36.4	125	13	Q9PWB5	Q9PWB5 coturnix co	953	4	36.4	135	10	Q9FVE0	Q9FVE0 arabidopsis
881	4	36.4	125	13	Q9PWB3	Q9PWB3 coturnix co	954	4	36.4	135	13	Q9W7A6	Q9W7A6 coturnix co
882	4	36.4	125	14	Q9WB4	Q9WB4 human immun	955	4	36.4	136	1	Q9YAR0	Q9YAR0 aeropyrum p
883	4	36.4	125	14	Q69271	Q69271 equine herp	956	4	36.4	136	2	Q51792	Q51792 alcaligenes
884	4	36.4	125	14	Q9DQW8	Q9DQW8 human immun	957	4	36.4	136	2	P74444	P74444 synechocyst
885	4	36.4	126	2	P74205	P74205 synechocyst	958	4	36.4	136	5	Q9GQZ8	Q9GQZ8 plasmidium
886	4	36.4	126	4	Q9UHE2	Q9UHE2 homo sapien	959	4	36.4	136	10	Q9J318	Q9J318 brassica na
887	4	36.4	126	5	Q94720	Q94720 paramedcum	960	4	36.4	136	10	Q9J319	Q9J319 brassica na
888	4	36.4	126	10	Q9SEF5	Q9SEF5 arabidopsis	961	4	36.4	136	10	Q43216	Q43216 triticum ae
889	4	36.4	127	2	Q9RLC9	Q9RLC9 pseudomonas	962	4	36.4	136	10	Q9S7N4	Q9S7N4 arabidopsis
890	4	36.4	127	2	Q9KLS8	Q9KLS8 vibrio chol	963	4	36.4	136	10	Q9FX60	Q9FX60 arabidopsis
891	4	36.4	127	5	Q9N128	Q9N128 plasmidium	964	4	36.4	137	2	Q47836	Q47836 enterococcu
892	4	36.4	127	10	Q9ZU00	Q9ZU00 arabidopsis	965	4	36.4	137	5	Q15689	Q15689 plasmidium
893	4	36.4	127	13	Q9W7A5	Q9W7A5 coturnix co	966	4	36.4	137	5	Q20468	Q20468 caenorhabdi
894	4	36.4	128	2	Q9WY58	Q9WY58 thermotoga	967	4	36.4	137	5	Q9N1Q4	Q9N1Q4 trypanosoma
895	4	36.4	128	2	Q9KXJ3	Q9KXJ3 streptomyc	968	4	36.4	137	11	Q35946	Q35946 rattus norv

677	4	36.4	102	2	053562	053562 methylolisin	750	4	36.4	112	14	079829	079829 human immun
678	4	36.4	102	5	09VED9	09VED9 drosophila	751	4	36.4	112	14	079836	079836 human immun
679	4	36.4	102	14	079847	079847 human immun	752	4	36.4	113	1	059655	059655 methanosarc
680	4	36.4	102	14	079848	079848 human immun	753	4	36.4	113	8	0913F9	0913F9 neptiroselmt
681	4	36.4	102	14	079849	079849 human immun	754	4	36.4	113	14	071164	071164 hepatitis c
682	4	36.4	102	14	091E50	091E50 human immun	755	4	36.4	113	14	079852	079852 human immun
683	4	36.4	103	1	059510	059510 pyrococcus	756	4	36.4	113	14	079853	079853 human immun
684	4	36.4	103	2	09PHX9	09PHX9 campylobact	757	4	36.4	113	14	079855	079855 human immun
685	4	36.4	103	2	09KRB8	09KRB8 vibrio chol	758	4	36.4	113	14	079856	079856 human immun
686	4	36.4	103	3	059673	059673 schizosacch	759	4	36.4	113	14	079857	079857 human immun
687	4	36.4	103	3	09PE69	09PE69 neurospora	760	4	36.4	113	14	079857	079857 human immun
688	4	36.4	103	5	022338	022338 caenorhabdi	761	4	36.4	113	14	079872	079872 human immun
689	4	36.4	103	5	09VZ98	09VZ98 drosophila	762	4	36.4	113	14	079873	079873 human immun
690	4	36.4	103	5	09NIO8	09NIO8 trypanosoma	763	4	36.4	113	14	079858	079858 human immun
691	4	36.4	103	5	09NIO8	09NIO8 trypanosoma	764	4	36.4	113	14	079859	079859 human immun
692	4	36.4	103	5	09NIO5	09NIO5 trypanosoma	765	4	36.4	113	14	079860	079860 human immun
693	4	36.4	104	8	09NIO2	09NIO2 plasmodium	766	4	36.4	113	14	079861	079861 human immun
694	4	36.4	104	10	09SUD3	09SUD3 beta vulgar	767	4	36.4	113	14	079862	079862 human immun
695	4	36.4	105	2	09WMP7	09WMP7 synchococc	768	4	36.4	113	14	079870	079870 human immun
696	4	36.4	105	2	025027	025027 helicobacte	769	4	36.4	113	14	079871	079871 human immun
697	4	36.4	105	2	09JTK2	09JTK2 neisseria m	770	4	36.4	114	2	098RC3	098RC3 listeria mo
698	4	36.4	105	5	09VRR8	09VRR8 drosophila	771	4	36.4	114	10	023138	023138 arbidopsist
699	4	36.4	105	14	076624	076624 human immun	772	4	36.4	114	14	079854	079854 human immun
700	4	36.4	105	14	012332	012332 human immun	773	4	36.4	115	5	09N129	09N129 plasmodium
701	4	36.4	105	14	09YTT7	09YTT7 human immun	774	4	36.4	115	5	09N130	09N130 plasmodium
702	4	36.4	105	14	09QTY8	09QTY8 tt virus. o	775	4	36.4	115	5	09N129	09N129 plasmodium
703	4	36.4	105	14	09QIT3	09QIT3 human immun	776	4	36.4	115	10	09XU07	09XU07 arbidopsist
704	4	36.4	105	14	09QIT3	09QIT3 human immun	777	4	36.4	115	10	09LYX0	09LYX0 arbidopsist
705	4	36.4	105	14	09PMT2	09PMT2 human immun	778	4	36.4	115	10	09LTRO	09LTRO arbidopsist
706	4	36.4	105	14	09PMT2	09PMT2 human immun	779	4	36.4	116	1	09YA88	09YA88 aeropyrum p
707	4	36.4	106	1	027467	027467 methanobact	780	4	36.4	116	2	09XAW0	09XAW0 pseudomonas
708	4	36.4	106	1	09YBC9	09YBC9 aeropyrum p	781	4	36.4	116	3	043034	043034 schizosacch
709	4	36.4	106	5	09Y9E1	09Y9E1 aeropyrum p	782	4	36.4	116	4	013138	013138 homo sapien
710	4	36.4	106	5	09NTO6	09NTO6 trypanosoma	783	4	36.4	116	5	P90590	P90590 parametium
711	4	36.4	106	10	065746	065746 ciccer arlet	784	4	36.4	116	5	09GQ27	09GQ27 plasmodium
712	4	36.4	106	10	09EY11	09EY11 picea abies	785	4	36.4	116	5	09GQ26	09GQ26 plasmodium
713	4	36.4	106	14	085590	085590 human t-cel	786	4	36.4	116	8	09XDF5	09XDF5 gonostoma g
714	4	36.4	106	14	098499	098499 parametium	787	4	36.4	116	10	09XFT6	09XFT6 chlamydom
715	4	36.4	107	5	09M4Z4	09M4Z4 drosophila	788	4	36.4	116	10	09SNU1	09SNU1 cryza sativ
716	4	36.4	107	5	09WOT5	09WOT5 drosophila	789	4	36.4	116	14	079826	079826 human immun
717	4	36.4	107	5	09UJ93	09UJ93 caenorhabdi	790	4	36.4	116	14	079830	079830 human immun
718	4	36.4	107	5	09NLP7	09NLP7 leishmania	791	4	36.4	116	14	079832	079832 human immun
719	4	36.4	107	5	09NEC8	09NEC8 leishmania	792	4	36.4	116	14	079834	079834 human immun
720	4	36.4	107	5	09XIL3	09XIL3 caenorhabdi	793	4	36.4	116	14	079835	079835 human immun
721	4	36.4	107	10	09ZRX4	09ZRX4 trititium ae	794	4	36.4	116	14	09YYV1	09YYV1 eyach virus
722	4	36.4	108	8	09ZYO8	09ZYO8 chordelies	795	4	36.4	116	14	09YYV0	09YYV0 eyach virus
723	4	36.4	109	2	P73607	P73607 synchocyst	796	4	36.4	117	2	0910H1	0910H1 pseudomonas
724	4	36.4	109	4	014325	014325 homo sapien	797	4	36.4	117	4	09NTE4	09NTE4 homo sapien
725	4	36.4	109	10	042347	042347 arbidopsist	798	4	36.4	117	4	09S166	09S166 homo sapien
726	4	36.4	110	2	09PEW3	09PEW3 xylella fas	799	4	36.4	117	4	09H0R8	09H0R8 homo sapien
727	4	36.4	110	2	09PEW2	09PEW2 neurospora	800	4	36.4	117	5	09VAJ4	09VAJ4 drosophila
728	4	36.4	110	5	09N316	09N316 caenorhabdi	801	4	36.4	117	10	048094	048094 leavenworth
729	4	36.4	110	6	09GWM6	09GWM6 macaca fasc	802	4	36.4	117	10	050049	050049 leavenworth
730	4	36.4	110	10	081061	081061 arbidopsist	803	4	36.4	117	10	050059	050059 leavenworth
731	4	36.4	110	11	09Z172	09Z172 mus musculu	804	4	36.4	117	10	050060	050060 leavenworth
732	4	36.4	110	14	011343	011343 mus musculu c	805	4	36.4	117	11	09QUIT7	09QUIT7 rattus norv
733	4	36.4	110	14	079840	079840 human immun	806	4	36.4	117	11	09J397	09J397 mus musculu c
734	4	36.4	110	14	079841	079841 human immun	807	4	36.4	117	14	098304	098304 molluscum c
735	4	36.4	110	14	079842	079842 human immun	808	4	36.4	117	14	079831	079831 human immun
736	4	36.4	110	14	P89815	P89815 human immun	809	4	36.4	117	14	079833	079833 human immun
737	4	36.4	111	5	094666	094666 plasmodium	810	4	36.4	118	2	024992	024992 helicobacte
738	4	36.4	111	5	09N136	09N136 plasmodium	811	4	36.4	118	2	09ZWN3	09ZWN3 helicobacte
739	4	36.4	111	5	09N135	09N135 plasmodium	812	4	36.4	118	2	09S1B5	09S1B5 arthropacte
740	4	36.4	111	5	09N134	09N134 plasmodium	813	4	36.4	118	4	09Y6B1	09Y6B1 homo sapien
741	4	36.4	111	10	024263	024263 pisum sativ	814	4	36.4	118	5	017150	017150 branchiostor
742	4	36.4	111	10	09SPK9	09SPK9 lactuca sat	815	4	36.4	118	5	097360	097360 phytophthor
743	4	36.4	112	1	09HNA4	09HNA4 halobacteri	816	4	36.4	118	5	09N1P8	09N1P8 solanum tub
744	4	36.4	112	1	09R2M7	09R2M7 delnoccoccu	817	4	36.4	118	10	09ZRD4	09ZRD4 arbidopsist
745	4	36.4	112	5	09JTH5	09JTH5 neisseria m	818	4	36.4	118	10	09ZRD4	09ZRD4 phytophthor
746	4	36.4	112	5	09GVD6	09GVD6 leishmania	819	4	36.4	118	10	09SMZ7	09SMZ7 arbidopsist
747	4	36.4	112	14	065509	065509 barmanh fore	820	4	36.4	118	10	09SMZ7	09SMZ7 arbidopsist
748	4	36.4	112	14	079827	079827 human immun	821	4	36.4	119	1	09Y9V6	09Y9V6 aeropyrum p
749	4	36.4	112	14	079828	079828 human immun	822	4	36.4	119	2	055617	055617 synchocyst

531	4	36.4	71	2	Q9PAE9	Q9paeg xyella f	604	4	36.4	84	14	Q9QJP8	Q9qjp8 human
532	4	36.4	71	10	Q9FTW6	Q9ftw6 oryza sativ	605	4	36.4	84	14	Q9QJP6	Q9qjp6 human
533	4	36.4	72	2	Q44953	Q44953 bacillus br	606	4	36.4	84	14	Q9QJP5	Q9qjp5 human
534	4	36.4	72	3	Q00411	Q00411 coccidioid	607	4	36.4	84	14	Q9QJP4	Q9qjp4 human
535	4	36.4	72	7	Q9FP71	Q9fp71 gadus morhu	608	4	36.4	84	14	Q9QJP3	Q9qjp3 human
536	4	36.4	72	14	Q84416	Q84416 paramecium	609	4	36.4	84	14	Q9QJP2	Q9qjp2 human
537	4	36.4	73	4	Q95576	Q95576 homo sapien	610	4	36.4	84	14	Q9QJP1	Q9qjp1 human
538	4	36.4	73	10	Q9M9P9	Q9m9p9 arabidopsis	611	4	36.4	84	14	Q9QJN9	Q9qjn9 human
539	4	36.4	74	2	Q43946	Q43946 azorhizobiu	612	4	36.4	84	14	Q9QJN8	Q9qjn8 human
540	4	36.4	74	2	Q31653	Q31653 bacillus su	613	4	36.4	85	6	Q9RHJ6	Q9rhj6 shewanella
541	4	36.4	74	2	Q32280	Q32280 bacillus su	614	4	36.4	85	6	Q29356	Q29356 sus scrofa
542	4	36.4	75	2	Q44890	Q44890 borellia bu	615	4	36.4	85	9	Q9WC17	Q9wc17 bacterioph
543	4	36.4	75	6	P79319	P79319 sus scrofa	616	4	36.4	86	4	Q99557	Q99557 homo sapien
544	4	36.4	76	2	Q06243	Q06243 mycobacteri	617	4	36.4	86	8	Q20119	Q20119 chlorella v
545	4	36.4	76	6	Q9N046	Q9n046 macaca fasc	618	4	36.4	86	14	Q00792	Q00792 human
546	4	36.4	76	10	P93382	P93382 nicotiana t	619	4	36.4	87	5	Q9U3U6	Q9u3u6 asterias ru
547	4	36.4	77	2	Q9X6M2	Q9x6m2 klebsiella	620	4	36.4	87	14	Q65930	Q65930 caprine art
548	4	36.4	77	2	Q9RVR7	Q9rvr7 delnoccocus	621	4	36.4	87	14	Q9WR53	Q9wr53 brazilian c
549	4	36.4	77	10	Q9FM16	Q9fm16 arabidopsis	622	4	36.4	87	14	Q9WR51	Q9wr51 brazilian c
550	4	36.4	78	10	Q9LDR0	Q9ldr0 oryza sativ	623	4	36.4	87	14	Q9WR49	Q9wr49 brazilian c
551	4	36.4	78	14	Q79844	Q79844 human	624	4	36.4	87	14	Q9W959	Q9w959 brazilian c
552	4	36.4	78	14	Q79846	Q79846 human	625	4	36.4	88	2	Q56971	Q56971 yersinia pe
553	4	36.4	79	5	Q23145	Q23145 caenorhabdi	626	4	36.4	88	2	Q3XA88	Q3xa88 streptomyc
554	4	36.4	79	11	Q63280	Q63280 rattus norv	627	4	36.4	88	5	Q9VFG8	Q9vfg8 drosophila
555	4	36.4	79	11	Q9Q358	Q9qj58 human herpe	628	4	36.4	89	1	Q9YAL2	Q9yal2 aetopyrum p
556	4	36.4	81	5	Q22861	Q22861 caenorhabdi	629	4	36.4	89	1	Q9HSU7	Q9hsu7 halobacteri
557	4	36.4	82	10	Q9SY18	Q9sy18 arabidopsis	630	4	36.4	89	13	Q42371	Q42371 brachydanio
558	4	36.4	82	14	Q55446	Q55446 sindbis vir	631	4	36.4	89	14	Q79821	Q79821 human
559	4	36.4	82	14	Q79824	Q79824 human	632	4	36.4	90	5	Q97102	Q97102 drosophila
560	4	36.4	82	14	Q79823	Q79823 human	633	4	36.4	90	14	Q79819	Q79819 human
561	4	36.4	83	14	Q79825	Q79825 human	634	4	36.4	90	14	Q79820	Q79820 human
562	4	36.4	83	1	Q9HHY5	Q9hhys halobacteri	635	4	36.4	91	2	Q9Z982	Q9z982 chlamydia p
563	4	36.4	83	1	Q9HHJ1	Q9hhj1 halobacteri	636	4	36.4	91	2	Q9RZR9	Q9rzr9 delnoccocus
564	4	36.4	83	2	Q85409	Q85409 pseudomonas	637	4	36.4	91	2	Q9R6C6	Q9r6c6 acrobacteri
565	4	36.4	83	2	Q85410	Q85410 pseudomonas	638	4	36.4	91	2	Q9JST1	Q9jsj1 chlamydia p
566	4	36.4	83	2	Q85411	Q85411 pseudomonas	639	4	36.4	91	14	Q69372	Q69372 cercopithec
567	4	36.4	83	2	Q85412	Q85412 pseudomonas	640	4	36.4	91	14	Q9YMG6	Q9ymg6 lymantria d
568	4	36.4	83	2	Q85413	Q85413 pseudomonas	641	4	36.4	92	6	Q9TV11	Q9tv11 canis famli
569	4	36.4	83	2	Q85414	Q85414 pseudomonas	642	4	36.4	92	13	Q9W7A7	Q9w7a7 coturnix co
570	4	36.4	83	2	Q85415	Q85415 pseudomonas	643	4	36.4	93	3	Q9USB9	Q9usb9 schizosacch
571	4	36.4	83	2	Q85416	Q85416 pseudomonas	644	4	36.4	93	5	Q9W2X9	Q9w2x9 drosophila
572	4	36.4	83	2	Q85418	Q85418 pseudomonas	645	4	36.4	93	5	Q9TVV9	Q9tvv9 caenorhabdi
573	4	36.4	83	2	Q85419	Q85419 pseudomonas	646	4	36.4	93	10	Q42409	Q42409 triticum tu
574	4	36.4	83	2	Q85420	Q85420 pseudomonas	647	4	36.4	93	10	P93609	P93609 triticum ae
575	4	36.4	83	2	Q85421	Q85421 pseudomonas	648	4	36.4	93	10	Q9SDN8	Q9sdd8 phytophthor
576	4	36.4	83	2	Q85422	Q85422 pseudomonas	649	4	36.4	94	2	Q9RSY3	Q9rsy3 azorhizobiu
577	4	36.4	83	2	Q85423	Q85423 pseudomonas	650	4	36.4	94	10	Q40830	Q40830 pisum elat
578	4	36.4	83	2	Q85424	Q85424 pseudomonas	651	4	36.4	94	10	Q24255	Q24255 pisum fulvu
579	4	36.4	83	2	Q85425	Q85425 pseudomonas	652	4	36.4	94	10	Q24262	Q24262 pisum sativ
580	4	36.4	83	2	Q85426	Q85426 pseudomonas	653	4	36.4	94	10	Q9M4X1	Q9m4x1 poa fendler
581	4	36.4	83	2	Q85427	Q85427 pseudomonas	654	4	36.4	94	10	Q9FSJ9	Q9fsj9 oryza sativ
582	4	36.4	83	2	Q85428	Q85428 pseudomonas	655	4	36.4	95	2	Q32887	Q32887 mycobacteri
583	4	36.4	83	2	Q85429	Q85429 pseudomonas	656	4	36.4	95	14	Q86553	Q86553 maedi-vlsna
584	4	36.4	83	2	Q85430	Q85430 pseudomonas	657	4	36.4	95	14	Q79868	Q79868 human
585	4	36.4	83	2	Q85431	Q85431 pseudomonas	658	4	36.4	95	14	Q79869	Q79869 human
586	4	36.4	83	2	Q85432	Q85432 pseudomonas	659	4	36.4	96	5	Q9V5Y7	Q9v5y7 drosophila
587	4	36.4	83	2	Q85433	Q85433 pseudomonas	660	4	36.4	97	5	Q9VOT1	Q9vot1 drosophila
588	4	36.4	83	2	Q85434	Q85434 pseudomonas	661	4	36.4	97	13	Q9W7A8	Q9w7a8 coturnix co
589	4	36.4	83	2	Q85435	Q85435 pseudomonas	662	4	36.4	98	5	Q96731	Q96731 phytophthor
590	4	36.4	83	2	Q85436	Q85436 pseudomonas	663	4	36.4	98	5	Q96732	Q96732 phytophthor
591	4	36.4	83	2	Q85437	Q85437 pseudomonas	664	4	36.4	98	5	Q96733	Q96733 phytophthor
592	4	36.4	83	2	Q85438	Q85438 pseudomonas	665	4	36.4	98	5	Q96734	Q96734 phytophthor
593	4	36.4	83	2	Q85439	Q85439 pseudomonas	666	4	36.4	98	10	Q9S9P8	Q9s9p8 phytophthor
594	4	36.4	83	2	Q85440	Q85440 pseudomonas	667	4	36.4	98	14	Q57056	Q57056 human
595	4	36.4	83	2	Q85441	Q85441 pseudomonas	668	4	36.4	98	14	Q9YEP0	Q9yep0 choristoneu
596	4	36.4	83	2	Q85442	Q85442 pseudomonas	669	4	36.4	99	2	Q07487	Q07487 rhizobium m
597	4	36.4	83	2	Q85443	Q85443 pseudomonas	670	4	36.4	99	2	Q9Z7I8	Q9z7i8 chlamydia p
598	4	36.4	83	2	Q85444	Q85444 pseudomonas	671	4	36.4	99	2	Q9ERT5	Q9ert5 corynebacte
599	4	36.4	83	2	Q85445	Q85445 pseudomonas	672	4	36.4	99	3	Q9HPH1	Q9hph1 pichia etch
600	4	36.4	83	2	P77431	P77431 escherichia	673	4	36.4	101	10	Q9W581	Q9w581 splinacia ol
601	4	36.4	83	2	Q9KU64	Q9ku64 vibrio chol	674	4	36.4	101	11	P70530	P70530 rattus norv
602	4	36.4	84	5	Q9XVZ8	Q9xvz8 caenorhabdi	675	4	36.4	101	11	Q9ERN9	Q9ern9 cavia porco
603	4	36.4	84	10	Q9XCQ9	Q9xcq9 oryza sativ	676	4	36.4	101	13	Q9PWB6	Q9pwb6 coturnix co

385	5	45.5	1550	4	092547	092547 homo sapien	458	4	36.4	46	2	086393	086393 nelisseria m
386	5	45.5	1586	13	09DFB7	09dfb7 gallus gall	459	4	36.4	47	5	09V5D6	09v5d6 drosophila
387	5	45.5	1621	2	09KXAS	09kas vibrio chol	460	4	36.4	47	14	087177	087177 chimpanzee
388	5	45.5	1654	11	09JIG0	09jig0 rattus norv	461	4	36.4	47	14	087178	087178 chimpanzee
389	5	45.5	1655	5	09VB55	09vb55 drosophila	462	4	36.4	47	14	087179	087179 chimpanzee
390	5	45.5	1663	5	09U001	09u001 homo sapien	463	4	36.4	47	14	087180	087180 chimpanzee
391	5	45.5	1664	5	09V9V5	09v9v5 drosophila	464	4	36.4	47	14	087181	087181 chimpanzee
392	5	45.5	1688	5	09N926	09n926 drosophila	465	4	36.4	47	14	087183	087183 chimpanzee
393	5	45.5	1696	11	09WTR8	09wtr8 rattus norv	466	4	36.4	47	14	087186	087186 chimpanzee
394	5	45.5	1703	5	09VGP8	09vgp8 drosophila	467	4	36.4	48	2	09KX20	09kx20 pseudomonas
395	5	45.5	1729	5	09U617	09u017 drosophila	468	4	36.4	48	4	012978	012978 homo sapien
396	5	45.5	1785	5	023685	023685 plasmodium	469	4	36.4	50	14	09YUW5	09yuw5 human coxa
397	5	45.5	1785	5	093636	093636 caenorhabdi	470	4	36.4	50	14	09YUW4	09yuw4 echovirus 3
398	5	45.5	1794	9	09TIA7	09tia7 bacterioph	471	4	36.4	50	14	09YUW2	09yuw2 human coxa
399	5	45.5	1825	3	09HFI5	09hfi5 neurospora	472	4	36.4	50	14	09YUW0	09yuw0 human coxa
400	5	45.5	1876	5	09VTR5	09vtr5 drosophila	473	4	36.4	52	14	091MS5	091ms5 prunus necr
401	5	45.5	1929	5	093537	093537 caenorhabdi	474	4	36.4	52	14	091MS4	091ms4 prunus necr
402	5	45.5	1930	5	09U600	09u600 drosophila	475	4	36.4	52	14	091MS2	091ms2 prunus necr
403	5	45.5	1991	5	09W244	09w244 drosophila	476	4	36.4	52	14	091MS1	091ms1 prunus necr
404	5	45.5	1994	10	09LP19	09lp19 arabidopsis	477	4	36.4	52	14	091MR9	091mr9 prunus necr
405	5	45.5	2023	4	075557	075557 homo sapien	478	4	36.4	52	14	091MR8	091mr8 prunus necr
406	5	45.5	2033	4	09UWD7	09ud7 homo sapien	479	4	36.4	52	14	091MR6	091mr6 prunus necr
407	5	45.5	2074	11	088542	088542 mus musculu	480	4	36.4	52	14	091MR4	091mr4 prunus necr
408	5	45.5	2135	4	043157	043157 homo sapien	481	4	36.4	52	14	091MR3	091mr3 prunus necr
409	5	45.5	2135	4	09U1V7	09u1v7 homo sapien	482	4	36.4	52	14	091MR1	091mr1 prunus necr
410	5	45.5	2187	11	P70670	P70670 mus musculu	483	4	36.4	52	14	091MR0	091mr0 prunus necr
411	5	45.5	2209	5	09U0G6	09u0g6 plasmodium	484	4	36.4	52	14	091MO8	091mo8 prunus necr
412	5	45.5	2212	5	09UHV6	09uhv6 homo sapien	485	4	36.4	52	14	091MO6	091mo6 prunus necr
413	5	45.5	2212	5	094657	094657 plasmodium	486	4	36.4	52	14	091MO5	091mo5 prunus necr
414	5	45.5	2376	11	09JIF2	09jif2 rattus norv	487	4	36.4	52	14	091MO4	091mo4 prunus necr
415	5	45.5	2382	4	09H4A3	09h4a3 homo sapien	488	4	36.4	52	14	091MO2	091mo2 prunus necr
416	5	45.5	2439	5	09VMS2	09vms2 drosophila	489	4	36.4	53	1	09HAW5	09haw5 frankia sp.
417	5	45.5	2635	14	P88955	P88955 kaposi's sa	490	4	36.4	53	2	09RAW5	09raw5 frankia sp.
418	5	45.5	2635	14	040942	040942 plasmodium	491	4	36.4	53	14	011370	011370 moluscum c
419	5	45.5	2647	5	P90580	P90580 shewanella	492	4	36.4	55	6	097747	097747 bos taurus
420	5	45.5	2756	2	033904	033904 leishmania	493	4	36.4	55	6	09UVM9	09uvm9 coprinus ci
421	5	45.5	2936	5	09NKP7	09nkp7 leishmania	494	4	36.4	56	3	09UVM9	09uvm9 coprinus ci
422	5	45.5	2959	11	09JIF1	09jif1 rattus norv	495	4	36.4	56	4	012976	012976 homo sapien
423	5	45.5	3112	5	09NKP1	09nkp1 leishmania	496	4	36.4	57	6	097900	097900 ateles belz
424	5	45.5	3132	14	P89459	P89459 herpes simp	497	4	36.4	59	4	012977	012977 homo sapien
425	5	45.5	3169	5	0917V8	0917v8 drosophila	498	4	36.4	60	2	09PGC0	09pgc0 xylella fas
426	5	45.5	3201	5	09NDJ2	09ndj2 drosophila	499	4	36.4	60	2	09KXN8	09kxn8 streptomyce
427	5	45.5	3257	5	09V736	09v736 drosophila	500	4	36.4	60	5	09VZL9	09vzl9 drosophila
428	5	45.5	3261	4	09Y556	09y556 homo sapien	501	4	36.4	60	5	09U3W3	09u3w3 caenorhabdi
429	5	45.5	3379	5	09V5N8	09v5n8 drosophila	502	4	36.4	61	2	09U3Z8	09u3z8 nelisseria m
430	5	45.5	3526	5	09VFL1	09vfl1 drosophila	503	4	36.4	61	5	018358	018358 caenorhabdi
431	5	45.5	6875	6	028733	028733 oryctolagus	504	4	36.4	62	1	09HL02	09hl02 thecnioplasm
432	5	45.5	26926	4	010466	010466 homo sapien	505	4	36.4	62	2	047216	047216 escherichia
433	4	36.4	17	13	P81904	P81904 ictalurus p	506	4	36.4	62	5	017536	017536 caenorhabdi
434	4	36.4	19	2	09R524	09r524 clostridium	507	4	36.4	62	14	010289	010289 orgyia pseu
435	4	36.4	20	2	09R424	09r424 proteus mir	508	4	36.4	63	5	016829	016829 drosophila
436	4	36.4	20	13	P81903	P81903 ictalurus p	509	4	36.4	63	13	090951	090951 gallus gall
437	4	36.4	21	5	09TWF7	09twf7 entamoeba h	510	4	36.4	63	14	085040	085040 pseudorabie
438	4	36.4	22	5	09TW08	09tw08 crithidia f	511	4	36.4	64	2	045170	045170 borrelia ga
439	4	36.4	22	13	09PS65	09ps65 oncorhynch	512	4	36.4	64	2	09JXF6	09jxf6 nelisseria m
440	4	36.4	24	10	09S825	09s825 spinacia ol	513	4	36.4	64	2	09JWJ3	09jwj3 nelisseria m
441	4	36.4	25	2	09R5H6	09r5h6 bacillus su	514	4	36.4	64	2	091026	091026 pseudomonas
442	4	36.4	32	14	084265	084265 human papil	515	4	36.4	64	10	09LGP2	09lgp2 oryza sativ
443	4	36.4	34	2	09RSB3	09rsb3 streptomyce	516	4	36.4	65	5	09W5R0	09w5r0 drosophila
444	4	36.4	36	2	09KS74	09ks74 vibrio chol	517	4	36.4	66	2	09JTC8	09jtc8 nelisseria m
445	4	36.4	37	10	09ZP81	09zp81 raphanus sa	518	4	36.4	66	14	084302	084302 human papil
446	4	36.4	38	5	024462	024462 drosophila	519	4	36.4	67	2	P76099	P76099 escherichia
447	4	36.4	38	8	079167	079167 drosophila	520	4	36.4	67	3	014391	014391 schizosacch
448	4	36.4	38	8	079172	079172 nitox novae	521	4	36.4	67	4	012975	012975 homo sapien
449	4	36.4	39	4	09U0N1	09u0n1 homo sapien	522	4	36.4	68	2	049119	049119 methyllobact
450	4	36.4	39	4	09U0N1	09u0n1 homo sapien	523	4	36.4	69	1	09HQE8	09hqe8 halobacteri
451	4	36.4	41	2	031327	031327 bacillus br	524	4	36.4	70	2	056716	056716 vibrio para
452	4	36.4	42	11	09X8F1	09x8f1 streptomyce	525	4	36.4	70	4	09N7C7	09n7c7 homo sapien
453	4	36.4	42	11	09ZIC3	09zic3 mus spretus	526	4	36.4	70	5	09N7C7	09n7c7 leishmania
454	4	36.4	43	4	013063	013063 homo sapien	527	4	36.4	70	14	065909	065909 human coxa
455	4	36.4	43	4	014909	014909 homo sapien	528	4	36.4	71	2	09ZFU3	09zfu3 mastigoclad
456	4	36.4	43	5	09VD93	09vd93 drosophila	529	4	36.4	71	2	09RSM1	09rsm1 delnecoccus
457	4	36.4	43	14	09Q1F1	09q1f1 polyomaviru	530	4	36.4	71	2	09RSM1	09rsm1 delnecoccus

239	5	45.5	528	10	022549	022549 lycopersico	312	5	45.5	859	4	09GR7	09gr7 homo sapien
240	5	45.5	534	5	044117	044117 drosophila	313	5	45.5	866	2	09KR26	09kr26 streptococ
241	5	45.5	536	1	09HPA2	09HPA2 halobacteri	314	5	45.5	869	4	09HCF3	09hcf3 homo sapien
242	5	45.5	537	2	046977	046977 escherichia	315	5	45.5	876	2	035376	035376 synechococ
243	5	45.5	540	10	048683	048683 arabiopsis	316	5	45.5	883	2	09X5P4	09x5p4 pseudomonas
244	5	45.5	545	11	060626	060626 mus musculu	317	5	45.5	891	2	09HYJ7	09hyj7 pseudomonas
245	5	45.5	550	5	09VN76	09VN76 drosophila	318	5	45.5	891	5	09V172	09v172 drosophila
246	5	45.5	559	5	016124	016124 drosophila	319	5	45.5	905	3	09P8C5	09p8c5 tolypoclad
247	5	45.5	569	10	P93543	P93543 sambucus n1	320	5	45.5	922	11	09OXJ2	09oxj2 mus musculu
248	5	45.5	576	2	031745	031745 bacillus su	321	5	45.5	923	11	09WVL2	09wvl2 mus musculu
249	5	45.5	576	4	09NTE7	09NTE7 homo sapien	322	5	45.5	925	11	09QZB4	09qzb4 mus musculu
250	5	45.5	578	3	09Y7N0	09Y7N0 schizosacch	323	5	45.5	927	5	021811	021811 caenorhabdi
251	5	45.5	579	4	09PI73	09PI73 homo sapien	324	5	45.5	932	5	09NH67	09nh67 drosophila
252	5	45.5	581	2	09RU45	09RU45 delinococcus	325	5	45.5	932	5	09VAM0	09vam0 drosophila
253	5	45.5	581	10	09ZTV1	09ZTV1 canavalia 1	326	5	45.5	934	4	09P2B0	09p2b0 homo sapien
254	5	45.5	583	2	09Z5K5	09Z5K5 mycobacteri	327	5	45.5	943	2	044109	044109 actinomyc
255	5	45.5	583	5	019275	019275 caenorhabdi	328	5	45.5	950	5	09VFO1	09vfo1 drosophila
256	5	45.5	587	2	044563	044563 anabena va	329	5	45.5	968	11	086522	086522 mus musculu
257	5	45.5	590	5	09GUG6	09GUG6 caenorhabdi	330	5	45.5	971	5	09TVL9	09tvl9 caenorhabdi
258	5	45.5	593	2	051191	051191 neisseria m	331	5	45.5	972	11	09OYX2	09oyx2 ratius norv
259	5	45.5	601	5	09W3V9	09W3V9 drosophila	332	5	45.5	973	4	09P203	09p203 homo sapien
260	5	45.5	610	14	084595	084595 paramecium	333	5	45.5	986	2	09PJT3	09pj3 chlamydia m
261	5	45.5	611	4	09NOE0	09NOE0 homo sapien	334	5	45.5	993	4	09HCC9	09hcc9 homo sapien
262	5	45.5	613	3	005785	005785 saccharomyc	335	5	45.5	993	5	017162	017162 brugia mala
263	5	45.5	613	4	09UFB1	09UFB1 homo sapien	336	5	45.5	1012	11	064028	064028 mus musculu
264	5	45.5	614	5	P91720	P91720 drosophila	337	5	45.5	1013	11	09JTH3	09jth3 ratius norv
265	5	45.5	622	2	031248	031248 actinobact	338	5	45.5	1028	5	09N5Y8	09n5y8 caenorhabdi
266	5	45.5	623	13	057602	057602 ictalurus p	339	5	45.5	1028	10	09F6H7	09f6h7 arabiopsis
267	5	45.5	626	5	09W1U4	09W1U4 drosophila	340	5	45.5	1039	5	09VTR6	09vtr6 drosophila
268	5	45.5	632	2	09KM53	09KM53 peptobacter	341	5	45.5	1040	4	09NTJ4	09ntj4 homo sapien
269	5	45.5	648	10	09M8Z4	09M8Z4 arabiopsis	342	5	45.5	1041	2	09JMD5	09jmd5 neisseria m
270	5	45.5	650	2	031382	031382 bradyrhizob	343	5	45.5	1049	3	013344	013344 emericeila
271	5	45.5	650	2	09RK05	09RK05 streptomyc	344	5	45.5	1052	4	060264	060264 homo sapien
272	5	45.5	652	4	015410	015410 homo sapien	345	5	45.5	1062	4	09UL64	09ul64 homo sapien
273	5	45.5	654	2	039656	039656 plectonema	346	5	45.5	1072	5	09N5Y6	09n5y6 caenorhabdi
274	5	45.5	659	10	09LMU4	09LMU4 arabiopsis	347	5	45.5	1077	5	097217	097217 leishmania
275	5	45.5	667	2	09WXA5	09WXA5 erwina car	348	5	45.5	1098	2	050733	050733 borrelia bu
276	5	45.5	668	10	09FUZ7	09FUZ7 zea mays (m	349	5	45.5	1105	4	09ULF3	09ulf3 homo sapien
277	5	45.5	680	2	052644	052644 ruminococcu	350	5	45.5	1127	2	09P843	09p843 mycobacteri
278	5	45.5	695	11	09ESB0	09ESB0 ratius norv	351	5	45.5	1132	5	002432	002432 drosophila
279	5	45.5	697	10	09FTG1	09FTG1 arabiopsis	352	5	45.5	1151	3	057580	057580 gallus gall
280	5	45.5	700	11	09ESB1	09ESB1 ratius norv	353	5	45.5	1151	13	057580	057580 gallus gall
281	5	45.5	711	4	09ULG6	09ULG6 homo sapien	354	5	45.5	1161	2	09JVR9	09jvr9 neisseria m
282	5	45.5	718	2	09JZD0	09JZD0 neisseria m	355	5	45.5	1177	5	021391	021391 caenorhabdi
283	5	45.5	722	5	09NKS5	09NKS5 leishmania	356	5	45.5	1178	5	09VCC5	09vc5 drosophila
284	5	45.5	722	13	09PSZ5	09PSZ5 lampetra ja	357	5	45.5	1182	5	024352	024352 drosophila
285	5	45.5	728	5	09XGX4	09XGX4 caenorhabdi	358	5	45.5	1198	4	09H9J4	09h9j4 homo sapien
286	5	45.5	730	2	09X6U0	09X6U0 streptococ	359	5	45.5	1215	5	09V787	09v787 drosophila
287	5	45.5	733	10	09ZVD0	09ZVD0 arabiopsis	360	5	45.5	1216	11	09Z0Y7	09z0y7 mus musculu
288	5	45.5	749	4	09UK04	09UK04 homo sapien	361	5	45.5	1224	13	09Y190	09y190 xenopus lae
289	5	45.5	756	4	09Y6W2	09Y6W2 homo sapien	362	5	45.5	1228	2	044334	044334 agrobacteri
290	5	45.5	756	4	09Y6W1	09Y6W1 homo sapien	363	5	45.5	1236	11	070349	070349 mus musculu
291	5	45.5	756	4	09Y6W1	09Y6W1 homo sapien	364	5	45.5	1237	13	091976	091976 gallus gall
292	5	45.5	768	4	09Y6W1	09Y6W1 pseudomonas	365	5	45.5	1238	5	09V8B6	09v8b6 drosophila
293	5	45.5	768	11	088797	088797 ratius norv	366	5	45.5	1249	5	09N8G4	09n8g4 trypanosoma
294	5	45.5	774	4	013598	013598 homo sapien	367	5	45.5	1257	2	P96746	P96746 cornebacte
295	5	45.5	774	4	094892	094892 drosophila	368	5	45.5	1262	5	09W110	09w110 drosophila
296	5	45.5	779	4	09Y2F4	09Y2F4 homo sapien	369	5	45.5	1266	2	09W4Q4	09w4q4 drosophila
297	5	45.5	782	4	09NKK3	09NKK3 homo sapien	370	5	45.5	1295	5	09F6T1	09f6t1 escherichia
298	5	45.5	782	10	041583	041583 homo sapien	371	5	45.5	1329	10	09ZUK1	09zuk1 arabiopsis
299	5	45.5	792	2	09L2I8	09L2I8 streptomyc	372	5	45.5	1331	4	09UHC6	09uhc6 homo sapien
300	5	45.5	797	3	09P7M6	09P7M6 schizosacch	373	5	45.5	1339	4	09U012	09u012 homo sapien
301	5	45.5	800	2	09EXG2	09EXG2 listeria mo	374	5	45.5	1356	5	021946	021946 caenorhabdi
302	5	45.5	806	10	09MBT5	09MBT5 arabiopsis	375	5	45.5	1376	5	09W5D0	09w5d0 drosophila
303	5	45.5	806	10	09MBT5	09MBT5 arabiopsis	376	5	45.5	1400	11	09ESU6	09esu6 mus musculu
304	5	45.5	820	10	09LFE0	09LFE0 arabiopsis	377	5	45.5	1403	5	09U6A2	09u6a2 drosophila
305	5	45.5	824	5	021737	021737 caenorhabdi	378	5	45.5	1409	5	002626	002626 caenorhabdi
306	5	45.5	832	2	09KZV7	09KZV7 streptomyc	379	5	45.5	1416	5	019378	019378 caenorhabdi
307	5	45.5	833	5	09USN8	09USN8 leishmania	380	5	45.5	1435	4	09UEB9	09ueb9 homo sapien
308	5	45.5	835	2	09K3E2	09K3E2 streptomyc	381	5	45.5	1435	4	09HCD7	09hcd7 homo sapien
309	5	45.5	838	4	09NTN9	09NTN9 homo sapien	382	5	45.5	1445	4	09ULI6	09uli6 homo sapien
310	5	45.5	841	3	09Y8B5	09Y8B5 cryptococcu	383	5	45.5	1520	2	09KTO4	09ktg4 vibrio chol
311	5	45.5	852	3	09PAQ2	09PAQ2 pneumocysti	384	5	45.5	1543	5	09WMA0	09wma0 drosophila

93	5	45.5	212	14	09WMH8	09wmh8 fish lympho	166	5	45.5	373	10	P93031	P93031 arbidopsis
94	5	45.5	217	5	09VLA1	09vla1 drosophila	167	5	45.5	373	10	09SD30	09sd30 arbidopsis
95	5	45.5	218	5	09PF65	09pf65 xylella fas	168	5	45.5	375	10	09RW21	09rw21 delnoccus
96	5	45.5	220	5	09VBE1	09vbe1 drosophila	169	5	45.5	375	4	014712	014712 homo sapien
97	5	45.5	223	5	021648	021648 caenorhabdi	170	5	45.5	376	13	09FWM1	09fwm1 gallus galli
98	5	45.5	224	3	042710	042710 schizosacch	171	5	45.5	381	5	09NDP7	09ndp7 clona lntes
99	5	45.5	225	13	093590	093590 xenopus lae	172	5	45.5	382	10	003990	003990 daucus caro
100	5	45.5	225	5	001833	001833 caenorhabdi	173	5	45.5	383	2	09X6L5	09x6l5 klebsiella
101	5	45.5	228	10	09ZPK9	09zpk9 hyacinthus	174	5	45.5	383	2	001678	001678 pneumocysti
102	5	45.5	229	3	09USP6	09usp6 schizosacch	175	5	45.5	384	2	056617	056617 vibrio chol
103	5	45.5	241	5	023790	023790 chironomus	176	5	45.5	385	5	020103	020103 caenorhabdi
104	5	45.5	241	5	017321	017321 chironomus	177	5	45.5	387	14	066407	066407 dashneen mos
105	5	45.5	241	5	09G0H1	09guh1 caenorhabdi	178	5	45.5	388	5	023232	023232 caenorhabdi
106	5	45.5	242	2	09EUQ7	09eug7 streptococc	179	5	45.5	395	14	069369	069369 cercopithec
107	5	45.5	243	5	023784	023784 chironomus	180	5	45.5	399	4	09H4K6	09h4k6 homo sapien
108	5	45.5	246	2	09EX05	09ex05 streptomyce	181	5	45.5	403	10	004772	004772 chlorococcu
109	5	45.5	256	11	09ESA6	09esa6 rattus norv	182	5	45.5	404	4	075177	075177 homo sapien
110	5	45.5	258	4	09NUD0	09nud0 homo sapien	183	5	45.5	405	2	09FCM7	09fcm7 streptomyce
111	5	45.5	258	13	091928	091928 bambusicola	184	5	45.5	405	13	091929	091929 bambusicola
112	5	45.5	262	5	015758	015758 trypanosoma	185	5	45.5	408	2	067062	067062 aquilex aeo
113	5	45.5	262	5	09VY35	09vy35 drosophila	186	5	45.5	412	1	09YBC6	09ybc6 aeropyrum p
114	5	45.5	262	5	09U396	09u396 caenorhabdi	187	5	45.5	412	5	008523	008523 ascaris suu
115	5	45.5	263	5	09VY34	09vy34 drosophila	188	5	45.5	415	10	09FEP4	09fep4 oryza saliv
116	5	45.5	267	5	09V6B8	09v6b8 drosophila	189	5	45.5	416	5	P90878	P90878 caenorhabdi
117	5	45.5	269	2	09KPI3	09kpi3 vibrio chol	190	5	45.5	416	9	09ZMW9	09zwm9 corynephage
118	5	45.5	269	2	09F2T4	09f2t4 streptomyce	191	5	45.5	423	5	09VBX3	09vbx3 drosophila
119	5	45.5	270	2	P73854	P73854 synechocyst	192	5	45.5	424	3	074211	074211 yarrowia ll
120	5	45.5	270	2	09KAR9	09kar9 bacillus ha	193	5	45.5	425	1	013358	013358 homo sapien
121	5	45.5	272	10	09FAC6	09fac6 pseudomonas	194	5	45.5	431	1	09U731	09u731 pyrococcus
122	5	45.5	272	10	09FY77	09fy77 arbidopsis	195	5	45.5	434	3	09P970	09p970 tricholoma
123	5	45.5	273	2	09LIR2	09lir2 streptomyce	196	5	45.5	437	3	09HEX2	09hex2 pneumocysti
124	5	45.5	274	13	091927	091927 bambusicola	197	5	45.5	437	5	09GVE6	09gve6 leishmania
125	5	45.5	274	13	091926	091926 bambusicola	198	5	45.5	439	5	09TX40	09tx40 dictyostell
126	5	45.5	276	10	09SNS1	09sns1 oryza sativ	199	5	45.5	442	5	026909	026909 trypanosoma
127	5	45.5	279	5	015759	015759 trypanosoma	200	5	45.5	444	5	026895	026895 trypanosoma
128	5	45.5	280	2	P95727	P95727 streptomyce	201	5	45.5	445	2	066913	066913 aquilex aeo
129	5	45.5	289	14	098505	098505 parametium	202	5	45.5	445	2	09KBS1	09kbs1 bacillus ha
130	5	45.5	296	5	018675	018675 caenorhabdi	203	5	45.5	448	2	09REQ3	09req3 zymomonas m
131	5	45.5	297	5	09V5R4	09v5r4 drosophila	204	5	45.5	448	5	023571	023571 caenorhabdi
132	5	45.5	298	11	09ESA9	09esa9 rattus norv	205	5	45.5	448	10	023100	023100 arbidopsis
133	5	45.5	301	10	09ZPH0	09zph0 arbidopsis	206	5	45.5	451	2	09K111	09k111 neisseria m
134	5	45.5	302	5	09U719	09u719 chaeopteru	207	5	45.5	451	2	09JSM6	09jsm6 neisseria m
135	5	45.5	303	2	09RS08	09rs08 delnoccus	208	5	45.5	455	10	09LJH2	09ljh2 arbidopsis
136	5	45.5	304	2	09URJ3	09urj3 neisseria m	209	5	45.5	456	2	09ZC76	09zc76 yersinia pe
137	5	45.5	306	5	09VRA8	09vra8 drosophila	210	5	45.5	458	5	09N3U1	09n3u1 caenorhabdi
138	5	45.5	307	10	09ZUP7	09zup7 arbidopsis	211	5	45.5	461	2	09LAX6	09lax6 streptococc
139	5	45.5	315	5	P91282	P91282 caenorhabdi	212	5	45.5	471	3	09P723	09p723 neutrospora
140	5	45.5	320	5	09VQ29	09vq29 drosophila	213	5	45.5	476	5	003996	003996 plasmodium
141	5	45.5	321	2	084847	084847 chlamydia t	214	5	45.5	479	2	09H2B7	09h2b7 pseudomonas
142	5	45.5	321	2	09R705	09r705 escherichia	215	5	45.5	480	5	09VMD5	09vmd5 drosophila
143	5	45.5	323	2	045621	045621 bacillus sp	216	5	45.5	480	10	004535	004535 arbidopsis
144	5	45.5	326	3	09P957	09p957 tricholoma	217	5	45.5	485	2	09ZNM1	09znm1 pseudomonas
145	5	45.5	326	3	09P957	09p957 tricholoma	218	5	45.5	489	10	065518	065518 arbidopsis
146	5	45.5	327	2	09Z908	09z908 bacillus ha	219	5	45.5	489	11	09W0H5	09wh05 mus musculi
147	5	45.5	330	5	018118	018118 caenorhabdi	220	5	45.5	500	5	P90972	P90972 caenorhabdi
148	5	45.5	330	14	09YTN3	09ytn3 ateline her	221	5	45.5	500	5	093289	093289 caenorhabdi
149	5	45.5	338	2	09HVA2	09hva2 pseudomonas	222	5	45.5	501	11	070399	070399 cavia porce
150	5	45.5	340	2	09PHN5	09phn5 campylobact	223	5	45.5	502	5	09VBR3	09vbr3 drosophila
151	5	45.5	345	4	09NRD1	09nrd1 homo sapien	224	5	45.5	503	5	09VLA8	09vla8 drosophila
152	5	45.5	347	2	005160	005160 synechococc	225	5	45.5	506	4	09NMW9	09nmw9 homo sapien
153	5	45.5	347	13	09DFG2	09dfg2 xenopus lae	226	5	45.5	509	5	09GUK1	09guk1 leishmania
154	5	45.5	349	4	015413	015413 homo sapien	227	5	45.5	510	5	015767	015767 babesia big
155	5	45.5	350	5	015760	015760 babesia big	228	5	45.5	511	5	09VVS5	09vvs5 drosophila
156	5	45.5	352	5	015761	015761 babesia big	229	5	45.5	511	10	09MB73	09mb73 citrus unsh
157	5	45.5	352	2	09XA14	09xa14 streptomyce	230	5	45.5	513	2	054044	054044 pseudomonas
158	5	45.5	354	5	026635	026635 sarcophaga	231	5	45.5	513	10	09FVB8	09fvb8 brassica na
159	5	45.5	357	2	053459	053459 mycobacteri	232	5	45.5	515	5	09TX44	09tx44 drosophila
160	5	45.5	364	5	002429	002429 dysderia cro	233	5	45.5	520	4	09H239	09h239 homo sapien
161	5	45.5	369	2	09RPE4	09rpe4 mycoplasma	234	5	45.5	520	10	09FVCO	09fvc0 brassica na
162	5	45.5	371	5	046169	046169 tribolium c	235	5	45.5	520	10	09FVB9	09fvb9 brassica na
163	5	45.5	371	5	046052	046052 drosophila	236	5	45.5	524	5	09VFE9	09vfe9 drosophila
164	5	45.5	372	5	09VZY1	09vzy1 drosophila	237	5	45.5	527	5	09VAK7	09vak7 drosophila
165	5	45.5	373	2	09PB07	09pb07 xylella fas	238	5	45.5	527	10	041479	041479 solanum tub

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: August 15, 2001, 12:42:32 ; Search time 58.01 Seconds
(without alignments)
25.088 Million cell updates/sec

Title: US-09-372-036-29
Perfect score: 11
Sequence: 1 OQQTAPKAPTE 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_16:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-unclassified:*
- 13: sp-vertebrate:*
- 14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	478	2	Q03493 listeria mo
2	10	90.9	76	2	Q48784 listeria mo
3	10	90.9	84	2	Q57205 listeria mo
4	10	90.9	86	2	Q48775 listeria mo
5	10	90.9	86	2	Q48782 listeria mo
6	10	90.9	88	2	Q48781 listeria mo
7	10	90.9	117	2	Q48774 listeria mo
8	10	90.9	236	5	Q9NAN3
9	6	54.5	288	5	Q9EMH8
10	6	54.5	329	2	Q9RGS0
11	6	54.5	343	5	Q19781
12	6	54.5	348	10	Q9FPA4
13	6	54.5	371	5	Q20966
14	6	54.5	388	5	Q9VMV9
15	6	54.5	606	2	Q86584
16	6	54.5	612	2	Q92614
17	6	54.5	663	2	Q9P196
18	6	54.5	672	5	Q25586
19	6	54.5	689	2	Q9RKV7

20	6	54.5	855	5	Q9NEW7	Q9new7 caenorhabdi
21	6	54.5	861	2	Q9HUA6	Q9hua6 pseudomonas
22	6	54.5	925	5	Q9YEW6	Q9yew6 drosophila
23	6	54.5	995	5	P90897	P90897 caenorhabdi
24	6	54.5	1052	11	Q88332	Q88332 mus musculu
25	6	54.5	1158	5	Q97169	Q97169 drosophila
26	6	54.5	1199	5	Q9V5G1	Q9v5g1 drosophila
27	6	54.5	1241	3	Q13617	Q13617 schizosacch
28	6	54.5	1257	5	Q9NMF04	Q9nfm04 caenorhabdi
29	6	54.5	2121	5	Q9NH54	Q9nh54 drosophila
30	6	54.5	2129	5	Q9VL23	Q9vl23 drosophila
31	6	54.5	2478	5	Q9VXZ5	Q9vxz5 drosophila
32	6	54.5	5233	5	Q9NB71	Q9nb71 drosophila
33	6	45.5	22	2	P81150	P81150 desulfovibr
34	5	45.5	23	2	P81149	P81149 desulfovibr
35	5	45.5	61	2	Q56859	Q56859 yersinia en
36	5	45.5	64	2	Q9S1E1	Q9s1e1 yersinia pe
37	5	45.5	82	10	Q9M4C9	Q9m4c9 hordeum vul
38	5	45.5	88	13	Q9YCP4	Q9ycp4 gallus gall
39	5	45.5	95	10	Q38792	Q38792 antirrhinum
40	5	45.5	103	2	Q91063	Q91063 streptomyce
41	5	45.5	110	5	Q9N3V6	Q9n3v6 caenorhabdi
42	5	45.5	111	11	Q9ESA8	Q9esa8 ratius norv
43	5	45.5	114	4	Q95014	Q95014 homo sapien
44	5	45.5	114	5	Q9YBH2	Q9ybh2 drosophila
45	5	45.5	114	5	Q9ULN7	Q9uln7 leishmania
46	5	45.5	117	5	Q9RTX9	Q9rtx9 deinococcus
47	5	45.5	118	2	Q9RTX9	Q9rtx9 pneumocysti
48	5	45.5	120	3	Q9PBW7	Q9pbw7 campylobact
49	5	45.5	121	2	Q9PP33	Q9pp33 campylobact
50	5	45.5	124	13	Q9PS90	Q9ps90 gallus gall
51	5	45.5	127	1	Q9Y8T9	Q9y8t9 aeropyrum p
52	5	45.5	133	14	Q9JSE3	Q9jse3 fowlpox vir
53	5	45.5	136	2	Q9K1X8	Q9k1x8 vibrio chol
54	5	45.5	136	11	Q9ESA7	Q9esa7 ratius norv
55	5	45.5	137	5	Q03997	Q03997 plasmodium
56	5	45.5	137	10	Q40043	Q40043 hordeum vul
57	5	45.5	139	9	P93179	P93179 hordeum vul
58	5	45.5	144	2	Q9KZN1	Q9kzn1 streptomyce
59	5	45.5	144	2	Q9TPP4	Q9tpf4 neisseria m
60	5	45.5	146	3	Q9HG53	Q9hg53 pneumocysti
61	5	45.5	146	3	Q9HG52	Q9hg52 pneumocysti
62	5	45.5	146	3	Q9HG51	Q9hg51 pneumocysti
63	5	45.5	148	2	Q9K173	Q9k173 neisseria m
64	5	45.5	156	10	Q64940	Q64940 lophopyrum
65	5	45.5	157	5	Q9YNB9	Q9ynb9 drosophila
66	5	45.5	158	10	Q41600	Q41600 triticum tu
67	5	45.5	159	2	Q9JTC9	Q9jtc9 neisseria m
68	5	45.5	159	4	Q9H8U1	Q9h8u1 homo sapien
69	5	45.5	166	2	Q44075	Q44075 aeromonas h
70	5	45.5	170	4	Q9H4W2	Q9h4w2 homo sapien
71	5	45.5	172	4	Q9P054	Q9p054 homo sapien
72	5	45.5	172	5	Q9N985	Q9n985 leishmania
73	5	45.5	174	1	Q59592	Q59592 pyrococcus
74	5	45.5	175	11	Q63571	Q63571 ratius norv
75	5	45.5	176	3	Q9P765	Q9p765 neurospora
76	5	45.5	176	10	Q9ST24	Q9st24 zea mays (m
77	5	45.5	177	10	Q9ZWL5	Q9zwl5 zea mays (m
78	5	45.5	181	2	Q05816	Q05816 mycobacteri
79	5	45.5	181	4	Q9Y6Z4	Q9y6z4 homo sapien
80	5	45.5	181	5	Q9YBZ0	Q9ybz0 drosophila
81	5	45.5	183	2	Q9RW99	Q9rw99 delinococcus
82	5	45.5	191	5	Q18649	Q18649 caenorhabdi
83	5	45.5	194	11	Q9JUK2	Q9juk2 mus musculu
84	5	45.5	197	2	Q9RC54	Q9rc54 bacillus ha
85	5	45.5	197	5	Q9YV38	Q9yv38 drosophila
86	5	45.5	200	2	Q9F459	Q9f459 anabaena sp
87	5	45.5	202	3	Q9HGF8	Q9hgf8 saccharomyc
88	5	45.5	205	2	Q9JYB8	Q9jyb8 neisseria m
89	5	45.5	207	2	Q9KAD3	Q9kad3 bacillus ha
90	5	45.5	207	10	Q9LY40	Q9ly40 arabidopsis
91	5	45.5	208	4	Q75852	Q75852 homo sapien
92	5	45.5	212	2	Q9RSN7	Q9rsn7 deinococcus

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RX MEDLINE-92347850; PubMed-1386335;
RA Inaba T., Matsushima H., Valentine M., Rousset M.F., Sherr C.J.,
RA Look A.T.;
RT "Genomic organization, chromosomal localization, and independent
RT expression of human cyclin D genes.";
RL Genomics 13:565-574(1992).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE Holoenzyme complex. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
CC -----
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DR EMBL: M90814; AAS1927.1; -
DR EMBL: M92287; AAS52337.1; -
DR EMBL: M88087; AAS1929.1; -
DR EMBL: M88084; AAS1929.1; JOINED.
DR EMBL: M88085; AAS1929.1; JOINED.
DR EMBL: M88086; AAS1929.1; JOINED.
DR PIR: BA2822; B42822.
DR PIR: A44022; A44022.
DR MIM: 123834; -
DR InterPro: IPR000553; -
DR Pfam: PF00134; CYCLIN: 1.
DR PROSITE: PS00292; CYCLINS: 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
FT CONFLICT 259 A -> S (IN REF. 2).
FT SEQUENCE 292 AA; 32503 MW; 16FE56FE2FEB0029 CRC64;
SQ
Query Match 45.5%; Score 5; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 AKAP 9
DB 266 AKAP 270

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CC ALTERNATIVE SPLICING. EXCEPT FOR SMDF THEY ARE IN ENTRY AC 002297.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS SYSTEM: SPINAL CORD MOTOR
CC NEURONS, DORSAL ROOT GANGLION NEURONS, AND BRAIN. PREDOMINANT
CC ISOFORM EXPRESSED IN SENSORY AND MOTOR NEURONS. NOT DETECTED IN
CC ADULT HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND
CC PANCREAS. NOT EXPRESSED IN FETAL LUNG, LIVER, AND KIDNEY.
CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN DEVELOPING SPINAL MOTOR
CC NEURONS AND IN DEVELOPING CRANIAL NERVE NUCLEI. EXPRESSION IS
CC MAINTAINED ONLY IN BOTH ADULT MOTOR NEURONS AND DORSAL ROOT
CC GANGLION NEURONS.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
CC -----
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CC -----
DR EMBL: I41827; AAC11764.1; -
DR MIM: 142445; -
DR InterPro: IPR000561; -
DR Pfam: PF00008; EGF_1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; FALSE-NEG.
KW Growth factor; EGF-like domain; Transmembrane; Multigene family;
KW Alternative splicing.
FT TRANSMEM 76 100
FT DOMAIN 58 91 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT DOMAIN 211 232 CYS-RICH.
FT DOMAIN 233 277 SER/THR-RICH.
FT DISULFID 237 251 EGF-LIKE.
FT DISULFID 245 265 BY SIMILARITY.
FT DISULFID 267 276 BY SIMILARITY.
FT SEQUENCE 296 AA; 31685 MW; 8DA1743217F7EB02 CRC64;
SQ
Query Match 45.5%; Score 5; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 OTAPK 7
DB 217 OTAPK 221

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Search completed: August 15, 2001, 12:43:01
Job time: 491 sec

-1- ALTERNATIVE PRODUCTS: AT LEAST 10 ISOFORMS OF NRG1 ARE PRODUCED BY

LBX1_HUMAN STANDARD; PRT; 280 AA.
 ID LBX1_HUMAN
 AC P52954;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE TRANSCRIPTION FACTOR LBX1.
 GN LBX1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=9627534; PubMed=8645601;
 RA Jagla K., Dolle P., Mattei M.-G., Jagla T., Schubaur B.,
 RT "Mouse Lbx1 and human LBX1 define a novel mammalian homeobox gene
 RL family related to the Drosophila lady bird genes."
 RL Mech. Dev. 53:345-356(1995).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -----
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 CC -----
 CC EMBL: X90828; CAA6342.1; -;
 DR HSSP: P22808; 1VND.
 DR InterPro: IPR001356; -;
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PR00024; HOMEBOX.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Transcription regulation; Nuclear protein.
 FT DNA_BIND 124 183 HOMEBOX.
 FT DOMAIN 219 225 POLY-GLY.
 FT DOMAIN 269 280 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT SEQUENCE 280 AA; 30307 MW; 8DDA14BDD7A40B97 CRC64;
 SQ
 Query Match 45.5%; Score 5; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 APKAP 9
 DB 240 APKAP 244
 RESULT 48
 LIPH_PSEAE STANDARD; PRT; 288 AA.
 ID LIPH_PSEAE
 AC Q01725;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LIPH PROTEIN.
 GN LIPH OR PA2863.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=92381478; PubMed=1512563;
 RA Wohlfarth S., Hoesche C., Strunk C., Winkler U.K.;
 RT "Molecular genetics of the extracellular lipase of Pseudomonas
 aeruginosa PA01.";

RL J. Gen. Microbiol. 138:1325-1335(1992).
 RN [2]
 RN REVISION TO 250-280.
 RA Wohlfarth S.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=2043737; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Ralzer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 CC -1- FUNCTION: HELPS TO PRODUCE AN EXTRACELLULARLY ACTIVE LIPASE.
 CC -----
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 CC -----
 CC EMBL: X63391; CAA4998.1; ALT_INIT.
 DR EMBL: AE004712; AAG06251.1; -;
 DR PIR: S25769; S25769.
 SQ SEQUENCE 288 AA; 32440 MW; 8BF64F42B79CF94 CRC64;
 OY 1 OQOYA 5
 DB 189 OQOYA 193
 RESULT 49
 CGD3_HUMAN STANDARD; PRT; 292 AA.
 ID CGD3_HUMAN
 AC P30281;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GI/S-SPECIFIC CYCLIN D3.
 GN CCND3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92347851; PubMed=1386336;
 RA Xiong Y., Meininger J., Beach D., Ward D.C.;
 RT "Molecular cloning and chromosomal mapping of CCND genes encoding
 RT human D-type cyclins.";
 RL Genomics 13:575-584(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93015922; PubMed=1383201;
 RA Motokura T., Keyomarsi K., Kronenberg H.M., Arnold A.;
 RT "Cloning and characterization of human cyclin D3, a cDNA closely
 RT related in sequence to the PRAD1/cyclin D1 proto-oncogene.";
 RL J. Biol. Chem. 267:20412-20415(1992).
 RN [3]
 RP SEQUENCE OF 52-237 FROM N.A.
 RC Tissue=Placenta;


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RL Nature 393:537-544(1998).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
CC -1- COFACTOR: BINDS A 2FE-2S CLUSTER (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 24 KDA SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL: Z83867; CAB06290.1; -.
CC Tubercolist: RV3149; -.
CC InterPro: IPR002023; -.
CC DR Pfam: PF01257; complex1_24kd.1.
CC DR PROSITE: PS01099; COMPLEX1_24K; FALSE_NEG.
CC KM Oxidoreductase; NAD; Ubiquinone; Iron-sulfur.
CC FT METAL 114 114 IRON-SULFUR (2FE-2S) (POTENTIAL).
CC FT METAL 119 119 IRON-SULFUR (2FE-2S) (POTENTIAL).
CC FT METAL 155 155 IRON-SULFUR (2FE-2S) (POTENTIAL).
CC FT METAL 159 159 IRON-SULFUR (2FE-2S) (POTENTIAL).
CC FT SEQUENCE 252 AA; 27197 MW; 07B62E1A282175A4 CRC64;
SQ
Query Match 45.5%; Score 5; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No.55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 PKAP 10
Db 192 PKAP 196
RESULT 44
HXC9_FUGRU STANDARD; PRT; 259 AA.
ID AC 042502;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HOMEOBOX PROTEIN HOX-C9 (HOXC-9).
GN HOXC9.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:97285126; PubMed:9140399;
RA Aparicio S., Hawker K., Cottage A., Mikawa Y., Zuo L., Venkatesh B.,
RA Chen E., Krumlauf R., Brenner S.;
RT "Organization of the Fugu rubripes Hox clusters: evidence for
RT continuing evolution of vertebrate Hox complexes.";
RL Nat. Genet. 16:79-83(1997).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
CC -----
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DR EMBL: U92572; AAB68680.1; -.
DR InterPro: IPR000047; -.
DR InterPro: IPR001356; -.
DR Pfam: PF000046; homeobox; 1.
DR PRINTS: PR00024; HOMEOBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DNA_BIND 191 250 HOMEOBOX.
FT SEQUENCE 259 AA; 29691 MW; 1BF5ACB7558F15D2 CRC64;
SQ
Query Match 45.5%; Score 5; DB 1; Length 259;
Best Local Similarity 100.0%; Pred. No.56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 APRAP 9
Db 57 APRAP 61
RESULT 45
H11_VOLCA STANDARD; PRT; 260 AA.
ID AC 008664;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HISTONE H1-I.
GN H1-I.
OS Volvox carteri.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Volvocaceae; Volvox.
OX NCBI_TaxID=3067;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=F. NAGARIENSIS / HK10;
RA MEDLINE:93328125; PubMed=8335260;
RA Lindauer A., Mueller K., Schmitt R.;
RT "Two histone H1-encoding genes of the green alga Volvox carteri with
RT features intermediate between plant and animal genes.";
RL Gene 129:59-68(1993).
CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS RESTRICTED TO EMBRYOGENESIS.
CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L07946; AAA74723.1; -.
CC PIR: JN0747; JN0747.
CC DR HSSP: P08287; IGHC.
CC DR InterPro: IPR001386; -.
CC DR Pfam: PF00538; linker_histone; 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
KW Repeat.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 55 132 GLOBULAR (BY SIMILARITY).
FT DNA_BIND 138 141 POTENTIAL.
FT DOMAIN 135 249 7 X 5 AA REPEATS OF K-K-[AS]-T-P.
FT REPEAT 135 139 1.
FT REPEAT 187 191 2.
FT REPEAT 198 202 3 (APPROXIMATE).
FT REPEAT 208 212 4.

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Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OTAPK 7
DB 29 OTAPK 33

RESULT 41

NOCM_AGRU ID NOCM_AGRU STANDARD: PRT: 241 AA.

AC P35113; 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DE 01-OCT-2000 (Rel. 40, Last annotation update)

NOPLINE TRANSPORT SYSTEM PERMEASE PROTEIN NOCM.

OS Agrobacterium tumefaciens.

OC Plasmid pRiC58.

CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OX NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

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CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

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CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

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CC NCBI_Taxid=362;

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CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

CC NCBI_Taxid=362;

DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HISTONE H1, ORPHON.
OS Chironomus thummi thummi (Midge).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OX NCBI_Taxid=7155;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94087747; PubMed=8263935;
RA Hankeln T., Schmidt E.R.;
RT "Divergent evolution of an 'orphan' histone gene cluster in
Chironomus";
RL J. Mol. Biol. 234:1301-1307(1993).
CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
CC -----
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CC -----
CC EMBL: X72803; CA51322.1; -.
DR HSSP: P08287; IGHC.
DR InterPro: IPR001386;
DR Pfam: PF00538; Linker histone: 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SQ SEQUENCE 244 AA; 25455 MW; 12A6D32C6690354 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ADKAP 9
DB 28 ADKAP 32

RESULT 43

NOOE_MYCTU ID NOOE_MYCTU STANDARD: PRT: 252 AA.

AC P95177; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 30-MAY-2000 (Rel. 39, Last annotation update)

NADH DEHYDROGENASE I CHAIN E (EC 1.6.5.3) (NADH-UBIQUINONE

OX NCBI_Taxid=1773;

CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

CC NCBI_Taxid=1773;

RX MEDLINE-92020152; PubMed-1923777;
 RA Yang P., Katsura M., Nakayama T., Mikami K., Iwabuchi M.;
 RT "Molecular cloning and nucleotide sequences of cDNAs for histone H1
 RT and H2B variants from wheat";
 CC Nucleic Acids Res. 19:5077-5077(1991).
 CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
 CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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 CC -----
 CC EMBL; X59872; CAA42529.1; -
 CC PIR; S22322; S22322.
 CC HSSP; P02259; 1HST.
 CC InterPro: IPR001386; -
 CC Pfam: PF00538; linker_histone; 1.
 CC Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
 CC SEQUENCE 236 AA; 24018 MW; 069105D1972C74BB CRC64;
 SQ

Query Match 45.5%; Score 5; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 APRAP 9
 Db 32 APRAP 36

RESULT 39
 H1E.CHITE STANDARD; PRT; 237 AA.
 AC P40278;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HISTONE H1E.
 OS Chironomus tentans (Midge).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.
 OC NCBI_TaxID=7153;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulze E., Winiowski J.R., Nagel S., Gavenis K., Grossbach U.;
 RL Submitted (AXX-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
 CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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 CC -----
 CC EMBL; L29105; AAB53945.1; -
 CC HSSP; P08287; IGHC.
 CC InterPro: IPR001386; -
 CC Pfam: PF00538; linker_histone; 1.
 CC Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
 CC SEQUENCE 237 AA; 24689 MW; D429364FFBCB1F3E CRC64;
 SQ

Query Match 45.5%; Score 5; DB 1; Length 237;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 APRAP 9
 Db 28 APRAP 32

RESULT 40
 OPAA.MEIGO STANDARD; PRT; 239 AA.
 ID OPAA.MEIGO
 AC 004876;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OPACITY PROTEIN OPA53 PRECURSOR (FRAGMENT).
 GN OPAA.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-MS11 / F3;
 RX MEDLINE-93178439; PubMed-8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells";
 RL EMBO J. 12:641-650(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-MS11 / V18;
 RX MEDLINE-92114767; PubMed-1815562;
 RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
 RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
 RT "The opacity proteins of Neisseria gonorrhoeae strain MS11 are
 RT encoded by a family of 11 complete genes";
 RL Mol. Microbiol. 5:1889-1901(1991).
 RN [3]
 RP ERRATUM.
 RA MEDLINE-92261323; PubMed-1584024;
 RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
 RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
 RL Mol. Microbiol. 6:1073-1076(1992).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
 CC -----
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 CC -----
 CC EMBL; Z18930; CAA79363.1; -
 CC EMBL; X60709; CAA43119.1; -
 CC PIR; S28630; S28630.
 CC PIR; S36331; S36331.
 CC Outer membrane; Multigene family; Signal.
 CC NON_TER 1
 FT SIGNS 1
 FT CHAIN 2
 FT VARIANT 92
 FT NON_TER 239
 FT SEQUENCE 239 AA; 26734 MW; 2F12E69DEB26CAA0 CRC64;
 SQ

Query Match 45.5%; Score 5; DB 1; Length 239;

Db 47 AKAP 51

RESULT 36

NAPG_ECOLI STANDARD: PRT: 231 AA.

AC P33936; P33935; (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE FERREDOXIN-TYPE PROTEIN NAPG.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RP SEQUENCE FROM N.A.

RC STRAIN-K12 / BHB2600;

RA Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K., Church G.M.;

RU Submitted (OCT-1993) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-K12 / MG1655;

RX MEDLINE=9742617; PubMed=9278503;

RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

RA "The complete genome sequence of Escherichia coli K-12."

RT Science 277:1453-1474(1997).

CC -1- FUNCTION: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF BACTERIAL-TYPE 4FE-4S FERREDOXINS.

CC -1- SIMILARITY: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 145.

CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 145.

CC -----

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CC -----

CC EMBL: U00008; AAA16398.1; ALT_FRAME.

DR EMBL: U00008; AAA16397.1; ALT_FRAME.

DR EMBL: AE000309; AAC75265.1; -.

DR HSSP: P00195; 1CLF.

DR EcGene: EGI2064; napg.

DR InterPro: IPR001450; -.

DR Pfam: PF00037; fer4_2.

DR PROSITE: PS00198; 4FE4S_FERREDOXIN; 1.

DR Electon transport; Iron-sulfur; 4Fe-4S.

FT METAL 61 61 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 64 64 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 67 67 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 71 71 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 99 99 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 102 102 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 107 107 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 111 111 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 139 139 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).

FT METAL 147 147 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).

FT METAL 150 150 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).

FT METAL 154 154 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).

FT METAL 186 186 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).

FT METAL 189 189 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).

FT METAL 192 192 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).

FT METAL 196 196 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).

SEQUENCE 231 AA; 24924 MW; 9DA55774D6A68AD5 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 231;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OQOTA 5

Db 35 OQOTA 39

RESULT 37

HIE_CHIPA STANDARD: PRT: 235 AA.

AC P40262;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HISTONE H1E.

OS Chironomus pallidivittatus (Midge).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;

OC Chironomidae; Chironomidae; Chironominae; Chironomus.

OX NCBI_TaxID=7151;

RN [1]

RP SEQUENCE FROM N.A.

RA Schulze E., Mislowski J.R., Nagel S., Gavenis K., Grossbach U.;

RU Submitted (XXX-1994) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.

CC -----

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CC -----

CC EMBL: L29106; AAA21714.1; -.

DR HSSP: P08287; 1GHC.

DR InterPro: IPR001386; -.

DR Pfam: PF00538; linker_histone; 1.

KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.

SEQUENCE 235 AA; 24446 MW; 340BC5B9A85002AC CRC64;

Query Match 45.5%; Score 5; DB 1; Length 235;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AKAP 9

Db 28 AKAP 32

RESULT 38

HI_WHEAT STANDARD: PRT: 236 AA.

AC P27806;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HISTONE H1.

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Poaceae; Poaceae;

OC Triticum.

OX NCBI_TaxID=4565;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-CV. HOROSHIRIKOMUGI; TISSUE=Seedling;

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CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
-----
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-----
CC EMBL: Z47767; CAAB7696.1; -.
CC HSSP: P05082; 2ECK.
CC InterPro: IPR000850; -.
CC Pfam: PF00406; adenylatekinase; 1.
CC PRINTS: PR00094; ADENYLTKINASE.
CC PROSITE: PS00113; ADENYLATE_KINASE; FALSE_NEG.
CC TRANSFERASE: Kinase; ATP-binding.
CC NE_BIND 7 15 ATP (BY SIMILARITY).
CC FT SEQUENCE 214 AA; 23755 MW; 55030EA82BDDAC7 CRC64;
-----
OY 2 QOTAP 6
DB 173 QOTAP 177

Query Match 45.5%; Score 5; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 34
KAD_YERPE STANDARD; PRT; 214 AA.
AC 069172;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).
GN AKK.
OS Versinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Versinia.
OC NCBI_TaxID=632;
RN 1]
RP SEQUENCE FROM N.A.
RA Munier-Lehmann H.;
RT "Adenylate kinase from Versinia pestis and Escherichia coli:
RT structural relatedness and differences linked to growth properties of
RT these two organisms.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS SMALL UNBIOGENOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
-----
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-----
CC EMBL: AF065382; AAC17436.1; -.
CC InterPro: IPR000850; -.
CC Pfam: PF00406; adenylatekinase; 1.
CC PRINTS: PR00094; ADENYLTKINASE.
CC PROSITE: PS00113; ADENYLATE_KINASE; 1.
CC TRANSFERASE: Kinase; ATP-binding.
CC NE_BIND 7 15 ATP (BY SIMILARITY).
CC FT SEQUENCE 214 AA; 23755 MW; 55030EA82BDDAC7 CRC64;

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SQ SEQUENCE 214 AA; 23672 MW; 36D9FD13558E86CA CRC64;
-----
OY 2 QOTAP 6
DB 173 QOTAP 177

Query Match 45.5%; Score 5; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 35
TONB_XANCP STANDARD; PRT; 223 AA.
AC 034261;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TONB PROTEIN.
GN TONB.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OC NCBI_TaxID=340;
RN 1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98037510; PubMed=9371459;
RA Wiggerich H.G., Klaue B., Koepflin R., Pfeifer U.B., Pehler A.;
RT "Unusual structure of the tonB-exb DNA region of Xanthomonas
RT campestris pv. campestris: tonB, exbB, and exbD1 are essential for
RT ferric iron uptake, but exbD2 is not.";
RL J. Bacteriol. 179:7103-7110(1997).
CC -1- FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT
CC CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO
CC THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO
CC TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-
CC REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE
CC RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER
CC MEMBRANE PROTEINS (BY SIMILARITY).
CC -1- SUBUNIT: THE ACCESSORY PROTEINS EXB AND EXB2 SEEM TO FORM A
CC COMPLEX WITH TONB (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC. ANCHORED TO THE CYTOPLASMIC
CC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE
CC PERIPLASM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TONB FAMILY.
-----
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-----
CC EMBL: Z95386; CAB08610.1; -.
CC Transport: Protein transport; Inner membrane; Periplasmic;
CC Transmembrane; Signal-anchor; Repeat.
CC FT DOMAIN 1 23 CYTOPLASMIC (POTENTIAL).
CC TRANSLEM 24 44 SIGNAL-ANCHOR (POTENTIAL).
CC FT DOMAIN 45 223 PERIPLASMIC (POTENTIAL).
CC FT DOMAIN 66 78 POLY-PRO.
CC FT DOMAIN 82 85 POLY-PRO.
CC FT DOMAIN 94 101 POLY-PRO.
CC FT DOMAIN 94 101 POLY-PRO.
CC FT SEQUENCE 223 AA; 23598 MW; D7C6886DF06FDA9 CRC64;
-----
OY 5 APKAP 9
DB 173 QOTAP 177

Query Match 45.5%; Score 5; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 31
Y319_MYCPN STANDARD: PRT: 193 AA.
ID Y319_MYCPN
AC P75329;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHEICAL PROTEIN MG319 HOMOLOG (H08_ORF193).
GN MP454 OR MP387.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
CX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfreid R., Hilbert H., Piagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC -----
DR EMBL: AE000037; AAB96035.1; -
KM Hypothetical protein; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 136 156
SQ SEQUENCE 193 AA; 21443 MW; BAE6806C6D80C1D CRC64;

Query Match 45.5%; Score 5; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
DB 68 TAPKA 72

RESULT 32
KAPS_YEAST STANDARD: PRT: 202 AA.
ID KAPS_YEAST
AC Q02196;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ADENYLYLSULFATE KINASE (EC 2.7.1.25) (APS KINASE) (ADENOSINE-
DE 5'-PHOSPHOSULFATE KINASE) (ATP ADENOSINE-5'-PHOSPHOSULFATE 3'-
DE PHOSPHOTRANSFERASE).
GN MET14 OR YKL001C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB320;
RX MEDLINE=91375456; PubMed=1654509;
RA Koroch C., Mountain H.A., Bystrom A.S.;
RT "Cloning, nucleotide sequence, and regulation of MET14, the gene
RT encoding the APS kinase of Saccharomyces cerevisiae.";
RL Mol. Gen. Genet. 229:96-108(1991).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93070612; PubMed=1441752;
RA Dusterhoeft A., Philippsen P.;
RT "DNA sequencing and analysis of a 24.7 kb segment encompassing
RT centromere CEN1 of Saccharomyces cerevisiae reveals nine previously
RT unknown open reading frames.";
RL Yeast 8:749-759(1992).
CC CC
CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
CC -1- CATALYTIC ACTIVITY: ATP + ADENYLYLSULFATE -> ADP +
CC 3'-PHOSPHOADENYLYLSULFATE.
CC -1- PATHWAY: SECOND STEP IN THE SULFATE ASSIMILATION PATHWAY THAT
CC LEADS TO THE BIOSYNTHESIS OF METHIONINE AND CYSTEINE.
CC -1- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
CC -----
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CC -----
DR EMBL: X57990; CAA41055.1; -
DR EMBL: S55315; AAB19854.1; -
DR EMBL: X65124; CAA46252.1; -
DR EMBL: 228001; CAA81833.1; -
DR PIR: S17244; S17244.
DR SGD: S0001484; MET14.
DR InterPro: IPR002891; -
DR Pfam: PF01583; APS_kinase; 1.
KW Methionine biosynthesis; Cysteine biosynthesis; Transferase;
KW Kinase; ATP-binding; Phosphorylation.
FT NP_BIND 31 38 ATP (BY SIMILARITY).
FT ACT_SITE 105 105 FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
FT SIMILARITY).
SQ SEQUENCE 202 AA; 23060 MW; 32F301FB6B2F41D3 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
DB 166 APKAP 170

RESULT 33
KAD_YEREN STANDARD: PRT: 214 AA.
ID KAD_YEREN
AC P43412;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ADENYLYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).
GN ADR.
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
CX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6471/76 / SEROTYPE O:3;
RX MEDLINE=96100456; PubMed=8559076;
RX Skurnik M., Venho R., Toivanen P., Al-Hendy A.;
RT "A novel locus of Yersinia enterocolitica serotype O:3 involved in
RT lipopolysaccharide outer core biosynthesis.";
RL Mol. Microbiol. 17:575-594(1995).
CC CC
CC -1- FUNCTION: THIS SMALL OBLIGATORY ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

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DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRANSLATION INITIATION FACTOR IF-3.
 GN INFC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=294;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0.
 RA Blumer C., Heeb S., Pessl G., Haas D.;
 RT "Global Gaca-steered control of secondary metabolism in Pseudomonas
 RT fluorescens acts on specific ribosome binding sites."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE
 CC EQUILIBRIUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN
 CC FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
 CC SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE IF-3 FAMILY.

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 CC EMBL; AF136400; AAD34787.1; -
 DR InterPro: IPR001288; -
 DR Pfam: PF00707; IF3; 1.
 DR PROSITE: PS00938; IF3; 1.
 KM Initiation factor; Protein biosynthesis.
 SQ SEQUENCE 183 AA; 20835 MW; 003E1B9155C066A CRC64;

Query Match 45.5%; Score 5; DB 1; Length 183;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APRAP 9
 [1111]
 Db 14 APRAP 18

RESULT 29
 IF3_PSESY STANDARD; PRT; 183 AA.
 AC P52834;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TRANSLATION INITIATION FACTOR IF-3.
 GN INFC.
 OS Pseudomonas syringae (pv. syringae).
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=321;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUP27;
 RX MEDLINE=96198155; Pubmed=8626280;
 RA Kitten T., Willis D.K.;
 RT "Suppression of a sensor kinase-dependent phenotype in Pseudomonas
 RT syringae by ribosomal proteins L35 and L20."
 RL J. Bacteriol. 178:1548-1555(1996).
 CC -1- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE
 CC EQUILIBRIUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN
 CC FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
 CC SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE IF-3 FAMILY.

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 CC EMBL; U44118; AAB05014.1; -
 DR HSSP: P02999; 2IFE.
 DR InterPro: IPR001288; -
 DR Pfam: PF00707; IF3; 1.
 DR PROSITE: PS00938; IF3; 1.
 KM Initiation factor; Protein biosynthesis.
 SQ SEQUENCE 183 AA; 20806 MW; 50ADD828F04831FE CRC64;

Query Match 45.5%; Score 5; DB 1; Length 183;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APRAP 9
 [1111]
 Db 14 APRAP 18

RESULT 30
 H12_CAEEL STANDARD; PRT; 190 AA.
 AC P15796;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HISTONE H1.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 [1]
 RN SEQUENCE.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=90165873; Pubmed=2407235;
 RA vanfleteren J.R., van Bun S.M., de Baere I., van Beeumen J.J.;
 RT "The primary structure of a minor isoform (H1.2) of histone H1 from
 RT the nematode Caenorhabditis elegans."
 RL Biochem. J. 265:739-746(1990).
 CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
 CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- MISCELLANEOUS: THERE ARE 2 FORMS OF H1 IN THIS NEMATODE: H1.2 IS
 CC THE MINOR FORM.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
 CC PIR: S08195; S08195.
 DR HSSP: P08287; 1GHC.
 DR InterPro: IPR001386; -
 DR Pfam: PF00358; linker_histone; 1.
 KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
 KW Acetylation.
 FT MOD_RES 1 1 ACETYLATION (PROBABLE).
 FT DOMAIN 36 112 GLOBULAR.
 SQ SEQUENCE 190 AA; 19830 MW; FCOA04429B14C7DD CRC64;

Query Match 45.5%; Score 5; DB 1; Length 190;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APRAP 9
 [1111]
 Db 17 APRAP 21

```
CC -----
DR EMBL: L33457; AAA67370.1; -.
DR EMBL: U50904; AAA93483.1; -.
DR HSSP: P02259; 1HST.
DR DICTYDB: DD01080; hsta.
DR InterPro: IPR001386; -.
DR Pfam: PF00538; linker_histone.1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Phosphorylation.
FT INIT_MET 0
FT CONFLICT 140 179
FT SEQUENCE 179 AA: 18729 MW; ESC4528BAE30CCFC CRC64;
SQ
Query Match
Best Local Similarity 45.5%; Score 5; DB 1; Length 179;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 PKAPT 10
DB 2 PKAPT 6
RESULT 26
YPOL_THEFL STANDARD: PRT; 179 AA.
ID YPOL_THEFL
AC P32438;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHELICAL PROTEIN IN POL 5' REGION (FRAGMENT).
OS Thermus aquaticus (subsp. flavus).
CC Bacteria; Thermus/Delnococcus group; Thermus group; Thermus.
OC NCBI_TaxId=273;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ACM B-1257;
RX MEDLINE=93087201; Pubmed=1454544;
RA Akhmetzhanov A.A., Vakhitov V.A.;
RT "Molecular cloning and nucleotide sequence of the DNA polymerase gene
from Thermus flavus."
RL Nucleic Acids Res. 20:5839-5839(1992).
RN [2]
RP IDENTIFICATION, AND SIMILARITY.
RX MEDLINE=94147966; Pubmed=8313894;
RA Koonin E.V., Bork P., Sander C.;
RT "Yeast chromosome III: new gene functions."
RL EMO J. 13:493-503(1994).
CC -1 SIMILARITY: BELONGS TO THE UPF0029 FAMILY.
CC -----
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CC -----
DR EMBL: X66105; -, NOT_ANNOTATED_CDS.
DR InterPro: IPR001498; -.
DR PROSITE: PS00910; UPF0029; 1.
KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 179 AA: 19362 MW; 1B02ED2403D39786 CRC64;
SQ
Query Match
Best Local Similarity 45.5%; Score 5; DB 1; Length 179;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 APKAP 9
DB 105 APKAP 109
```

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RESULT 27
NOO9_THETH STANDARD: PRT; 182 AA.
ID NOO9_THETH
AC Q56224;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 9 (EC 1.6.5.3) (NADH
DE DEHYDROGENASE 1, CHAIN 9) (NDH-1, CHAIN 9).
GN NOO9.
OS Thermus aquaticus (subsp. thermophilus).
OC Bacteria; Thermus/Delnococcus group; Thermus group; Thermus.
OC NCBI_TaxId=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HB8 / ATCC 27634;
RX MEDLINE=97172490; Pubmed=9020134;
RA Yano T., Chu S.S., Sled V.D., Ohnishi T., Yagi T.;
RT "The proton-translocating NADH-quinone oxidoreductase (NDH-1) of
the thermophilic bacterium Thermus thermophilus HB-8. Complete DNA
sequence of the gene cluster and thermostable properties of the
expressed NOO2 subunit."
RL J. Biol. Chem. 272:4201-4211(1997).
CC -1 CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1 COPFACTOR: MAY BIND TWO 4FE-4S CLUSTERS.
CC -1 SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS.
CC -1 SIMILARITY: BELONGS TO THE COMPLEX I 23 KDA SUBUNIT FAMILY.
CC -1 SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
CC -----
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CC -----
DR EMBL: U52917; AAA97946.1; -.
DR HSSP: P00198; 1FBN.
DR InterPro: IPR001450; -.
DR Pfam: PF00037; fer4; 1.
DR PRINTS: PR00353; 4FE4SFERDOXIN.
DR PROSITE: PS00198; 4FE4S-FERREDOXIN; 2.
KW Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S.
FT METAL 53
FT METAL 53
FT METAL 56
FT METAL 59
FT METAL 59
FT METAL 63
FT METAL 63
FT METAL 98
FT METAL 98
FT METAL 101
FT METAL 101
FT METAL 104
FT METAL 104
FT METAL 108
FT METAL 108
FT SEQUENCE 182 AA: 20080 MW; 054A9E7942C64C66 CRC64;
SQ
Query Match
Best Local Similarity 45.5%; Score 5; DB 1; Length 182;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 7 KAPTE 11
DB 174 KAPTE 178
RESULT 28
IF3_PSEFL STANDARD: PRT; 183 AA.
ID IF3_PSEFL
AC Q9X6E7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
```

RP SEQUENCE FROM N.A.
 RA MEDLINE=84011052; Pubmed=6413701;
 RA Costanzo M., Hannett N., Brzustowicz L., Pero J.;
 RT "Bacteriophage SPO1 gene 27: location and nucleotide sequence.";
 RL J. Virol. 48:555-560(1983).
 RN [2]
 RP SEQUENCE OF 1-11 FROM N.A.
 RX MEDLINE=83144054; Pubmed=6402778;
 RA Costanzo M., Pero J.;
 RT "Structure of a Bacillus subtilis bacteriophage SPO1 gene encoding
 RT RNA polymerase sigma factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1236-1240(1983).
 CC -1- FUNCTION: REQUIRED FOR LATE GENE TRANSCRIPTION AND DNA
 CC REPLICATION.
 CC -1- SIMILARITY: TO PHAGE SPO1 GENES 44 AND 51 PROTEINS.
 CC -----
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 CC -----
 CC EMBL; K01137; AAA32598.1; -;
 DR EMBL; V01375; CAA24663.1; -;
 KM Transcription regulation; DNA replication.
 SQ SEQUENCE 155 AA; 17538 MW; 67B008ACB48C3A3 CRC64;
 SO
 Query Match 45.5%; Score 5; DB 1; Length 155;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TAPKA 8
 11111
 DB 86 TAPKA 90
 RESULT 24
 FLIN_PSEAE STANDARD; PRT; 157 AA.
 AC Q51466;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FLAGELLAR MOTOR SWITCH PROTEIN FLIN.
 GN FLIN OR PA1444.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_Taxid=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PAK;
 RX MEDLINE=95347807; Pubmed=7622217;
 RA Simpson D.A., Ramphal R., Lory S.;
 RT "Characterization of Pseudomonas aeruginosa fllo, a gene involved in
 RT flagellar biosynthesis and adherence.";
 RL Infect. Immun. 63:2950-2957(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PAO1;
 RX MEDLINE=20437337; Pubmed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).

CC -1- FUNCTION: FLIN IS ONE OF THREE PROTEINS (FLIC, FLIN, FLIM) THAT
 CC FORM A SWITCH COMPLEX THAT IS PROPOSED TO BE LOCATED AT THE BASE
 CC OF THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEY AND CHEZ
 CC CHEMOTAXIS PROTEINS, IN ADDITION TO CONTACTING COMPONENTS OF THE
 CC MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE FLIN/MOPA/SPA0 FAMILY.
 CC -----
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 CC -----
 CC EMBL; L39832; AAA79754.1; -;
 DR EMBL; AE004574; AAG04833.1; -;
 DR InterPro; IPR001172; -;
 DR Pfam; PF01052; SpoA; 1.
 DR PRINTS; PR00956; FLGMOTORFLIN.
 KM Chemotaxis; Flagella; Flagellar rotation; Inner membrane.
 FT CONFLICT 48 48 P -> S (IN REF. 1).
 SQ SEQUENCE 157 AA; 16620 MW; B3D91C0182ACB775 CRC64;
 SO
 Query Match 45.5%; Score 5; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PKAPT 10
 11111
 DB 62 PKAPT 66
 RESULT 25
 H1_DICDI STANDARD; PRT; 179 AA.
 ID H1_DICDI
 AC P54671;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HISTONE H1.
 GN H5TA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 OX NCBI_Taxid=44689;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-16.
 RX MEDLINE=95172391; Pubmed=7867938;
 RA Hauser L.J., Pham M.S., Oline D.E.;
 RT "Dictyostelium discoideum contains a single-copy gene encoding a
 RT unique subtype of histone H1.";
 RL Gene 154:119-122(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JH10;
 RA O'Day D.H., Mackay L., Lydan M.A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
 CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: PHOSPHORYLATED BY H1 HISTONE KINASE (HKG).
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
 CC -----
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RN [1]
RP SEQUENCE FROM N.A.
RA Cavan J.F., Darlows V.A., Davies C.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE UPF0076 (UK114) FAMILY.
CC -----
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CC -----
DR EMBL: U50749; AAB48552.1; -
DR InterPro: IPR000543; -
DR Pfam: PF01042; UPF0076; 1.
DR PROSITE: PS01094; UPF0076; 1.
KW Hypothetical protein.
SQ SEQUENCE 130 AA; 14232 MW; 74531BAD1F2CA525 CRC64;

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Query Match 45.5%; Score 5; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4 TAPKA 8
    11111
DB 10 TAPKA 14

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RESULT 21
ID YT47_CABEL STANDARD; PRT; 132 AA.
AC Q11074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHEICAL 14.8 KDA PROTEIN B0416.7 IN CHROMOSOME X.
GN B0416.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RL Favallo T.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: SOME, TO C.ELEGANS F36A4.2 AND F36A4.4.
CC -----
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CC -----
DR EMBL: U23516; AAG38883.1; -
DR WormPep; B0416.7; CE02437.
KW Hypothetical protein.
SQ SEQUENCE 132 AA; 14811 MW; 16C3FC7580732E40 CRC64;

```

```

Query Match 45.5%; Score 5; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 6 PRAPT 10
    11111
DB 111 PRAPT 115

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RESULT 22
ID DH1_HORVU STANDARD; PRT; 139 AA.
AC P12951;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE DEHYDRIN DHN1 (B8).
GN DHN1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae;
OC Hordeum.
OX NCBI_Taxid=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV, HIMALAYA; TISSUE=Seedling;
RX MEDLINE-93357436; PubMed-2562763;
RA Close T.J., Kortt A.A., Chandler P.M.;
RT "A CDNA-based comparison of dehydration-induced proteins (dehydrins)
RT in barley and corn".
RL Plant Mol. Biol. 13:95-108(1989).
CC -1- INDUCTION: BY ABSCISIC ACID AND WATER-STRESS.
CC -1- SIMILARITY: VERY SIMILAR TO DHN3 AND DHN4, MAIZE DHN1, AND
CC ESPECIALLY TO BARLEY DHN2. TWO EXTREMELY CONSERVED BLOCKS WERE
CC IDENTIFIED, WITH A LESS CONSERVED REPEATING UNIT POSITIONED
CC BETWEEN THEM. DEHYDRIN DHN1 HAS ONLY ONE SUCH SEMI-CONSERVED
CC TANDEM REPEATING UNITS.
CC -----
CC -1- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
CC -----
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CC -----
DR EMBL: X15288; CAA3362.1; -
DR PIR: S05544; S05544.
DR InterPro: IPR000167; -
DR Pfam: PF00257; dehydrin.1.
DR PROSITE: PS00315; DEHYDRIN.1; 1.
DR PROSITE: PS00823; DEHYDRIN.2; 2.
KW dehydrin.
FT DOMAIN 61 69 POLY-SER.
FT SEQUENCE 139 AA; 14236 MW; BCE6A93923BFCB CRC64;
SQ SEQUENCE 132 AA; 14811 MW; 16C3FC7580732E40 CRC64;

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Query Match 45.5%; Score 5; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 QOOTA 5
    11111
DB 102 QOOTA 106

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RESULT 23
ID GP27_BPSP1 STANDARD; PRT; 155 AA.
AC P06228; Q38590;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENE 27 PROTEIN.
GN 27.
OS Bacteriophage SP01.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
OC SP01-like viruses.
OX NCBI_Taxid=10685;
RN [1]

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FT TURN 79 80
 FT TURN 84 85
 FT STRAND 86 86
 FT HELIX 87 92
 FT HELIX 101 109
 FT TURN 110 111
 FT HELIX 113 120
 SO SEQUENCE 129 AA; 13976 MW; 78C2A85F3B18441 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
 |||||
 Db 23 APRAP 27

RESULT 19
 CYC3_DESVM STANDARD; PRT; 130 AA.
 ID CYC3_DESVM STANDARD; PRT; 130 AA.
 AC P00132; 046607; 01, Created)
 DT 21-JUL-1986 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME C3 PRECURSOR.
 OS Desulfovibrio vulgaris (strain Miyazaki).
 OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
 OX NCBI_TaxID=883;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kitanuma M., Ozawa K., Kojima S., Kumagai I., Akutsu H., Miura K.I.;
 RT "The primary structure of pre-cytochrome c(3) from Desulfovibrio
 RT vulgaris (Miyazaki F) as determined by nucleotide sequencing."
 RT gene and partial amino acid sequencing."
 RL Protein Seq. Data Anal. 5:193-196(1993).
 [2]
 RP SEQUENCE OF 24-130.
 RX MEDLINE=80249474; PubMed=6249799;
 RA Shinkai W., Hase T., Yagi T., Matsubara H.;
 RT "Amino acid sequence of cytochrome c3 from Desulfovibrio vulgaris,
 RT Miyazaki.";
 RL J. Biochem. 87:1747-1756(1980).
 [3]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=82007753; PubMed=6268619;
 RA Higuchi Y., Bando S., Kusunoki M., Matsuura Y., Yasuoka N., Kakudo M.,
 RA Yamanaka T., Yagi T., Inokuchi H.;
 RT "The structure of cytochrome c3 from Desulfovibrio vulgaris Miyazaki
 RT at 2.5-A resolution."
 RL J. Biochem. 89:1659-1662(1991).
 [4]
 RN STRUCTURE BY NMR.
 RX MEDLINE=93044358; PubMed=1668723;
 RA Park J.-S., Kano K., Morimoto Y., Higuchi Y., Yasuoka N., Ogata M.,
 RA Niki K., Akutsu H.;
 RT "1H NMR studies on ferricytochrome c3 from Desulfovibrio vulgaris
 RT Miyazaki F and its interaction with ferredoxin I.";
 RL J. Biomol. NMR 1:271-282(1991).
 CC -1- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
 CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
 CC DEHYDROGENASE TO FERREDOXIN.
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC -1- PPM: BINDS 4 HEMES.
 CC -1- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
 CC -----
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 CC -----
 CC EMBL: D31702; BAA06511.1; -.
 DR PIR; A00125; CCDV3M.
 DR PDB; 2CDV; 21-FEB-84.
 DR InterPro; IPR000345; -.
 DR InterPro; IPR002322; -.
 DR Pfam; PF02085; Cytochrome CIII; 1.
 DR PRINTS; PR00609; CYTOCHROME C3.
 DR PROSITE; PS00190; CYTOCHROME C; 2.
 DR Electron transport; Sulfate respiration; Heme; Periplasmic; Signal;
 KW 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 130
 FT METAL 45 45
 FT METAL 48 48
 FT METAL 53 53
 FT BINDING 56 56
 FT METAL 57 57
 FT METAL 58 58
 FT BINDING 69 69
 FT BINDING 74 74
 FT METAL 75 75
 FT METAL 93 93
 FT BINDING 102 102
 FT BINDING 105 105
 FT METAL 106 106
 FT BINDING 123 123
 FT BINDING 128 128
 FT METAL 129 129
 FT METAL 65 65
 FT CONFLICT 32 34
 FT STRAND 41 43
 FT HELIX 46 48
 FT TURN 49 50
 FT HELIX 53 56
 FT STRAND 59 60
 FT TURN 61 62
 FT STRAND 63 64
 FT TURN 69 70
 FT TURN 72 73
 FT STRAND 77 77
 FT TURN 80 81
 FT TURN 85 86
 FT STRAND 87 87
 FT STRAND 88 93
 FT HELIX 102 110
 FT HELIX 111 112
 FT TURN 114 121
 SO SEQUENCE 130 AA; 13843 MW; CCBBA60351B9EF8E CRC64;

Query Match 45.5%; Score 5; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
 |||||
 Db 24 APRAP 28

RESULT 20
 Y142_LEUWC STANDARD; PRT; 130 AA.
 ID Y142_LEUWC STANDARD; PRT; 130 AA.
 AC P97117;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HYPOTHETICAL 14.2 KDA PROTEIN.
 OS Leuconostoc mesenteroides (subsp. cremoris).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 CC Leuconostoc.
 OX NCBI_TaxID=33965;

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 DR EMBL: U37245; AAC22286.1; -
 DR TIGR: H10626; -
 DR InterPro: IPR001185; -
 DR Pfam: PF01741; MSCL: 1.
 DR PRINTS: PS01264; MECHANNEL.
 DR PROSITE: PS01327; MSCL: 1.
 KW Transmembrane; Inner membrane; Ionic channel.
 FT DOMAIN 1 15 CYTOPLASMIC (BY SIMILARITY).
 FT TRANSMEM 16 42 BY SIMILARITY.
 FT DOMAIN 43 74 PERIPLASMIC (BY SIMILARITY).
 FT TRANSMEM 75 96 BY SIMILARITY.
 FT DOMAIN 97 128 CYTOPLASMIC (BY SIMILARITY).
 FT SEQUENCE 128 AA: 14198 MW: 803A68D2720DE51A CRC64;
 SO
 Query Match 45.5%; Score 5; DB 1; Length 128;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 TAPKA 8
 Db 110 TAPKA 114
 RESULT 18
 CYC3_DESVH STANDARD: PRT: 129 AA.
 ID CYC3_DESVH STANDARD: PRT: 129 AA.
 AC P00131;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME C3 PRECURSOR.
 OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87004646; PubMed=3019687;
 RA Voordouw G., Brenner S.;
 RT "Cloning and sequencing of the gene encoding cytochrome c3 from
 RT Desulfovibrio vulgaris (Hildenborough).";
 RL Eur. J. Biochem. 159:347-351(1986).
 RN [2]
 RP SEQUENCE OF 23-129.
 RC STRAIN=NCIB 8303;
 RA MEDLINE=74070664; PubMed=4358550;
 RA Trousel E.B., Campbell L.L.;
 RT "Amino acid sequence of cytochrome c3 from Desulfovibrio vulgaris,";
 RL J. Biol. Chem. 249:386-393(1974).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RA MEDLINE=92138655; PubMed=1663945;
 RA Morimoto Y., Tani T., Okumura H., Higuchi Y., Yasuoka N.;
 RT "Effects of amino acid substitution on three-dimensional structure:
 RT an x-ray analysis of cytochrome c3 from Desulfovibrio vulgaris
 RT Hildenborough at 2-A resolution.";
 RL J. Biochem. 110:532-540(1991).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE=94076344; PubMed=825467;
 RA Matias P.M., Prazao C., Morais J., Coll M., Carrondo M.A.;
 RT "Structure analysis of cytochrome c3 from Desulfovibrio vulgaris
 RT Hildenborough at 1.9-A resolution.";
 RL J. Mol. Biol. 234:680-699(1993).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS).
 RA Simoes P., Matias P.M., Morais J., Wilson K., Dauter Z.,
 RA Carrondo M.A.;
 RL Submitted (JUN-1997) to the PDB data bank.
 RN [6]

RP STRUCTURE BY NMR.
 RX MEDLINE=93093162; PubMed=1333991;
 RA Salgueiro C.A., Turner D.L., Santos H., Legall J., Xavier A.V.;
 RT "Assignment of the redox potentials to the four hemes in
 RT Desulfovibrio vulgaris cytochrome c3 by 2D-NMR.";
 RL FEBS Lett. 314:155-158(1992).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98378464; PubMed=9710542;
 RA Mesias A.C., Kastner D.H.W., Costa H.S., Legall J., Turner D.L.,
 RA Santos H., Xavier A.V.;
 RT "Solution structure of desulfovibrio vulgaris (Hildenborough)
 RT ferredoxin cytochrome c3: structural basis for functional cooperativity.";
 RL J. Mol. Biol. 281:719-739(1998).
 CC -I- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
 CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
 CC DEHYDROGENASE TO FERREDOXIN.
 CC -I- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC -I- PTM: BINDS 4 HEMES.
 CC -I- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X04304; CAA27847.1; -
 DR PIR: A00124; CDDV3.
 DR PIR: A24799; A24799.
 DR PDB: 2CTH; 24-DEC-97.
 DR PDB: 2CYM; 30-APR-94.
 DR PDB: 3CYR; 28-JAN-98.
 DR PDB: 1A21; 08-JUL-98.
 DR InterPro: IPR000345; -
 DR InterPro: IPR002322; -
 DR Pfam: PF02085; Cytochrome_C11; 1.
 DR PRINTS: PRO0609; CYTOCHROME_C3.
 DR PROSITE: PS00190; CYTOCHROME_C; 2.
 KW Electron transport; Sulfate respiration; Heme; Periplasmic; Signal;
 KW 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 129
 FT METAL 34 34 CYTOCHROME C3
 FT METAL 37 37 IRON (HEME 1 AXIAL LIGAND).
 FT BINDING 52 52 IRON (HEME 3 AXIAL LIGAND).
 FT BINDING 55 55 HEME 1 (COVALENT).
 FT METAL 56 56 HEME 1 (COVALENT).
 FT METAL 57 57 IRON (HEME 1 AXIAL LIGAND).
 FT BINDING 68 68 IRON (HEME 2 AXIAL LIGAND).
 FT BINDING 73 73 HEME 2 (COVALENT).
 FT METAL 74 74 HEME 2 (COVALENT).
 FT METAL 92 92 IRON (HEME 2 AXIAL LIGAND).
 FT BINDING 101 101 IRON (HEME 4 AXIAL LIGAND).
 FT BINDING 104 104 HEME 3 (COVALENT).
 FT METAL 105 105 IRON (HEME 3 AXIAL LIGAND).
 FT BINDING 122 122 HEME 4 (COVALENT).
 FT BINDING 127 127 HEME 4 (COVALENT).
 FT METAL 128 128 IRON (HEME 4 AXIAL LIGAND).
 FT STRAND 31 33
 FT STRAND 40 42
 FT HELIX 45 47
 FT TURN 48 49
 FT HELIX 52 54
 FT TURN 55 55
 FT STRAND 58 59
 FT TURN 60 61
 FT STRAND 62 63
 FT TURN 68 69
 FT TURN 71 72
 FT STRAND 76 76

DR Pfam: PF00379; Insect_cuticle; 1.
 DR PRINTS: PR00947; CUTICLE.
 DR PROSITE: PS00233; CUTICLE; 1.
 KM Structural protein; Cuticle.
 FT DOMAIN 73
 SQ SEQUENCE 126 AA; 12421 MW; F9633E26A877F6DE CRC64;

Query Match 45.5%; Score 5; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 83 APKAP 87

RESULT 15
 CU26_ARADI STANDARD; PRT; 127 AA.
 AC P80517;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 13-JUL-1998 (Rel. 36, Last annotation update)
 DE ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 12.6 (ACP 12.6).
 OS Araneus diadematus (Spider).
 CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 CC Araneomorphae; Entelegynae; Araneidae; Araneidae; Araneus;
 CC NCBI_Taxid=45920;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Cuticle;
 RX MEDLINE=97166616; Pubmed-9014336;
 RA Norup T., Berg T., Stenholm H., Andersen S.O., Hoefjup P.;
 RT "Purification and characterization of five cuticular proteins from
 the spider Araneus diadematus";
 RL Insect Biochem. Mol. Biol. 26:907-915(1996).
 CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
 CC -1- MASS SPECTROMETRY: MW=12587.5; METHOD-ELECTROSPRAY.
 CC -1- SIMILARITY: CONTAINS A CUTICLE CONSENSUS DOMAIN.
 DR Interpro: IPR000618;
 DR Pfam: PF00379; Insect_cuticle; 1.
 DR PRINTS: PR00947; CUTICLE.
 DR PROSITE: PS00233; CUTICLE; 1.
 KM Structural protein; Cuticle.
 FT DOMAIN 73
 SQ SEQUENCE 127 AA; 12589 MW; 9BFBCFB2B6AA4B9 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 127;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 83 APKAP 87

RESULT 16
 ULB0_HCMVA STANDARD; PRT; 127 AA.
 ID ULB0_HCMVA
 AC P16830;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE HYPOTHETICAL PROTEIN ULI10.
 GN ULI10.
 OS Human cytomegalovirus (strain AD169).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Betaherpesvirinae; Cytomegalovirus.
 CC NCBI_Taxid=10360;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=90269039; Pubmed-2161319;
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
 RA Horsnell T., Hutchison C.A. III, Kourzides T., Martignetti J.A.,
 RA Predde E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 RT "Analysis of the protein-coding content of the sequence of human
 cytomegalovirus strain AD169.";
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 CC -----

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DR EMBL: X17403; CA35348.1; -.
 DR PIR: S09877; S09877.
 DR Hypothetical protein.
 SQ SEQUENCE 127 AA; 14224 MW; D788B65C864F5AB CRC64;

Query Match 45.5%; Score 5; DB 1; Length 127;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QOTAP 6
 |||||
 Db 23 QOTAP 27

RESULT 17
 MSCL_HAEIN STANDARD; PRT; 128 AA.
 ID MSCL_HAEIN
 AC P44789;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL.
 GN MSCL OR H10626
 OS Haemophilus influenzae.
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus.
 CC NCBI_Taxid=727;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; Pubmed-7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Wetman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RL Science 269:496-512(1995).
 CC -1- FUNCTION: CHANNEL THAT OPENS IN RESPONSE TO STRETCH FORCES IN THE
 CC MEMBRANE LIPID BILAYER. MAY PARTICIPATE IN THE REGULATION OF
 CC OSMOTIC PRESSURE CHANGES WITHIN THE CELL (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOPENTAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (BY SIMILARITY).
 CC -----

CC -1- SIMILARITY: BELONGS TO THE MSCL FAMILY.

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FT NON_TER 123 123
SQ SEQUENCE 123 AA: 14162 MW: B2E73FB457EBB51C CRC64:

Query Match 45.5%; Score 5; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KAPTE 11
DB 56 KAPTE 60

RESULT 12

WN3A_MELGA STANDARD; PRT: 123 AA.
AC P28125;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE WNT-3A PROTEIN (FRAGMENT).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxId=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92279273; PubMed=1534411;
RA Sidorow A.;
RT "Diversification of the Wnt gene family on the ancestral lineage of vertebrates."
RL Proc. Natl. Acad. Sci. U.S.A. 89:5098-5102(1992).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC -----
CC EMBL: M91281; AAA49630.1; -
CC InterPro: IPR000970; -
CC Pfam: PF00110; wnt: 1.
CC PROSITE: PS00246; WNT1; PARTIAL.
KW Developmental protein; Glycoprotein.
FT NON_TER 1 123
FT NON_TER 123 123
SQ SEQUENCE 123 AA: 14268 MW: 66B6CEFF05BBA576 CRC64:

Query Match 45.5%; Score 5; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KAPTE 11
DB 56 KAPTE 60

RESULT 13

WN3A_SCEOC STANDARD; PRT: 123 AA.
AC P28142;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE WNT-3A PROTEIN (FRAGMENT).
GN WNT-3A.

OS Sceloporus occidentalis (Western fence lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxId=8519;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92279273; PubMed=1534411;
RA Sidorow A.;
RT "Diversification of the Wnt gene family on the ancestral lineage of vertebrates."
RL Proc. Natl. Acad. Sci. U.S.A. 89:5098-5102(1992).

CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----

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CC -----

CC EMBL: M91299; AAA49542.1; -
CC InterPro: IPR000970; -
CC Pfam: PF00110; wnt: 1.
CC PROSITE: PS00246; WNT1; PARTIAL.
KW Developmental protein; Glycoprotein.
FT NON_TER 1 123
FT NON_TER 123 123
SQ SEQUENCE 123 AA: 14296 MW: 66A1E9CF05BBBC6F CRC64:

Query Match 45.5%; Score 5; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KAPTE 11
DB 56 KAPTE 60

RESULT 14

CN24_ARADI STANDARD; PRT: 126 AA.
AC P80516;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 12.4 (ACP 12.4).
OS Araneus diadematus (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneidae; Araneidae; Araneus.
OX NCBI_TaxId=45920;
RN [1]
RP SEQUENCE.
RX TISSUE-Cuticle; PubMed=9014336;
RX MEDLINE=9716616; PubMed=9014336;
RA Norup T., Berg T., Stenholm H., Andersen S.O., Hoejrup P.;
RT "Purification and characterization of five cuticular proteins from the spider Araneus diadematus."
RL Insect Biochem. Mol. Biol. 26:907-915(1996).
CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
CC -1- MASS SPECTROMETRY: MM=12420.5; METHOD-ELECTROSPRAY.
CC -1- SIMILARITY: CONTAINS A CUTICLE CONSENSUS DOMAIN.
DR InterPro: IPR000618; -

FT MOD.RES 6 6 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13339 MW; 826ECB33A26BD873 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
DB 102 TAPKA 106

RESULT 9
CU9_ARADI STANDARD; PRT; 120 AA.

AC P80515;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9).
OS Araneus diadematus (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneidae; Araneidae; Araneus.
OX NCBI_TaxID=45920;
RN [1]
RP SEQUENCE.
RC TISSUE=Cuticle;
RX MEDLINE=97166616; PubMed=9014336;
RA Norup T., Berg T., Stenholm H., Andersen S.O., Hoerjrup P.;
RT "Purification and characterization of five cuticular proteins from
the spider Araneus diadematus".
RL Insect Biochem. Mol. Biol. 26:907-915(1996).
CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
CC -1- MASS SPECTROMETRY: MW=11872.1; METHOD-ELECTROSPRAY.
CC -1- SIMILARITY: CONTAINS A CUTICLE CONSENSUS DOMAIN.
DR HSSP: P04002; IATF.
DR InterPro: IPR000618; .
DR Pfam: PF00379; Insect_cuticle; 1.
DR PRINTS: PR00947; CUTICLE.
DR PROSITE: PS00233; CUTICLE; 1.
KW Structural protein; Cuticle.
FT DOMAIN 73 83 POLY-ALA.
SQ SEQUENCE 120 AA; 11871 MW; 8D3E577C6199DC2 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
DB 83 APRAP 87

RESULT 10
H2B_HOLTU STANDARD; PRT; 123 AA.

AC P48557;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HISTONE H2B.
OS Holothuria tubulosa (Sea cucumber).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Holothuroidea; Aspidochelonea; Aspidochelonea; Holothuriidae;
OC Holothuria.
OX NCBI_TaxID=7685;
RN [1]
RP SEQUENCE FROM N.A.
RA Drabant B., Louroutzlatis A., Prats E., Cornudella L., Doenecke D.;
CL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
FT -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF

CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.

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CC EMBL: Z46225; CAA86297.1; .
DR InterPro: IPR000166; .
DR InterPro: IPR000558; .
DR Pfam: PF00123; histone; 1.
DR PRINTS: PR00621; HISTONEH2B.
DR PROSITE: PS00357; HISTONE_H2B; 1.
KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
SQ SEQUENCE 123 AA; 13649 MW; 35503AFB1400FE6E CRC64;

Query Match 45.5%; Score 5; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
DB 2 APRAP 6

RESULT 11
WN3A_ALOVU STANDARD; PRT; 123 AA.

AC P28101;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE WNT-3A PROTEIN (FRAGMENT).
GN WNT-3A.
OS Alopias vulpinus (Thresher shark).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Lamniformes; Alopiidae;
OC Alopiidae; Alopias.
OX NCBI_TaxID=7852;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92279273; PubMed=1534411;
RA Sidow A.;

RT "Diversification of the Wnt gene family on the ancestral lineage of
vertebrates".
RL Proc. Natl. Acad. Sci. U.S.A. 89:5098-5102(1992).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIMETERS.
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.

CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

CC EMBL: M91252; AAA48538.1; .
DR InterPro: IPR000970; .
DR Pfam: PF00110; wnt; 1.
DR PROSITE: PS00246; WNT1; PARTIAL.
KW Developmental protein; Glycoprotein.
FT NON_TER 1 1

DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (150 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DIIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
OS Strawberry mild yellow edge-associated virus (SMYAV).
CC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12187;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MY-18;
RX MEDLINE=92166762; PubMed=1339469;
RA Jekmann W., Maiss E., Martin R.R.;
RT "The nucleotide sequence and genome organization of strawberry mild
yellow edge-associated potexvirus.";
RL J. Gen. Virol. 73:475-479(1992).
CC -1- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D12517; BAA02082.1; -;
DR PIR: J01426; RRMGSM.
DR InterPro: IPR000606; -;
DR Pfam: PF01443; Viral_helicase1; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW NP_BIND
FT NP_BIND 605 612 POTENTIAL.
SQ SEQUENCE 1323 AA; 149593 MW; D6BC35133E3CAD26 CRC64;

Query Match 54.5%; Score 6; DB 1; Length 1323;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAPT 10
DB 463 APKAPT 468
IIIIII

RESULT 7
ANT1_ONCVO STANDARD: PRT; 2022 AA.
ID ANT1_ONCVO
AC P21249;
DT 01-MAY-1991 (Rel. 18, Created)
RT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MAJOR ANTIGEN.
GN OVT1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
CC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95287898; PubMed=7770081;
RA Tlitteraprabh S., Ritchie T.L., Tuan R.S., Shepley K.J., Dimman J.D.,
RA Neubert T.A., Scott A.L.;
RT "Molecular cloning of a gene expressed during early embryonic
development in Onchocerca volvulus.";
RT Mol. Biochem. Parasitol. 69:161-171(1995).
RL [2]
RP SEQUENCE OF 733-866 FROM N.A.
RX MEDLINE=89127417; PubMed=2464764;
RA Donelson J.E., Duke B.O.L., Moser D., Zeng W., Erondy N.E.,
RA Lucius R., Renz A., Karan M., Flores G.Z.;
RT "Construction of Onchocerca volvulus cDNA libraries and partial
characterization of the cDNA for a major antigen.";
RL Mol. Biochem. Parasitol. 31:241-250(1988).

CC -1- FUNCTION: MAY BE A MYOFIBRILLAR PROTEIN.
CC -----
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CC -----
DR EMBL: U12681; AAA80009.1; -;
DR PIR: J03995; AAA29412.1; -;
DR PIR: A54513; A54513.
DR HSSP: P02633; 3ICB.
KW Antigen; Coiled coil.
FT DOMAIN 74 120 COILED COIL (POTENTIAL).
FT DOMAIN 151 251 COILED COIL (POTENTIAL).
FT DOMAIN 327 384 COILED COIL (POTENTIAL).
FT DOMAIN 417 1879 COILED COIL (POTENTIAL).
SQ SEQUENCE 2022 AA; 237341 MW; B7132ACF1520317 CRC64;

Query Match 54.5%; Score 6; DB 1; Length 2022;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OQQTAP 6
DB 302 OQQTAP 307
IIIIII

RESULT 8
GSP1_AERHY STANDARD: PRT; 119 AA.
ID GSP1_AERHY
AC P31737;
DT 01-JUL-1993 (Rel. 26, Created)
RT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE GENERAL SECRETION PATHWAY PROTEIN I PRECURSOR.
GN EXEL.
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
CC Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AH65;
RX MEDLINE=94012544; PubMed=8407845;
RA Howard S.P., Critch J., Bedi A.;
RT "Isolation and analysis of eight exo genes and their involvement in
extraacellular protein secretion and outer membrane assembly in
Aeromonas hydrophila.";
RL J. Bacteriol. 175:6695-6703(1993).
CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
EXPORT OF PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE PULI/OUTI/XPSI/EXEL/XCPV FAMILY.
CC -----
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CC -----
DR EMBL: X66504; CAA47130.1; -;
DR PIR: S22912; S22912.
DR PIR: B49905; B49905.
DR InterPro: IPR001120; -;
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Transport; Methylation.
FT PROPEP 1 5 BY SIMILARITY.
FT CHAIN 6 119 GENERAL SECRETION PATHWAY PROTEIN I.

FT NON_TER 314 314
SQ SEQUENCE 314 AA: 34618 MW: 4F949656A8BED1F6 CRC64:

Query Match 54.5%; Score 6; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAPT 10
Db 49 APRAPT 54

RESULT 3

P53_MARMO STANDARD: PRT: 391 AA.
AC 036006:
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376966; PubMed=9233767;
RA Feltzson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT "Partial characterization of the woodchuck tumor suppressor, p53, and
its interaction with woodchuck hepatitis virus X antigen in
hepatocarcinogenesis.";
RT Oncogene 15:327-336(1997).
RL -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
EXPRESSION.
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
IN MANY TYPES OF CANCER.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: AJ001022; CA004478.1; -
DR HSSP: P04637; ITRF.
DR InterPro: IPR002117; -
DR Pfam: PF008070; P53; 1.
DR PRINTS: PRO0386; P53SUPPRESSR.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNM_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 354 OLIGOMERIZATION.
FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA: 43468 MW: E1DE5DB84BA0182 CRC64:

Query Match 54.5%; Score 6; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAPT 10
Db 69 APRAPT 74

RESULT 4

IF2_SYNY3 STANDARD: PRT: 1001 AA.
AC P72689:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TRANSLATION INITIATION FACTOR IF-2.
GN INFB OR SLR0744.
GN Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpou S., Takeuchi C., Wada T., Watanabe A.,
RA Yanada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synecocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RT DNA Res. 3:109-136(1996).
RL -1- FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION
OF PROTEIN SYNTHESIS IN VITRO, PROTECTS FORMYL METHIONYL-TRNA FROM
SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S
RIBOSOMAL SUBUNIT. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP
DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
CC -----
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CC -----
DR EMBL: D90900; BA016696.1; -
DR HSSP: P02990; IETU.
DR InterPro: IPR000178; -
DR InterPro: IPR000795; -
DR Pfam: PF000009; GTP_EFTU; 1.
DR Pfam: PF02131; IF2; 1.
DR PROSITE: PS01176; IF2; 1.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT DOMAIN 494 648 G-DOMAIN.
FT NP_BIND 502 509 GTP (BY SIMILARITY).
FT NP_BIND 552 556 GTP (BY SIMILARITY).
FT NP_BIND 606 609 GTP (BY SIMILARITY).
SQ SEQUENCE 1001 AA: 108118 MW: 4C7F00DEB56CE3C CRC64:

Query Match 54.5%; Score 6; DB 1; Length 1001;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAPT 10

Accession	Length	Score	DB 1	Length	DB 1
983	4	36.4	437	1	E2F2_HUMAN
984	4	36.4	437	1	SAH1_CABEL
985	4	36.4	438	1	FUMC_SULSO
986	4	36.4	438	1	PRIL_DROME
987	4	36.4	438	1	SYD_PYRO
988	4	36.4	438	1	SYD_PYRO
989	4	36.4	438	1	Y281_HAEIN
990	4	36.4	439	1	CK13_SCHPO
991	4	36.4	439	1	RHGI_HUMAN
992	4	36.4	440	1	MANA_CANAL
993	4	36.4	441	1	CG22_ANTMA
994	4	36.4	442	1	Y141_ECOLI
995	4	36.4	443	1	AROA_BACNO
996	4	36.4	443	1	CAR4_DICDI
997	4	36.4	443	1	DCUA_HELPJ
998	4	36.4	443	1	DCUA_HELPJ
999	4	36.4	443	1	SOX3_HUMAN
1000	4	36.4	443	1	YJ11_ECOLI

ALIGNMENTS

RESULT 1

ID P60_LISMO STANDARD: PRT: 484 AA.

AC P21171:

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN).

GN IAP.

OS Listeria monocytogenes.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Listeria.

OX NCBI_TaxID=1639;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-49.

RC STRAIN-SV1/2A EGD(KAUFMANN);

RX MEDLINE-90256283; PubMed-2111287;

RA Koehler S., Leimeister-Waechter M., Chakraborty T., Lottspeich F., Goebel W.;

RT "The gene coding for protein p60 of Listeria monocytogenes and its use as a specific probe for Listeria monocytogenes.";

RL Infect. Immun. 58:1943-1950(1990).

RN [2]

RP DISCUSSION OF SEQUENCE.

RX MEDLINE-93094153; PubMed-1459966;

RA Hubert A., Kuhn M., Goebel W., Koehler S.;

RT "Structural and functional properties of the p60 proteins from different Listeria species.";

RL J. Bacteriol. 174:8166-8171(1992).

CC -1- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE INVASION OF NONPROFESSIONAL PHAGOCYTTIC CELLS BY LISTERIA.

CC -1- SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA P60 FAMILY.

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CC EMBL: X53268; CA36509.1; -.

DR PIR: A41487; A41487.

DR InterPro: IPR000064; -.

DR InterPro: IPR002482; -.

DR Pfam: PF00877; NLPC_P60; 1.

DR Pfam: PF01476; PG_binding_2; 2.

KW Signal: Repeat.

FT SIGNAL 1 27

FT CHAIN 28 484 PROTEIN P60.

Accession	Length	Score	DB 1	Length	DB 1
FT DOMAIN	311	355	19	X 2	AA TANDEN REPEATS OF T-N.
SQ SEQUENCE	484 AA;	50587 MW;	3CCOF05091E14E0F		CRC64;

Query Match

Best Local Similarity 100.0%; Score 11; DB 1; Length 484;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 000TAPKAPTE 11

Db 291 000TAPKAPTE 301

RESULT 2

ID P53_SPEBE STANDARD: PRT: 314 AA.

AC 064662;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53) (FRAGMENT).

GN TP53.

OS *Spermophilus beecheyi* (Beechey ground squirrel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae; OC Spermophilus.

OX NCBI_TaxID=34862;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Thymus;

RX MEDLINE-95007566; PubMed-7923176;

RA Rivkina M.B., Cullen J.M., Robinson W.S., Marlon P.L.;

RT "State of the p53 gene in hepatocellular carcinomas of ground squirrels and woodchucks with past and ongoing infection with hepadnaviruses.";

RL Cancer Res. 54:5430-5437(1994).

CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND BCL-2 EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.

CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC EMBL: U43902; AA85628.1; -.

DR HSP: P04637; 1YCS.

DR InterPro: IPR002117; -.

DR PIR: P00870; P53; 1.

DR Pfam: PF00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

FT NON_TER 1 1

FT DOMAIN <1 24

FT DNA_BIND 80 270

FT DOMAIN 303 >314

FT DOMAIN 289 301

TRANSCRIPTION ACTIVATION (ACIDIC).

BY SIMILARITY.

OLIGOMERIZATION.

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

837	4	36.4	383	1	OPS4_DROVI	P17646	drosophila	910	4	36.4	414	1	LMPI_CHICK	P05300	gallus gall
838	4	36.4	384	1	5X18_HUMAN	P35713	homo sapien	911	4	36.4	415	1	HEMI_NEIGO	O9zhd6	neisseria m
839	4	36.4	384	1	Y039_MYCCE	P47285	mycoplasma	912	4	36.4	415	1	HEMI_NEIMB	O9zhd5	neisseria g
840	4	36.4	385	1	FADH_YEAST	P32771	saccharomyc	913	4	36.4	415	1	HEMI_NEIMB	P56994	neisseria m
841	4	36.4	386	1	GATM_PIG	P50441	sus scrofa	914	4	36.4	415	1	CTG_HAELN	P44945	haemophilus
842	4	36.4	387	1	ADHA_BACSU	O05239	baecillus su	915	4	36.4	416	1	IDH_ECOLI	P08200	escherichia
843	4	36.4	387	1	INVO_TARBA	P24711	tarsius ban	916	4	36.4	416	1	R23B_MOUSE	P54728	mus musculus
844	4	36.4	387	1	SAT_DEIRA	P56864	delinococcus	917	4	36.4	417	1	FTSA_PSEAE	P47203	pseudomonas
845	4	36.4	388	1	ARGJ_CORGL	O59280	cornebacte	918	4	36.4	417	1	LYOX_HUMAN	P28300	homo sapien
846	4	36.4	388	1	CZFI_CANAL	P28875	candida alb	919	4	36.4	417	1	MAC1_YEAST	P31192	saccharomyc
847	4	36.4	388	1	VE2_HPV29	P50772	human papil	920	4	36.4	417	1	ODO2_BACSU	P16263	baecillus su
848	4	36.4	389	1	YB82_YEAST	O04951	saccharomyc	921	4	36.4	418	1	FTS2_TREPA	O83405	treponema p
849	4	36.4	390	1	ADHB_BACSU	O05240	baecillus su	922	4	36.4	419	1	KAS2_STRCN	O02579	streptomyce
850	4	36.4	390	1	RIR2_MOUSE	P11157	mus musculus	923	4	36.4	419	1	LPB1_NEIMA	P57038	neisseria m
851	4	36.4	391	1	BCHP_RHOCA	P26172	rhodobacter	924	4	36.4	419	1	LPB1_NEIMB	O05014	neisseria m
852	4	36.4	391	1	NIRE_PSEST	O52521	pseudomonas	925	4	36.4	419	1	MANA_PSEFL	P49424	pseudomonas
853	4	36.4	391	1	V506_ROTGA	P26015	rotavirus (926	4	36.4	421	1	ACDM_HUMAN	P11310	homo sapien
854	4	36.4	392	1	CG2B_CHLYR	P51987	chlorophytra	927	4	36.4	421	1	ACDM_PIG	P41367	sus scrofa
855	4	36.4	392	1	HRCA_CHLMU	P54306	chlamydia m	928	4	36.4	421	1	FXJ1_MOUSE	O61660	mus musculus
856	4	36.4	393	1	GC1M_MOUSE	P01869	mus musculus	929	4	36.4	421	1	FXJ1_RAT	O63247	rattus norv
857	4	36.4	393	1	TRUA_MOUSE	O9wu56	mus musculus	930	4	36.4	421	1	MYB2_PHYPA	P80073	physcomitre
858	4	36.4	394	1	VGID_HSV11	O69091	herpes simp	931	4	36.4	421	1	SYS_THERM	P34945	thermus aqu
859	4	36.4	394	1	VGLD_HSV1A	P36318	herpes simp	932	4	36.4	422	1	CG2A_SPIRO	P04962	spisula sol
860	4	36.4	394	1	VGLD_HSV1P	P37083	herpes simp	933	4	36.4	422	1	SYH_HAEIN	P43823	haemophilus
861	4	36.4	395	1	YCHF_HSVB	P36342	simian herp	934	4	36.4	423	1	GATM_HUMAN	P50440	homo sapien
862	4	36.4	395	1	YCHP_CAEEL	P51917	caenorhabdi	935	4	36.4	423	1	GATM_RAT	P50442	rattus norv
863	4	36.4	395	1	C121_MYCTU	O59571	mycobacteri	936	4	36.4	423	1	IDH_BACSU	P39126	baecillus su
864	4	36.4	396	1	EPSC_BURSO	P52641	burkholderi	937	4	36.4	423	1	TYD_HUMAN	P32440	homo sapien
865	4	36.4	396	1	YD61_MYCTU	O11031	mycobacteri	938	4	36.4	423	1	SHIP1_YEAST	P32223	saccharomyc
866	4	36.4	397	1	SEPL_MOUSE	O62170	mus musculus	939	4	36.4	424	1	ASP_ANCCA	O16937	ancyllostoma
867	4	36.4	398	1	EF1G_CAEEL	P54412	caenorhabdi	940	4	36.4	424	1	IVD_RAT	P12007	rattus norv
868	4	36.4	398	1	ODO2_AZOVI	P20708	azotobacter	941	4	36.4	424	1	KAS2_STRCO	P21156	streptomyce
869	4	36.4	398	1	TAP_DROME	O18657	drosophila	942	4	36.4	425	1	IDH_HELPJ	O59636	halicobacte
870	4	36.4	400	1	NICM_PROWI	O37619	protosheca	943	4	36.4	425	1	IDH_HELPJ	O59297	chlorobium
871	4	36.4	401	1	NODE_RHIT	P04684	rhizodium 1	944	4	36.4	425	1	LMP2_CHICK	O90617	gallus gall
872	4	36.4	402	1	ARGJ_METUA	O57645	m putative	945	4	36.4	426	1	DHMH_PARVE	P23006	paracoccus
873	4	36.4	402	1	CAR1_CANPA	P32951	candida par	946	4	36.4	426	1	GSA_ECOLI	P23893	escherichia
874	4	36.4	402	1	HEM2_CHICK	O42479	gallus gall	947	4	36.4	426	1	GSA_SALTY	P42476	salmonella
875	4	36.4	402	1	KPPR_SPIOL	P09559	splanctia ol	948	4	36.4	426	1	HEMI_XANCH	P24808	xanthomonas
876	4	36.4	402	1	OPS4_CANAL	P46596	candida alb	949	4	36.4	427	1	CYB6_CHILT	O59297	chlorobium
877	4	36.4	402	1	PA11_MOUSE	P22777	mus musculus	950	4	36.4	427	1	TI31_HUMAN	P78552	homo sapien
878	4	36.4	402	1	PA11_RAT	P20961	rattus norv	951	4	36.4	427	1	YBHC_ECOTI	P46130	escherichia
879	4	36.4	402	1	PG11_ERMCA	P18192	erwinia car	952	4	36.4	428	1	HEM2_HORVU	O42836	hordium vul
880	4	36.4	402	1	RDS1_SCHPO	P53693	schizosacch	953	4	36.4	428	1	MOD5_YEAST	P07884	saccharomyc
881	4	36.4	403	1	CSB3_CHICK	P39963	gallus gall	954	4	36.4	428	1	SOCK_HUMAN	P98077	homo sapien
882	4	36.4	403	1	G3PA_MAIZE	P09315	zea mays (m	955	4	36.4	429	1	EP1G_ARPSA	P12261	artemia sal
883	4	36.4	403	1	I23O_HUMAN	P14902	homo sapien	956	4	36.4	429	1	MYCS_RAT	P23999	rattus norv
884	4	36.4	405	1	CAR8_CANAL	O42778	candida alb	957	4	36.4	429	1	YVFO_BACSU	O07013	baecillus su
885	4	36.4	405	1	GDPB_MOUSE	O921w4	mus musculu	958	4	36.4	430	1	CINA_MYCTU	O07731	mycobacteri
886	4	36.4	405	1	THRC_METUA	O58860	methanococc	959	4	36.4	430	1	CRE1_NEUCR	O59598	neurospora
887	4	36.4	405	1	YIS1_STRCO	P19780	streptomyce	960	4	36.4	430	1	GNL1_HUMAN	P36915	homo sapien
888	4	36.4	405	1	YIU3_CAEEL	P34397	caenorhabdi	961	4	36.4	430	1	GSA_BACSU	P30949	baecillus su
889	4	36.4	407	1	COAT_BBY	P04329	black beeti	962	4	36.4	430	1	GSA_HELPJ	O92md0	halicobacte
890	4	36.4	407	1	COAT_FHV	P12870	flock house	963	4	36.4	430	1	GSA_HELPJ	P56115	halicobacte
891	4	36.4	407	1	CPXD_AGRU	P24467	agrobacteri	964	4	36.4	431	1	OAPA_HAEIN	P44415	haemophilus
892	4	36.4	408	1	GDPB_HUMAN	O95390	homo sapien	965	4	36.4	431	1	P2X6_HUMAN	O15547	homo sapien
893	4	36.4	408	1	YJ95_YEAST	P47160	saccharomyc	966	4	36.4	432	1	CGA2_HUMAN	P20248	homo sapien
894	4	36.4	409	1	HEM1_PARDE	P43089	paracoccus	967	4	36.4	432	1	ENV2_MOUSE	P11370	mus musculus
895	4	36.4	409	1	KAS2_STRGA	P15539	streptomyce	968	4	36.4	432	1	TNU_RAT	P19332	rattus norv
896	4	36.4	409	1	R23B_HUMAN	P54727	homo sapien	969	4	36.4	433	1	TIG_HAEIN	P44837	haemophilus
897	4	36.4	410	1	CPIX_BACME	P14762	baecillus me	970	4	36.4	433	1	GAG_HTLV2	P03346	human t-cell
898	4	36.4	410	1	ENB_FLYCA	O02076	feline leuk	971	4	36.4	433	1	HEM2_SPIOL	P42493	spincacia ol
899	4	36.4	410	1	FB12_ADEG1	O64762	avian adeno	972	4	36.4	433	1	HRR2_HAIVA	P42258	halicobacte
900	4	36.4	411	1	T3RE_BACCE	O9w1p7	drosophila	973	4	36.4	433	1	RTCI_DICDI	O15746	dictyostell
901	4	36.4	412	1	T3RE_BACCE	P25241	baecillus ce	974	4	36.4	433	1	TNBI_AGRU	P54917	agrobacteri
902	4	36.4	412	1	Y360_MYCPN	P75241	mycoplasma	975	4	36.4	434	1	INXE_CAEEL	O62136	caenorhabdi
903	4	36.4	413	1	ESCI_SCHPO	O04635	schizosacch	976	4	36.4	434	1	PRSA_YEAST	P32397	saccharomyc
904	4	36.4	413	1	HMFT_DROME	P02835	drosophila	977	4	36.4	434	1	Y61O_METUA	O58027	methanococc
905	4	36.4	413	1	OR7A_DROME	O9w315	drosophila	978	4	36.4	436	1	ENV_FLYCS	O02077	feline leuk
906	4	36.4	413	1	OST4_CHICK	P46440	gallus gall	979	4	36.4	436	1	RHO_AOUAE	O07683	halobacteri
907	4	36.4	413	1	PKK_DROME	P91622	drosophila	980	4	36.4	436	1	STD_HAUNI	V010_HSV6U	human herpe
908	4	36.4	413	1	Y50_YEAST	P45819	saccharomyc	981	4	36.4	436	1			
909	4	36.4	414	1	IDH1_VIBAL	P41560	vibrio sp.	982	4	36.4	437	1	AAC3_DICDI	P14197	dictyostell

691	4	36.4	337	1	HAIR_DROME	P14003 drosophila	764	4	36.4	363	1	TOBI_MOUSE	O61471 mus musculus
692	4	36.4	337	1	VGH_BPC4	P03647 bacterioph	765	4	36.4	364	1	LIP_BURCE	P22088 burkholderi
693	4	36.4	337	1	YDTR_SCHPO	O14216 schizosap	766	4	36.4	364	1	LIP_PERS5	P25275 pseudomonas
694	4	36.4	338	1	NH52_CAEEL	O17928 caenorhabd	767	4	36.4	364	1	MRP_AOURB	O66946 aqualifx aeo
695	4	36.4	338	1	SED1_YRSTN	O01369 saccharomyc	768	4	36.4	364	1	TAU2_MOUSE	P10638 mus musculu
696	4	36.4	338	1	TAP4_HUMAN	O01664 homo sapien	769	4	36.4	364	1	ZRP4_MAIZE	P47917 zea mays (m
697	4	36.4	339	1	E281_ARCFU	O29877 archaeoglob	770	4	36.4	365	1	MEFB_HUMAN	O02080 homo sapien
698	4	36.4	339	1	FMRE_DROVI	P18767 drosophila	771	4	36.4	365	1	OMLA_ACPPL	O02937 actinobacil
699	4	36.4	339	1	SRPA_SYNP7	O55025 synchococc	772	4	36.4	365	1	TRUA_HUMAN	O97606 homo sapien
700	4	36.4	340	1	CAG4_HUMAN	O11201 h cmp-n ace	773	4	36.4	366	1	CYCR_RHOGE	P51758 rhodocyclu
701	4	36.4	340	1	CATR_CHICK	P43223 gallus-gall	774	4	36.4	366	1	HNLS_SORBI	P52708 sorghum bic
702	4	36.4	340	1	RECA_MYCCE	P47581 mycoplasma	775	4	36.4	366	1	VF72_HAEIN	P46495 haemophilus
703	4	36.4	340	1	VP35_EBOZM	O05127 ebola virus	776	4	36.4	367	1	DNAJ_COXBU	P42381 coxiella bu
704	4	36.4	341	1	COA2_BFDV	P13892 budgerigar	777	4	36.4	368	1	GUN1_ECOLI	P37651 escherichia
705	4	36.4	341	1	TAU3_MOUSE	P10637 mus musculu	778	4	36.4	368	1	MLTA_VIBCH	O98994 vibrio chol
706	4	36.4	342	1	TONB_PSEAE	O51368 pseudomonas	779	4	36.4	368	1	MYCL_MOUSE	P10166 mus musculu
707	4	36.4	342	1	VU84_HSV6U	P52532 human herpe	780	4	36.4	368	1	SH31_HUMAN	O99961 homo sapien
708	4	36.4	343	1	COAL_BFDV	P13891 budgerigar	781	4	36.4	368	1	VE2_HPV6A	O84294 human papil
709	4	36.4	343	1	TRA_CORDI	P35879 corynebacte	782	4	36.4	368	1	YBHR_ECOLI	P44087 haemophilus
710	4	36.4	344	1	ASTA_ECOLI	P76218 escherichia	783	4	36.4	368	1	Y974_HAEIN	P75774 escherichia
711	4	36.4	344	1	CHER_THEMA	O9WYN9 thermotoga	784	4	36.4	369	1	LMXB_MESAU	O60564 mesocricetu
712	4	36.4	344	1	HRCA_BACST	O45500 bacillus st	785	4	36.4	370	1	HMC2_DESVH	P33389 desulfotibtr
713	4	36.4	344	1	NUN2_RHIME	P56911 thizobium m	786	4	36.4	370	1	HUPK_RHILV	P28183 thizobium l
714	4	36.4	344	1	Y401_HUMAN	O43151 homo sapien	787	4	36.4	370	1	TRPD_MYCTU	Q10382 mycobacteri
715	4	36.4	344	1	YAAA_SCHPO	O09801 schizosacch	788	4	36.4	370	1	V2R_PIG	P32307 sus scrofa
716	4	36.4	345	1	GDPE_RAT	O92217 rattus norv	789	4	36.4	372	1	ADHA_RANPE	O57380 rana perezi
717	4	36.4	345	1	NU2M_MOUSE	P03893 mus musculu	790	4	36.4	372	1	ADHA_POVMK	P24595 mouse polyo
718	4	36.4	345	1	NU2M_RAT	P11662 rattus norv	791	4	36.4	372	1	DBPA_HUMAN	P16989 homo sapien
719	4	36.4	345	1	PANC_YEAST	P40439 saccharomyc	792	4	36.4	372	1	LMXB_MOUSE	O88609 mus musculu
720	4	36.4	346	1	ARCC_BACSU	P23715 bacillus su	793	4	36.4	372	1	MSSP_HUMAN	P29558 homo sapien
721	4	36.4	346	1	BIOB_ECOLI	P12996 escherichia	794	4	36.4	373	1	MP91_POAPR	P22284 poa pratens
722	4	36.4	346	1	BIOB_SERMA	P36569 serrattia ma	795	4	36.4	374	1	GDPE_BRARE	O42222 brachydanio
723	4	36.4	346	1	T2D7_YEAST	O04254 saccharomyc	796	4	36.4	375	1	ACRG_EMENTI	P20319 emerticella
724	4	36.4	346	1	YIC3_YEAST	P40564 saccharomyc	797	4	36.4	375	1	ADHG_GADMO	P81600 gadus morhu
725	4	36.4	347	1	DDL_HELPJ	O92485 helicobacte	798	4	36.4	375	1	FENS_TOBAC	O04397 nicotiana t
726	4	36.4	347	1	DDL_HELPY	P56191 helicobacte	799	4	36.4	375	1	GDPE_BOVIN	O18836 bos taurus
727	4	36.4	347	1	DHAS_LEGPN	O31219 legionella	800	4	36.4	375	1	GDPE_CHICK	O42220 gallus gall
728	4	36.4	347	1	UL88_HSV7J	P52364 human herpe	801	4	36.4	375	1	GDPE_HUMAN	O14273 melagris g
729	4	36.4	349	1	SAPD_HAEIN	P45288 haemophilus	802	4	36.4	375	1	GDPE_MELGA	O42221 melagris g
730	4	36.4	350	1	FLAO_TREPA	P18193 treponema p	803	4	36.4	375	1	GDPE_PAPHA	O18888 papio hamad
731	4	36.4	350	1	FLAO_HALYO	P41198 halobacteri	804	4	36.4	375	1	GDPE_PIG	O18831 sus scrofa
732	4	36.4	352	1	NU2M_STRPU	P15349 strongyloce	805	4	36.4	375	1	GDPE_SHEEP	O18830 ovis aries
733	4	36.4	352	1	SMP_SERNA	O06517 serrattia ma	806	4	36.4	375	1	INTE_ECOLI	P75965 escherichia
734	4	36.4	353	1	HEM2_BRAJA	P45622 bradyrhizob	807	4	36.4	375	1	SRE_CHICK	P78605 coriolinus hi
735	4	36.4	353	1	YF91_MYCPN	O50336 mycoplasma	808	4	36.4	375	1	DM2PM_STRIP	O90718 gallus gall
736	4	36.4	354	1	YMA3_MYCBO	O02279 mycobacteri	809	4	36.4	376	1	VASP_MOUSE	P422712 streptomyce
737	4	36.4	355	1	NIPS_LACDE	P31672 laccobacilli	810	4	36.4	376	1	VE2_HPV10	P70460 mus musculu
738	4	36.4	355	1	VAL1_ABRVW	O25747 abutilon mo	811	4	36.4	377	1	FENS_PEA	P36781 human papil
739	4	36.4	355	1	Y644_SYNY3	O55724 synchocyst	812	4	36.4	377	1	LMXB_CHICK	O41014 pium sativ
740	4	36.4	358	1	KLRF_MOUSE	P46099 mus musculu	813	4	36.4	378	1	DHA_BACSU	P53413 gallus gall
741	4	36.4	358	1	TRMU_SYNY3	P73755 synchocyst	814	4	36.4	378	1	FENS_ORYSA	O08352 bacillus su
742	4	36.4	358	1	VAL1_BCVY	P14991 beet curly	815	4	36.4	378	1	FENT_ORYSA	P41335 oryza sativ
743	4	36.4	359	1	HIS8_SALTY	P10369 salmonella	816	4	36.4	378	1	MRG_HUMAN	O23877 oryza sativ
744	4	36.4	359	1	TMOD_HUMAN	P28289 homo sapien	817	4	36.4	378	1	SVY_HAEPA	P35410 homo sapien
745	4	36.4	359	1	TMOD_MOUSE	P49813 mus musculu	818	4	36.4	378	1	OPS4_DROME	O08255 drosophila
746	4	36.4	359	1	VAL1_TYLCM	P27260 tomatto yell	819	4	36.4	378	1	VE2_HPV30	P36432 haemophilus
747	4	36.4	359	1	VAL1_TYLCU	P38609 tomatto yell	820	4	36.4	378	1	VE2_HPV55	P36790 human papil
748	4	36.4	360	1	GPRP_HUMAN	O00155 homo sapien	821	4	36.4	379	1	LMXE_HUMAN	O80937 human papil
749	4	36.4	360	1	VG47_BRMU	O91122 bacterioph	822	4	36.4	379	1	P2X6_RAT	O60663 homo sapien
750	4	36.4	361	1	DBPA_RAT	O62764 rattus norv	823	4	36.4	379	1	VAT1_TORCA	P51579 rattus norv
751	4	36.4	361	1	DCAM_HELAN	O65354 hellianthus	824	4	36.4	379	1	YAD2_YEAST	P19333 rufus cal
752	4	36.4	361	1	OSHI_ORYSA	P46609 oryza sativ	825	4	36.4	380	1	CAGD_MOUSE	P28004 saccharomyc
753	4	36.4	361	1	RTCI_DROME	O77264 drosophila	826	4	36.4	380	1	VGLI_HSVB5	O64669 mus musculu
754	4	36.4	362	1	UFED1_YEAST	P53044 saccharomyc	827	4	36.4	380	1	YMH7_CAEEL	O08102 bovine herp
755	4	36.4	362	1	CKRA_HUMAN	P46092 homo sapien	828	4	36.4	380	1	GRK1_ECOLI	P34474 caenorhabd
756	4	36.4	362	1	HUPK_MOUSE	O91121 mus musculu	829	4	36.4	381	1	LYSI_CANAL	P77354 escherichia
757	4	36.4	362	1	HUPK_BRAJA	P48342 bradyrhizob	830	4	36.4	382	1	MSN1_YEAST	P43065 candida alb
758	4	36.4	362	1	RLPA_ECOLI	P10100 escherichia	831	4	36.4	382	1	NU2M_CHLRE	P22148 saccharomyc
759	4	36.4	362	1	ADA_HUMAN	P32779 borrella he	832	4	36.4	382	1	OP53_DROPS	P08740 chlamydomon
760	4	36.4	363	1	AGLK_RHIME	P00813 homo sapien	833	4	36.4	383	1	RA27_YEAST	P28660 drosophila
761	4	36.4	363	1	R23A_HUMAN	O92329 rhizobium m	834	4	36.4	383	1	HOXV_AUCEU	P26793 saccharomyc
762	4	36.4	363	1	R23A_MOUSE	P54725 homo sapien	835	4	36.4	383	1	METR_MYCPN	P31914 alcaligenes
763	4	36.4	363	1	R23A_MOUSE	P54726 mus musculu	836	4	36.4	383	1		P78003 mycoplasma

545	4	36.4	272	1	THIM_BACSU	P39593	bacillus su	618	4	36.4	309	1	CHBX_RHOSH	P95648	rhodobacter
546	4	36.4	273	1	MYBC_MWIZE	P10230	zea mays (m	619	4	36.4	309	1	YESP_HSVU	O31519	bacillus su
547	4	36.4	275	1	APAH_ACTAC	O52655	actinobacil	620	4	36.4	310	1	V084_HSVU	P52534	human herpes
548	4	36.4	275	1	NAD6_ECOLI	P18843	escherichia	621	4	36.4	310	1	EY99_SCHHO	O13771	schizosach
549	4	36.4	275	1	RK2_PICAB	O62954	plcea abies	622	4	36.4	311	1	MENA_BACSU	P35582	bacillus su
550	4	36.4	275	1	TRPD_ARTSF	O17468	artemia san	623	4	36.4	311	1	M1AA_RICR	O96d37	ricketsia
551	4	36.4	277	1	TRFB_DROME	P41900	drosophila	624	4	36.4	312	1	SNAG_HUMAN	O99747	homo sapien
552	4	36.4	277	1	VNST_CVBO	P18517	bovine coro	625	4	36.4	312	1	YAKK_RHISN	P55529	rhizobium s
553	4	36.4	278	1	HUM3_CAEEL	O93356	caenorhabdi	626	4	36.4	314	1	GCR_SHEEP	P35547	ovis aries
554	4	36.4	278	1	HP0J_RHOCA	O03309	rhodobacter	627	4	36.4	314	1	MAG2_HUMAN	P43356	homo sapien
555	4	36.4	279	1	TRT3_RABIT	P02641	oryctolagus	628	4	36.4	314	1	SSAK_SALTU	P74853	salmonella
556	4	36.4	278	1	UDP_KLEPN	P52671	klebsiella	629	4	36.4	315	1	CCP1_ENTHI	O01957	entamoeba h
557	4	36.4	280	1	MSA2_PLAFK	O03643	plasmidium	630	4	36.4	315	1	TSJ1_STRLA	O53608	streptomyces
558	4	36.4	281	1	Y125_MYCPN	P74511	mycoplasma	631	4	36.4	316	1	GBLP_BIOL	O93134	blomphalari
559	4	36.4	282	1	GDA3_WHEAT	P04723	triticum ae	632	4	36.4	316	1	LDH1_PLAD	O27743	plasmidium
560	4	36.4	283	1	T150_ECOLI	P19769	escherichia	633	4	36.4	316	1	YK95_MYCTU	O10704	mycobacteri
561	4	36.4	283	1	Y1FO_ECOLI	P32677	escherichia	634	4	36.4	317	1	3MG_RAT	P23571	rattus norv
562	4	36.4	284	1	DRNL_MOUSE	P49183	mus musculu	635	4	36.4	317	1	AR34_SCHHO	O14241	schizosach
563	4	36.4	284	1	DRNL_RAT	P21704	rattus norv	636	4	36.4	317	1	CBXQ_ALCEU	P40118	alcaligenes
564	4	36.4	284	1	YPV2_METTF	P29571	methanobact	637	4	36.4	317	1	CBXP_ALCEU	O04540	alcaligenes
565	4	36.4	285	1	PARP_ECOLI	P19071	escherichia	638	4	36.4	317	1	CFXQ_XANPL	P23013	xanthobacter
566	4	36.4	285	1	T13B_HUMAN	O9Y275	homo sapien	639	4	36.4	317	1	FLGL_ECOLI	P29744	escherichia
567	4	36.4	286	1	CFXQ_CYACA	O22034	cyanidium c	640	4	36.4	319	1	FMFN_ECOLI	P29131	escherichia
568	4	36.4	286	1	PROC_YEAST	P32263	saccharomyc	641	4	36.4	319	1	YDFC_SCHHO	O14484	schizosach
569	4	36.4	287	1	HI_LICRS	P37218	lycoperisico	642	4	36.4	319	1	YDFC_SCHHO	P34553	bacillus su
570	4	36.4	288	1	PCDI_HUMAN	O15116	homo sapien	643	4	36.4	320	1	LDH_LACPE	P56512	lactobacilli
571	4	36.4	288	1	PHNS_DESGI	P12943	desulfovibr	644	4	36.4	320	1	YDJE_BACSU	P56512	lactobacilli
572	4	36.4	288	1	SUCD_ECOLI	P07459	escherichia	645	4	36.4	320	1	YDJE_BACSU	O34768	bacillus su
573	4	36.4	288	1	VP30_EBOZM	O05323	ebola virus	646	4	36.4	321	1	FLIM_AGRU	O44457	agrobacteri
574	4	36.4	289	1	Y134_MYCTU	O50599	mycobacteri	647	4	36.4	321	1	ISP_BACCS	P23140	bacillus ci
575	4														

399	4	36.4	209	1	RL3_BACHD	092914 bacillus ha	472	4	36.4	242	1	MTGA_KLEPN	048465 klebsiella
400	4	36.4	209	1	RL3_BACSU	P42920 bacillus su	473	4	36.4	242	1	PDXJ_AOUAE	067171 aquifex ae
401	4	36.4	209	1	YC02_KLEPN	P48448 klebsiella	474	4	36.4	242	1	YD05_SCHPO	013725 schizosacch
402	4	36.4	210	1	NIP3_CAEEL	009969 caenorhabdi	475	4	36.4	244	1	SCS2_YEAST	P40075 saccharomyc
403	4	36.4	210	1	YACE_HAEIN	P44520 haemophilus	476	4	36.4	245	1	HI_MAIZE	P23444 zea mays (m
404	4	36.4	210	1	YCFO_ECOLI	P75952 escherichia	477	4	36.4	245	1	YM29_MYCTU	010513 mycobacteri
405	4	36.4	211	1	MAUD_METME	050332 methylophil	478	4	36.4	246	1	HEM4_CHLVI	059335 chlorobium
406	4	36.4	211	1	TUB8_SOLTU	P33191 solanum tub	479	4	36.4	246	1	MTGA_HAEIN	P44690 haemophilum
407	4	36.4	211	1	YFDX_ECOLI	P76520 escherichia	480	4	36.4	246	1	MYF5_COTJA	P34061 coturnix co
408	4	36.4	211	1	YPTS_SCHPO	P36586 schizosacch	481	4	36.4	246	1	YEBF_ECOLI	P24337 escherichia
409	4	36.4	212	1	RERC_ARATH	092417 arabidopsis	482	4	36.4	246	1	YEBF_HAEIN	P44634 haemophilus
410	4	36.4	212	1	RL14_HUMAN	P50914 homo sapien	483	4	36.4	247	1	ATPI_CHLUV	P56295 chlorella v
411	4	36.4	212	1	SODP_VITVI	065199 vitis vinif	484	4	36.4	247	1	C21U_HUMAN	09umt2 homo sapien
412	4	36.4	213	1	HL3_RABIT	P02251 oryctolagus	485	4	36.4	247	1	CFL_RAPSA	012451 raphanus sa
413	4	36.4	213	1	RL14_RAT	063507 rattus norv	486	4	36.4	247	1	GRAB_HUMAN	P10144 h granzyne
414	4	36.4	213	1	RL3_BACST	P28600 bacillus st	487	4	36.4	247	1	YECO_ECOLI	P76290 escherichia
415	4	36.4	213	1	YCFM_ECOLI	P75947 escherichia	488	4	36.4	248	1	AMPW_MYCPN	011132 mycoplasma
416	4	36.4	214	1	YBFT_YEAST	P34222 saccharomyc	489	4	36.4	248	1	DJ_DROME	001352 drosophila
417	4	36.4	214	1	YPUS_RHOCA	P26161 rhodobacter	490	4	36.4	248	1	SOD1_PLEBO	P50058 plectonema
418	4	36.4	215	1	RL25_MYCTU	P96385 mycobacteri	491	4	36.4	249	1	BTUD_ECOLI	P06611 escherichia
419	4	36.4	215	1	RS6_MYCPN	P75543 mycoplasma	492	4	36.4	250	1	YXBO_BACSU	P54854 bacillus su
420	4	36.4	216	1	HIC1_XENLA	P15866 xenopus lae	493	4	36.4	250	1	HXB9_MOUSE	P20615 mus musculu
421	4	36.4	217	1	OTCI_SALTY	008016 salmonella	494	4	36.4	251	1	RA11_ARATH	Q38942 arabidopsis
422	4	36.4	217	1	YB47_YEAST	P38306 saccharomyc	495	4	36.4	252	1	END4_MYCLE	P30770 mycobacteri
423	4	36.4	217	1	YD67_SCHPO	010319 schizosacch	496	4	36.4	252	1	MYBD_MAIZE	P23592 zea mays (m
424	4	36.4	218	1	SCOB_MYCTU	006166 mycobacteri	497	4	36.4	252	1	TRT3_COTJA	P06398 coturnix co
425	4	36.4	219	1	ATPD_CHLRE	042687 chlamydomon	498	4	36.4	253	1	ADP1_DROME	P05552 drosophila
426	4	36.4	219	1	BASP_RAT	005175 rattus norv	499	4	36.4	254	1	PMFD_PROMI	P53520 proteus mir
427	4	36.4	219	1	H1B_XENLA	P06693 xenopus lae	500	4	36.4	255	1	PT22_YEAST	P10355 saccharomyc
428	4	36.4	219	1	P1MT_PYRAB	09uxx0 pyrococcus	501	4	36.4	255	1	RS3A_CANAL	P40910 candida alb
429	4	36.4	220	1	HL3_MOUSE	P43277 mus musculu	502	4	36.4	255	1	SOLA_YEAST	P53315 saccharomyc
430	4	36.4	220	1	HIC2_XENLA	P15867 xenopus lae	503	4	36.4	255	1	TONB_YEREN	005740 yeastinia en
431	4	36.4	221	1	HIC_CHITE	P40277 chironomus	504	4	36.4	256	1	Y166_METJA	057630 methanococc
432	4	36.4	222	1	CASB_CAPHI	P33048 capra hircu	505	4	36.4	256	1	CB22_SORYN	P09355 glycine max
433	4	36.4	222	1	CASB_SHEEP	P11839 ovis aries	506	4	36.4	256	1	FIXA_ECOLI	P31373 escherichia
434	4	36.4	223	1	AOP2_RAT	035244 r antioxi	507	4	36.4	256	1	TATC_HAEIN	P44560 haemophilus
435	4	36.4	223	1	VTAT_LAMB	P03730 bacterioph	508	4	36.4	257	1	BF41_MOUSE	P28565 mus musculu
436	4	36.4	224	1	CASB_BOVIN	P02666 bos taurus	509	4	36.4	257	1	MODA_ECOLI	P33729 escherichia
437	4	36.4	224	1	RL4_CHLPN	092798 chlamydia p	510	4	36.4	257	1	TRT3_HUMAN	P45728 homo sapien
438	4	36.4	226	1	BASP_BOVIN	P80724 bos taurus	511	4	36.4	258	1	MYP5_CHICK	008856 gallus gall
439	4	36.4	226	1	BASP_HUMAN	P80723 homo sapien	512	4	36.4	258	1	TRT3_RAT	P09373 rattus norv
440	4	36.4	228	1	HS30_NEUCR	P19752 neuropept	513	4	36.4	258	1	UL49_HSVBC	P30022 bovine herp
441	4	36.4	228	1	LEXA_RHOSE	09ztia4 rhodobacter	514	4	36.4	260	1	1433_PEA	P46366 plasmu saliv
442	4	36.4	229	1	RNS6_PYRPP	080324 pyrus pyrif	515	4	36.4	260	1	MTKB_METEX	P53595 methyllobact
443	4	36.4	229	1	SRY_BISBO	027949 bison bonas	516	4	36.4	260	1	TNFS_CANFA	097625 canis fami
444	4	36.4	229	1	SRY_BOVIN	003255 bos taurus	517	4	36.4	260	1	TNFS_FELCA	097605 felis silve
445	4	36.4	230	1	CPSB_STRAG	004662 streptococc	518	4	36.4	260	1	UPB8_BACSU	031751 bacillus su
446	4	36.4	231	1	HL_CHITH	P21895 chironomus	519	4	36.4	260	1	VP33_APLCA	Q16943 aplysia cal
447	4	36.4	231	1	NU4M_BOTLA	003700 bothriechis	520	4	36.4	260	1	YK07_YEAST	P36639 saccharomyc
448	4	36.4	232	1	CASB_CAMDR	09tvd0 camelus dro	521	4	36.4	261	1	RS4_DROME	P41442 drosophila
449	4	36.4	232	1	CASH_PIG	P39037 sus scrofa	522	4	36.4	261	1	YK83_CAEEL	P34349 caenorhabdi
450	4	36.4	232	1	CYSH_SYNP7	055309 synchococc	523	4	36.4	261	1	Y182_CAEEL	P34440 caenorhabdi
451	4	36.4	232	1	HL2_GLYBA	P40264 glyptotendi	524	4	36.4	262	1	CORT_SHVX	004572 shalioct vit
452	4	36.4	232	1	HLA_CHITE	P40275 chironomus	525	4	36.4	262	1	FDHD_BACSU	P39756 bacillus su
453	4	36.4	232	1	H1B_CHITE	P40276 chironomus	526	4	36.4	262	1	TRT3_CHICK	P12620 gallus gall
454	4	36.4	232	1	TONB_CAMCO	007650 campylobact	527	4	36.4	264	1	MSA2_PLAUF	P19599 plasmodium
455	4	36.4	233	1	HL1_GLYBA	P40263 glyptotendi	528	4	36.4	264	1	MSA2_PLAUF	P50499 plasmodium
456	4	36.4	233	1	HL1_GLYSA	P40266 glyptotendi	529	4	36.4	264	1	OTP_DROME	P56672 drosophila
457	4	36.4	233	1	SN64_MOUSE	092112 mus musculu	530	4	36.4	266	1	REF2_RAT	063528 rattus norv
458	4	36.4	234	1	ARGR_HUMAN	P55145 homo sapien	531	4	36.4	267	1	MM21_YEAST	P38633 saccharomyc
459	4	36.4	234	1	SN64_HUMAN	095473 homo sapien	532	4	36.4	267	1	FKBA_AERYH	P47403 mycoplasma
460	4	36.4	234	1	YER0_YEAST	P40011 saccharomyc	533	4	36.4	268	1	EXBD_SYNY3	008437 aeromonas h
461	4	36.4	234	1	YGIB_ECOLI	P24195 escherichia	534	4	36.4	269	1	PIR5_PREDI	P72942 synchocyst
462	4	36.4	235	1	Y101_YEAST	P40449 saccharomyc	535	4	36.4	269	1	PIR5_PREDI	P11401 firemyella d
463	4	36.4	235	1	PDXJ_AOUPI	P46212 aquifex pyr	536	4	36.4	270	1	FKBA_ECOLI	P45523 escherichia
464	4	36.4	237	1	DCOP_LACPL	P77888 lactobacill	537	4	36.4	270	1	ISPD_STRCO	Q91098 streptomyce
465	4	36.4	237	1	HETI_ANASP	P37695 anabaena sp	538	4	36.4	270	1	PANB_HELPY	Q92598 helicobacte
466	4	36.4	238	1	RK5_ODOSI	P49547 odontella s	539	4	36.4	270	1	PEAZ_HUMAN	025698 helicobacte
467	4	36.4	238	1	Y939_HAEIN	P44080 haemophilus	540	4	36.4	270	1	PEAZ_HUMAN	P15927 homo sapien
468	4	36.4	240	1	H12_VOICA	008865 volvox cart	541	4	36.4	270	1	REF2_MOUSE	062193 mus musculu
469	4	36.4	240	1	SFSA_METH	027565 methanobact	542	4	36.4	271	1	YD11_SCHPO	010247 schizosacch
470	4	36.4	241	1	SPIR_SPIME	P21635 spiroplasma	543	4	36.4	271	1	DJ1A_ECOLI	P31680 escherichia
471	4	36.4	242	1	MTGA_ECOLI	P46022 escherichia	544	4	36.4	271	1	VA04_VARV	P33832 variola vir

253	4	36.4	133	1	RCSF_ECOLI	P28633	escheric	326	4	36.4	172	1	RL10_BRUAB	P41107	bruce
254	4	36.4	134	1	ANFB_HUMAN	P16860	homo sap	327	4	36.4	173	1	Y013_BPHN1	P51715	bacteri
255	4	36.4	137	1	H2B4_MAIZE	P42120	zea mays (m	328	4	36.4	175	1	OLE2_BRANA	P29111	brassica
256	4	36.4	138	1	GRIM_DROME	O24570	droso	329	4	36.4	176	1	AROK_MYCTU	P55014	mycobact
257	4	36.4	139	1	THI2_ECOLI	P3636	escheric	330	4	36.4	176	1	ET2_RAT	P23943	rattus norv
258	4	36.4	140	1	18K2_MYCT	P46732	mycobact	331	4	36.4	177	1	IMP2_YEAST	P46972	saccharomyc
259	4	36.4	140	1	HYPI_PIST1	P52748	pisolithus	332	4	36.4	178	1	ET2_HUMAN	P20800	homo sap
260	4	36.4	140	1	YOIB_ECOLI	P36652	escheric	333	4	36.4	179	1	RK6_GUTH	O46908	quillardi
261	4	36.4	141	1	NEUV_RANES	P11858	rana escul	334	4	36.4	184	1	GRPE_CHLPN	O92484	chlamydia p
262	4	36.4	141	1	YO10_MYCTU	P15580	mycobact	335	4	36.4	184	1	LSPA_MYCPN	P54478	mycoplasma
263	4	36.4	141	1	ZRAP_ECOLI	P36682	escheric	336	4	36.4	184	1	NOSG_THERP	P35878	thermus aqu
264	4	36.4	142	1	H2AX_HUMAN	P16104	homo sap	337	4	36.4	184	1	YK17_YEAST	O02205	saccharomyc
265	4	36.4	142	1	H2AX_MOUSE	P27661	mus muscu	338	4	36.4	185	1	KAD_SYNY3	P23302	synecocyst
266	4	36.4	142	1	HBAA_ANGAN	P80945	anguilla an	339	4	36.4	185	1	RM05_MARPO	P26786	marichanta
267	4	36.4	143	1	CMG4_BACSU	P25956	bacillus su	340	4	36.4	186	1	YBAY_ECOLI	P27717	saccharomyc
268	4	36.4	143	1	LG81_VICRA	P02232	vicia faba	341	4	36.4	186	1	MLE1_MUGCA	P62159	muiggli capit
269	4	36.4	143	1	VLI_BPV3	P50805	bovine pap	342	4	36.4	186	1	RL18_YEAST	P07279	saccharomyc
270	4	36.4	143	1	VLI1_ADE41	P23688	human adeno	343	4	36.4	187	1	RL18_ARATH	P42791	arabidops
271	4	36.4	144	1	CORA_MOUSE	O62266	mus muscu	344	4	36.4	188	1	RM05_MARPO	P6860	marichanta
272	4	36.4	145	1	H2B_CAPAN	O49118	capsicum an	345	4	36.4	189	1	RS7A_YEAST	P26786	saccharomyc
273	4	36.4	146	1	SODM_STRPA	O33756	streptococ	346	4	36.4	190	1	YBAY_ECOLI	P27717	saccharomyc
274	4	36.4	146	1	PUR_HAETI	P4561	haemophilus	347	4	36.4	190	1	YCH3_SCHPO	P7885	escheric
275	4	36.4	146	1	YIAC_ECOLI	P37664	escheric	348	4	36.4	191	1	EX01_RHIME	O32928	rhizobium m
276	4	36.4	147	1	CYPA_CAEEL	P52017	caenorhabd	349	4	36.4	191	1	PGHD_SHEEP	O49414	xenopus lae
277	4	36.4	147	1	H2B_GOSHI	O25582	gossypium h	350	4	36.4	191	1	SDC2_XENLA	P49414	xenopus lae
278	4	36.4	147	1	RL13_MYCLE	P38014	mycobact	351	4	36.4	191	1	YGL2_STRCO	P40182	streptomyc
279	4	36.4	147	1	RL13_MYCTU	O06260	mycobact	352	4	36.4	192	1	UBC1_CAEEL	P52478	caenorhabd
280	4	36.4	150	1	H2B2_MAIZE	P30756	zea mays (m	353	4	36.4	192	1	VG49_BPMO2	O64239	mycobact
281	4	36.4	150	1	NNA4_BPT3	P20313	ze mays (m	354	4	36.4	193	1	H10_HUMAN	P07303	homo sap
282	4	36.4	150	1	NNA4_BPT7	P08086	bacterioph	355	4	36.4	193	1	VANI_VIBAN	P74945	vibrio angu
283	4	36.4	150	1	TAAI_VACC	P20982	vaccinia vi	356	4	36.4	193	1	Y455_METJA	O57897	methanococ
284	4	36.4	150	1	TAI1_VACCV	P07610	vaccinia vi	357	4	36.4	194	1	H1_SALT	P02254	salmo trutt
285	4	36.4	150	1	TAAL_VARY	P33814	vario	358	4	36.4	194	1	MEV_HUMAN	P08590	homo sap
286	4	36.4	150	1	VAO2_SCHRO	O10081	schizosacch	359	4	36.4	195	1	COAG_LIMPO	P03099	limulus pol
287	4	36.4	151	1	H2B1_MAIZE	P30755	zea mays (m	360	4	36.4	196	1	ANOD_ARCFU	O30011	archaeoglob
288	4	36.4	151	1	RBSD_ECOLI	P04982	escheric	361	4	36.4	196	1	MOBA_STACA	O08116	staphylococ
289	4	36.4	151	1	SYRB_RHIME	O33685	rhizobium m	362	4	36.4	196	1	RGS1_HUMAN	O08116	homo sap
290	4	36.4	152	1	ADOM_BPT3	P07693	bacterioph	363	4	36.4	196	1	TRAP_ECOLI	P41066	escheric
291	4	36.4	152	1	CORA_RAT	O63532	rattus norv	364	4	36.4	197	1	SDC4_CHICK	P49416	gallus gall
292	4	36.4	152	1	H2B1_MHEAT	P27807	triticum ae	365	4	36.4	197	1	WRBA_ECOLI	P30844	escheric
293	4	36.4	153	1	CORB_MOUSE	O62267	mus muscu	366	4	36.4	197	1	YI01_MYCTU	O07723	mycobact
294	4	36.4	153	1	H2B3_MAIZE	O43261	zea mays (m	367	4	36.4	198	1	CSP_BOVIN	O29455	bos taurus
295	4	36.4	153	1	PYRI_SERMA	P19936	seratila ma	368	4	36.4	198	1	NDUC_EMENT	P54101	mus muscu
296	4	36.4	154	1	H2B5_MAIZE	P54348	zea mays (m	369	4	36.4	198	1	NIDC4_MOUSE	P17624	emerice
297	4	36.4	155	1	YFH3_YEAST	P43587	saccharomyc	370	4	36.4	198	1	SDC4_HUMAN	P31431	homo sap
298	4	36.4	156	1	RU2B_HUMAN	P29316	homo sap	371	4	36.4	198	1	SDC4_MOUSE	O35988	mus muscu
299	4	36.4	157	1	RAP_TAROF	O49065	taraxacum o	372	4	36.4	198	1	YH13_YEAST	P38596	saccharomyc
300	4	36.4	157	1	RL24_HUMAN	P38663	homo sap	373	4	36.4	198	1	YH8G_PSEBU	P20162	pseudomonas
301	4	36.4	157	1	YM75_YEAST	O05027	saccharomyc	374	4	36.4	199	1	DS22_CRAPL	O01931	craterosifig
302	4	36.4	158	1	ILVH_BUCAI	P57320	buchnera ap	375	4	36.4	199	1	MLEV_RAT	P10765	toxodonta a
303	4	36.4	158	1	ILVH_BUCAP	O85294	buchnera ap	376	4	36.4	199	1	PRL_TOXAF	P10765	toxodonta a
304	4	36.4	159	1	DRR1_PEA	P12329	pisum sativ	377	4	36.4	199	1	PSBQ_CHURE	P12852	chlamydomon
305	4	36.4	160	1	ET2_MOUSE	P22389	mus muscu	378	4	36.4	201	1	GDIS_HUMAN	P32566	homo sap
306	4	36.4	160	1	RL10_METH	O27191	methanobact	379	4	36.4	201	1	IF3_MYCTU	P4975	mycobact
307	4	36.4	160	1	VLPC_MYCHR	P29230	mycoplasma	380	4	36.4	201	1	SDC2_HUMAN	P34741	homo sap
308	4	36.4	161	1	CAMP_BRAFL	O01305	branchiosto	381	4	36.4	201	1	SDC2_RAT	P34900	rattus norv
309	4	36.4	161	1	CAVP_BRAVA	P04573	branchiosto	382	4	36.4	201	1	YKDO_YEAST	P36099	saccharomyc
310	4	36.4	161	1	H33_HORVU	P19348	hordeum vul	383	4	36.4	201	1	YPT1_PHYTN	O01890	phytocthor
311	4	36.4	161	1	HS13_ARATH	P19037	arabidops	384	4	36.4	202	1	SDC2_MOUSE	P43407	mus muscu
312	4	36.4	162	1	GVPI1_HALME	O02234	halobacteri	385	4	36.4	202	1	SDC4_RAT	P34901	rattus norv
313	4	36.4	162	1	YB09_SCHPO	P87150	schizosacch	386	4	36.4	202	1	YIC2_AGRRH	P13460	agrobacteri
314	4	36.4	163	1	GSPM_AERHY	P41850	aeromonas h	387	4	36.4	202	1	YGE7_YEAST	P53178	saccharomyc
315	4	36.4	163	1	NTEB_HERSE	P27714	herbaspil	388	4	36.4	203	1	BCRC_BACLI	P42333	bacillus li
316	4	36.4	164	1	PTPA_STRCO	P53433	streptomyc	389	4	36.4	203	1	HYCB_ECOLI	P16428	escheric
317	4	36.4	164	1	Y400_SYNY3	O35129	synecocyst	390	4	36.4	204	1	VATD_BORBU	O51119	bortetia bu
318	4	36.4	167	1	PLMP_GRIFF	P81054	grifolia fto	391	4	36.4	204	1	YMA4_CAEEL	P34449	caenorhabd
319	4	36.4	167	1	TCCTP_YEAST	P35691	saccharomyc	392	4	36.4	206	1	AMIS_RHOER	O33185	rhodococcus
320	4	36.4	167	1	YVGS_YEAST	P40366	saccharomyc	393	4	36.4	206	1	HI_ONCMY	P06350	oncorhynch
321	4	36.4	168	1	GLP_MOUSE	P14220	mus muscu	394	4	36.4	206	1	KAD_AQUAE	O66499	aquifex ae
322	4	36.4	169	1	GLP_MOUSE	P14220	mus muscu	395	4	36.4	207	1	COX3_BACSU	P24012	macaca mla
323	4	36.4	171	1	IF3_BACST	O15589	homo sap	396	4	36.4	207	1	HIT_MACMO	P40286	bacillus su
324	4	36.4	171	1	Y008_CAEEL	P34646	caenorhabd	397	4	36.4	208	1	FTS0_STRGR	P5503	streptomyc
325	4	36.4	172	1	ILVH_METJA	O57625	methanococ	398	4	36.4	208	1	V23K_PEBV	P16261	pea early b

107	5	45.5	714	1	FRDA_HELIPY	006913	helicobacte	180	4	36.4	105	1	APL1_PETMA	P07095	petromyzon
108	5	45.5	766	1	DAB2_MOUSE	P98078	mus musculu	181	4	36.4	105	1	LAC_HUMAN	P01442	homo sapien
109	5	45.5	770	1	DAB2_HUMAN	P98082	homo sapien	182	4	36.4	105	1	THIO_RHOSH	P08058	rhodobacter
110	5	45.5	788	1	IF41_WHEAT	003387	tritricum ae	183	4	36.4	105	1	VPR_HV2D1	P17761	human immun
111	5	45.5	800	1	INLA_LISMO	P25166	listeria mo	184	4	36.4	105	1	VPR_HV2G1	P18046	human immun
112	5	45.5	883	1	IMB1_SCPPO	013864	schizosacch	185	4	36.4	105	1	VPR_HV2N2	P05930	human immun
113	5	45.5	893	1	YM92_CAEEL	P34531	caenorhabdi	186	4	36.4	105	1	VPR_HV2RO	P06938	human immun
114	5	45.5	894	1	KDPD_ECOLI	P21865	escherichia	187	4	36.4	105	1	Y027_MYCTU	P71597	mycobacteri
115	5	45.5	1027	1	ISWI_DROME	024368	drosoophila	188	4	36.4	105	1	YIF4_YEAST	P40524	saccharomyc
116	5	45.5	1040	1	MAN1_RAT	P21139	rattus norv	189	4	36.4	107	1	COL_RABIT	P42890	oryctolagus
117	5	45.5	1051	1	ULK1_MOUSE	070405	mus musculu	190	4	36.4	108	1	KVIR_HUMAN	P01610	homo sapien
118	5	45.5	1061	1	RNE_ECOLI	P21513	escherichia	191	4	36.4	108	1	THIO_ECOLI	P00274	escherichia
119	5	45.5	1070	1	AGLO_CANTS	P29054	candida tsu	192	4	36.4	109	1	LVH1_HUMAN	P06888	homo sapien
120	5	45.5	1218	1	MGPC_MYCPN	050341	mycoplasma	193	4	36.4	109	1	NUOM_BOVIN	P25712	homo sapien
121	5	45.5	1301	1	PTP9_DROME	P35832	drosoophila	194	4	36.4	109	1	VP26_BRAPS	091352	bacterioph
122	5	45.5	1403	1	PRO_DROME	P29617	drosoophila	195	4	36.4	111	1	IM98_CAEEL	091092	caenorhabdi
123	5	45.5	1552	1	TP2A_CHICK	042130	gallus gall	196	4	36.4	111	1	LVIC_HUMAN	P01701	homo sapien
124	5	45.5	1612	1	TP2B_CHILO	064399	criceulius	197	4	36.4	111	1	LVID_HUMAN	P01702	homo sapien
125	5	45.5	1612	1	TP2B_MOUSE	064511	mus musculu	198	4	36.4	111	1	LV2H_HUMAN	P01711	homo sapien
126	5	45.5	1663	1	HAPP_HUMAN	060229	homo sapien	199	4	36.4	112	1	COL_CANFA	P19090	cantis fami
127	5	45.5	1919	1	HAPP_RAT	P97924	rattus norv	200	4	36.4	112	1	LV1B_HUMAN	P01700	homo sapien
128	5	45.5	2134	1	Y192_HUMAN	093074	homo sapien	201	4	36.4	112	1	LV1H_HUMAN	P06887	homo sapien
129	5	45.5	2278	1	FAB1_YEAST	P34756	saccharomyc	202	4	36.4	113	1	KV2F_MOUSE	P01630	mus musculu
130	5	45.5	4358	1	DYHC_CAEEL	019020	caenorhabdi	203	4	36.4	113	1	RSBV_STRCO	Q9VWX8	streptomyce
131	5	45.5	34	1	PYSB_METBA	P80522	methanosarc	204	4	36.4	113	1	SS12_STRRO	P29607	streptomyce
132	4	36.4	35	1	NEUY_ONCMY	Q10726	pandinus im	205	4	36.4	114	1	RK20_CHLVU	P56352	chlorella v
133	4	36.4	36	1	SCKG_PANIM	P29071	oncorhynch	206	4	36.4	114	1	RSBV_LISMO	085016	listeria mo
134	4	36.4	51	1	MLEY_MOUSE	P09542	mus musculu	207	4	36.4	114	1	YHIT_BUCAI	P57483	buchnera ap
135	4	36.4	56	1	VG36_BPMD2	022001	mycobacteri	208	4	36.4	116	1	ANSR_BACSU	007683	bacillus su
136	4	36.4	67	1	VPR_HV2B2	P51772	bacterioph	209	4	36.4	116	1	MCS_HUMAN	P49901	homo sapien
137	4	36.4	70	1	FMFL_AERHY	P19369	aeromonas h	210	4	36.4	116	1	RLJ3_CHLRE	P45841	chlamydomon
138	4	36.4	70	1	PSAE_NOSS8	Q9W911	nostoc sp.	211	4	36.4	117	1	RLJ3_CHLRE	P22992	chlamydomon
139	4	36.4	75	1	YEIL_ECOLI	P33921	escherichia	212	4	36.4	117	1	AMC2_PIG	046204	chlamydia p
140	4	36.4	79	1	ET2_MACRA	Q28470	macaca fasc	213	4	36.4	117	1	YVIO_CAEEL	P34485	caenorhabdi
141	4	36.4	81	1	HEMP_YEREN	P31516	yersinia en	214	4	36.4	118	1	ELI1_PHYCR	P41892	phytophthor
142	4	36.4	81	1	RLJ3_MERTH	027649	methanobact	215	4	36.4	118	1	ELI1_PHYCR	P15570	phytophthor
143	4	36.4	83	1	MULI_PSEAE	P12221	pseudomonas	216	4	36.4	118	1	ELI1_PHYCR	P41801	phytophthor
144	4	36.4	83	1	VPP_BPMD2	P27331	bacterioph	217	4	36.4	118	1	LHG2_RHOCA	P23430	rhodobacter
145	4	36.4	83	1	Y9KD_BPMD2	P19195	bacterioph	218	4	36.4	118	1	RL7_MICLU	P02395	micrococcu
146	4	36.4	85	1	COXG_BOVIN	P00429	bos taurus	219	4	36.4	119	1	B2MG_CHISA	077552	chitropotes
147	4	36.4	85	1	YRBA_HAETN	P45026	haemophilus	220	4	36.4	119	1	PA21_OXYS	P00614	oxytarranus s
148	4	36.4	87	1	TAT_CAEVG	P21125	caprine art	221	4	36.4	119	1	YEAR_ECOLI	P76248	escherichia
149	4	36.4	87	1	VPR_HV2BE	P18100	human immun	222	4	36.4	120	1	RLJ3_NICGU	P46290	nicotiana g
150	4	36.4	87	1	YN55_CAEEL	P34589	caenorhabdi	223	4	36.4	120	1	RLJ3_PICMA	065071	picea maria
151	4	36.4	89	1	RS15_PSEPU	087151	pseudomonas	224	4	36.4	120	1	RL34_ARATH	042331	arabidopsis
152	4	36.4	90	1	HEO_HAETN	P44437	haemophilus	225	4	36.4	121	1	AMEL_ORMAN	097646	ornithothyrn
153	4	36.4	90	1	TEGP_HSVSB	P30025	simlan heip	226	4	36.4	121	1	H2B1_TERTH	P08993	tetrahymena
154	4	36.4	91	1	VE4_HPV58	P26349	human papil	227	4	36.4	121	1	H2B2_TERTH	P08994	tetrahymena
155	4	36.4	94	1	RUXE_YEAST	Q12330	saccharomyc	228	4	36.4	122	1	RL14_SYNY3	P73310	synecocyst
156	4	36.4	95	1	ADXX_DROME	P37193	dirosophila	229	4	36.4	123	1	ELI2_PHYCR	P41803	phytophthor
157	4	36.4	95	1	SM32_HUMAN	P55855	homo sapien	230	4	36.4	123	1	Y944_METJA	058359	methanococc
158	4	36.4	97	1	CSOA_THINE	P45689	thiobacteri	231	4	36.4	124	1	RL7_BORBU	051353	borrella bu
159	4	36.4	97	1	VG45_BPMD5	Q05256	mycobacteri	232	4	36.4	124	1	RL7_BORBU	P41106	bruceella ab
160	4	36.4	98	1	COXB_BOVIN	P00428	bos taurus	233	4	36.4	125	1	PSAE_SPTOL	P12334	splachia ol
161	4	36.4	98	1	CSOC_THINE	P45688	thiobacteri	234	4	36.4	125	1	RP09_SCHPO	009171	schizosacch
162	4	36.4	98	1	ELIA_PHYCP	P15571	phytophthor	235	4	36.4	125	1	RS6_CAMEE	Q09213	campylobact
163	4	36.4	98	1	ELIA_PHYDR	P35696	phytophthor	236	4	36.4	125	1	Y364_AQUAE	066689	aquiflex aeo
164	4	36.4	98	1	ELIA_PHYME	P35668	phytophthor	237	4	36.4	125	1	Y944_HELPT	P46964	saccharomyc
165	4	36.4	98	1	ELIB_PHYCI	P15569	phytophthor	238	4	36.4	125	1	Y944_HELPT	025558	helicobacte
166	4	36.4	98	1	ELIB_PHYDR	P35687	phytophthor	239	4	36.4	126	1	US05_HCMVA	P16840	human cytom
167	4	36.4	98	1	ELIB_PHYME	P35699	phytophthor	240	4	36.4	127	1	RL20_STRCO	088008	streptomyce
168	4	36.4	100	1	V07K_NMY	P15098	narcissus m	241	4	36.4	128	1	HISX_AZOBR	P18766	azospirillum
169	4	36.4	100	1	FLIO_ECOLI	P22586	escherichia	242	4	36.4	129	1	LVIX_HUMAN	P04432	homo sapien
170	4	36.4	101	1	LSM3_HUMAN	094419	homo sapien	243	4	36.4	129	1	OSTE_YEAST	P61964	saccharomyc
171	4	36.4	101	1	VG25_BPMD2	064219	mycobacteri	244	4	36.4	130	1	LVIG_HUMAN	P06316	homo sapien
172	4	36.4	101	1	VG25_BPMD5	Q05232	mycobacteri	245	4	36.4	130	1	YHLD_YEAST	P38793	saccharomyc
173	4	36.4	101	1	Y0XC_BACSU	P28670	bacillus su	246	4	36.4	131	1	DFRA_MYXXA	052178	myxococcus
174	4	36.4	102	1	MODX_RHLIT	052846	rhizobium 1	247	4	36.4	131	1	FRDC_ECOLI	P02093	proteus vul
175	4	36.4	103	1	LVIE_HUMAN	P01703	homo sapien	248	4	36.4	131	1	ILI3_MOUSE	P20109	mus musculu
176	4	36.4	103	1	SM31_HUMAN	P55854	homo sapien	249	4	36.4	132	1	TLA_CANFA	077782	canis fami
177	4	36.4	104	1	VGU3_YEAST	P53097	saccharomyc	250	4	36.4	132	1	TV42_MOUSE	R01729	mus musculu
178	4	36.4	104	1	VPR_HV2CA	P24111	human immun	251	4	36.4	132	1	Y035_ARCFU	030161	archaeoglob
179	4	36.4	104	1	VPR_HV2ST	P20884	human immun	252	4	36.4	132	1			

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:42:54 ; Search time 20.38 seconds
(without alignments)
18.489 Million cell updates/sec

Title: US-09-372-036-29

Perfect score: 11

Sequence: 1 QOQTAPKAPTE 11

Scoring table: OLIGO

Searched: 93435 seqs, 3425486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	11	100.0	P60_LISMO	P21171 listeria mo
2	6	54.5	P53_SPEBE	Q64662 spermophilu
3	6	54.5	P53_MARMO	Q36006 maroma mon
4	6	54.5	IF2_SYNY3	P72689 synchocyst
5	6	54.5	NFC2_MOUSE	Q60591 mus musculu
6	6	54.5	RPRO_SMYEA	P28897 strawberry
7	6	54.5	ANT1_ONCYO	P21249 onchocerca
8	5	45.5	GSP1_AERYH	P31737 aeromonas h
9	5	45.5	CU19_ARADI	P80515 araneus dia
10	5	45.5	H2B_HOLVU	P48557 holothuria
11	5	45.5	WN3A_HOLVU	P28101 alopias vul
12	5	45.5	WN3A_MELGA	P28125 melagris g
13	5	45.5	WN3A_SCEOC	P28142 sceloporius
14	5	45.5	CU24_ARADI	P80516 araneus dia
15	5	45.5	CU26_ARADI	P80517 araneus dia
16	5	45.5	ULB0_HCMVA	P16830 human cytom
17	5	45.5	MSCL_HAETN	P44789 haemophilus
18	5	45.5	CYC3_DESYH	P00131 desulfovibr
19	5	45.5	CYC3_DESYA	P00132 desulfovibr
20	5	45.5	Y142_LEUMC	P97117 leuconostoc
21	5	45.5	Y147_CAEEL	Q11074 caenorhabdi
22	5	45.5	DH1_HORVU	P12951 hordeum vul
23	5	45.5	GP27_BPSP1	P06228 bacterioph
24	5	45.5	FLUN_PSEAB	Q51466 pseudomonas
25	5	45.5	H1_DICDI	P54671 dictyostell
26	5	45.5	YPOL_THETL	P32438 thermus aqu
27	5	45.5	NOO9_THETL	Q56224 thermus aqu
28	5	45.5	IF3_PSEPL	Q95627 pseudomonas
29	5	45.5	IF3_PSESY	P52834 pseudomonas
30	5	45.5	H12_CAEEL	P15736 mycoplasma
31	5	45.5	Y319_MYCPN	Q02196 saccharomyc
32	5	45.5	KAP5_YEAST	P43412 yersinia en
33	5	45.5	KAD_YEREN	

34	5	45.5	214	1	KAD_YERPE	069172 yersinia pe
35	5	45.5	223	1	TONB_XANCP	Q34261 xanthomonas
36	5	45.5	231	1	NAPG_ECOLI	P33936 escherichia
37	5	45.5	235	1	HIE_CHIPA	P40262 chironomus
38	5	45.5	236	1	H1_WHEAT	P27806 triticum ae
39	5	45.5	237	1	HIE_CHITE	P40278 chironomus
40	5	45.5	239	1	OPAA_NEIGO	Q04876 neisseria g
41	5	45.5	241	1	NOCM_AGRU	P33113 agrobacteri
42	5	45.5	244	1	H1O_CHITH	Q07134 chironomus
43	5	45.5	252	1	NDOE_MYCTU	P95177 mycobacteri
44	5	45.5	259	1	HXC9_FUGRU	Q42502 fugu rubrip
45	5	45.5	260	1	H11_VOLCA	Q08864 volvox cart
46	5	45.5	279	1	THET_THEVU	P04072 thermactin
47	5	45.5	280	1	LXLI_HUMAN	P52954 homo sapien
48	5	45.5	288	1	LIPH_PSEAN	Q01725 pseudomonas
49	5	45.5	292	1	CDG3_HUMAN	P30281 homo sapien
50	5	45.5	296	1	SMDF_HUMAN	Q15491 homo sapien
51	5	45.5	298	1	XERC_ECOLI	P22885 escherichia
52	5	45.5	300	1	XERC_SALTY	P55888 salmonella
53	5	45.5	313	1	DRPE_CRAPL	P22242 craterostig
54	5	45.5	316	1	MANA_STRMU	O59935 streptococ
55	5	45.5	318	1	KITH_FLVD	P22176 fish lympho
56	5	45.5	319	1	SSUA_ECOLI	P75853 escherichia
57	5	45.5	320	1	TAUA_ECOLI	Q47537 escherichia
58	5	45.5	320	1	YD33_YEAST	Q12117 saccharomyc
59	5	45.5	321	1	Y377_MYCTU	O53712 mycobacteri
60	5	45.5	325	1	CYF_STNP2	P28293 synchococ
61	5	45.5	332	1	SR4_PHYPO	P11113 physarum po
62	5	45.5	340	1	LIMA_PSEAE	Q04591 pseudomonas
63	5	45.5	341	1	VP3_GELV	P17768 grapevine f
64	5	45.5	343	1	CAG4_PIG	Q02745 s cmp-n-ace
65	5	45.5	362	1	ILVC_LACLA	Q00138 lactococcus
66	5	45.5	380	1	YCHE_HAETN	P44681 haemophilus
67	5	45.5	380	1	VASP_HUMAN	P50552 homo sapien
68	5	45.5	398	1	DAP3_HUMAN	P51398 homo sapien
69	5	45.5	398	1	RA23_YEAST	P32628 saccharomyc
70	5	45.5	414	1	KAS2_STRHA	Q05357 streptomyce
71	5	45.5	415	1	KAS2_STRVN	P16541 streptomyce
72	5	45.5	448	1	PSA4_SCHPO	P36612 schizosacch
73	5	45.5	451	1	WORD_BACSU	Q03522 bacillus su
74	5	45.5	457	1	ODR7_CAEEL	P51933 caenorhabdi
75	5	45.5	470	1	DAX1_HUMAN	P41843 homo sapien
76	5	45.5	474	1	P2X2_CAVPO	O70397 cavia porce
77	5	45.5	479	1	PK2_DICDI	P28178 dictyostell
78	5	45.5	481	1	P60_LISIN	Q01836 listeria in
79	5	45.5	485	1	OPRM_PSEAE	O01487 pseudomonas
80	5	45.5	493	1	PDI_CHICK	P09102 gallus gall
81	5	45.5	508	1	GSPB_CHICK	P12244 gallus gall
82	5	45.5	508	1	PDI_HUMAN	P07237 homo sapien
83	5	45.5	509	1	PDI_MOUSE	P09103 mus musculu
84	5	45.5	509	1	PDI_RABIT	P21195 oryctolagus
85	5	45.5	509	1	PDI_RAT	P04785 rattus norv
86	5	45.5	510	1	BMP6_MOUSE	P207072 mus musculu
87	5	45.5	510	1	PDI_BOVIN	P05307 bos taurus
88	5	45.5	520	1	CP84_ARATH	Q42600 arabidopsi
89	5	45.5	523	1	P60_LISSE	Q01838 listeria se
90	5	45.5	524	1	P60_LISWE	Q01839 listeria we
91	5	45.5	537	1	CNE3_HUMAN	O75131 homo sapien
92	5	45.5	546	1	RUB1_BRANA	P10406 drosophila
93	5	45.5	550	1	CCE_DROME	Q13046 mycobacteri
94	5	45.5	553	1	ODO2_MYCTU	P38707 saccharomyc
95	5	45.5	554	1	SYNC_YEAST	O54465 shewanella
96	5	45.5	557	1	MERA_SHEBU	P23795 bos taurus
97	5	45.5	583	1	ACES_BOVIN	Q09144 yarrowia il
98	5	45.5	584	1	YMB3_YEAST	P54929 azospirillum
99	5	45.5	598	1	PEX5_YARLI	P04408 haemophilus
100	5	45.5	624	1	NIFA_AZOLI	P17412 wolfinella s
101	5	45.5	637	1	DNAK_ECOLI	O03185 giardia lam
102	5	45.5	638	1	YHES_HAETN	P33720 human papil
103	5	45.5	656	1	FRDA_WOLSU	Q95mpo helicobacte
104	5	45.5	667	1	TS11_GIALA	
105	5	45.5	681	1	VEL_HPV10	
106	5	45.5	714	1	FRDA_HELPJ	

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C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
A>Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
F:80-85/Region: nucleotide-binding motif B #status atypical

F:126/Active site: His #status predicted

Query Match

Best Local Similarity 45.5%; Score 5; DB 2; Length 214;
Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAP 6

DB 173 QOTAP 177

RESULT 50

T38907

hypothetical protein SPAC56E4.05 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000

C:Accession: T38907

R:Conor, R.; Church, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997

A:Reference number: Z21813

A:Accession: T38907

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-216 <CON>

A:Cross-references: EMBL:Z99261; PIDN:CAB16396.1; GSPDB:GN00066; SPDB:SPAC56E4.05

A:Experimental source: strain 972h; cosmid c56E4

C:Genetics:

A:Gene: SPDB:SPAC56E4.05

A:Map position: 1

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC56E4.05

Query Match

Best Local Similarity 45.5%; Score 5; DB 2; Length 216;
Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 KAPTE 11

DB 196 KAPTE 200

Search completed: August 15, 2001, 12:34:40
Job time: 105 sec

RESULT 45
H81057
C:Species: Neisseria meningitidis (strain C-125)
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81057
R:Retelink, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlata, V.; Maignan, V.; Pizzo, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; Vg
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: AB1000; MWID:2015755
A:Accession: H81057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <TET>
A:Cross-references: GB:AE002516; GB:AE002098; NID:g7226905; PIDN:AAF42006.1; PID:g722690
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1657

Query Match 45.5%; Score 5; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
|||||
Db 191 APRAP 195

RESULT 46
T49218
hypothetical protein F27H5.20 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cross)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49218
R:Reger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
Submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25018
A:Accession: T49218
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-207 <RIE>
A:Cross-references: EMBL:AL163852; GSPDB:GNO0061; ATSP:F27H5.20
C:Genetics:
A:Experimental source: cultivar Columbia; BAC clone F27H5
A:Gene: ATSP:F27H5.20
A:Map position: 3
A:Introns: 66/2; 104/1; 149/1; 169/3

Query Match 45.5%; Score 5; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPT 10
|||||
Db 126 PKAPT 130

RESULT 47
DB3944
SOS regulon transcription repressor *lexA* [Imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C:Accession: DB3944
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: AB3650; MWID:20263314
A:Accession: DB3944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <STO>
A:Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06075.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: *lexA*

Query Match 45.5%; Score 5; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOOTA 5
|||||
Db 145 QOOTA 149

RESULT 48
H75317
translation initiation factor IF-3 - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: H75317
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MWID:20036896
A:Accession: H75317
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <WHI>
A:Cross-references: GB:AE002044; GB:AE000513; NID:g6459872; PIDN:AAF11633.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2087
A:Map position: 1
C:Superfamily: translation initiation factor IF-3

Query Match 45.5%; Score 5; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
|||||
Db 169 APRAP 173

RESULT 49
S70734
adenylate kinase (EC 2.7.4.3) - *Yersinia enterocolitica*
N:Alternate names: ATP-AMP transphosphorylase
C:Species: *Yersinia enterocolitica*
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: S70734; S51258
R:Skurnik, M.; Venho, R.; Tolvanen, P.; Al-Hendy, A.
Mol. Microbiol. 17, 575-594, 1995
A:Title: A novel locus of *Yersinia enterocolitica* serotype O:3 involved in lipopolysa
A:Reference number: S70734; MWID:96100456
A:Accession: S70734
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-214 <SKU>
A:Cross-references: EMBL:Z47767; NID:g633689; PIDN:CAA87696.1; PID:g633690
A:Experimental source: strain 6471/76 serotype O:3
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C:Genetics:
A:Gene: *ack*

R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A'Reference number: AF5250; MUID:20036896
 A'Accession: E75435
 A>Status: Preliminary
 A'Molecule type: DNA
 A'Residuals: 1-183 <WHI>
 A'Cross-references: GB:AE001961; GB:AE000513; NID:g6458643; PIDN:AAF10683.1; PID:g645864
 A'Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1110
 A:Map position: 1
 C:Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 45.5%; Score 5; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
 |||||
 DB 2 TAPKA 6

RESULT 42
 T42232
 histone H1.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
 R:Jedrusik, M.; Schulze, E.
 Submitted to the EMBL Data Library, August 1997
 A'Description: The histone H1 complement of *Caenorhabditis elegans*.
 A'Reference number: 232091
 A'Accession: T42232
 A>Status: translated from GB/EMBL/DBJ
 A'Molecule type: mRNA
 A'Residuals: 1-191 <JED>
 A'Cross-references: EMBL:AF017811; NID:g2407322; PIDN:AA070666.1; PID:g2407323
 R:Vanlenteren, J.R.; Van Bun, S.M.; de Baere, I.; van Beunnen, J.J.
 Biochem. J. 265, 739-746, 1990
 A>Title: The primary structure of a minor isoform (H1.2) of histone H1 from the nematode
 A'Reference number: S08195; MUID:90165873
 A'Accession: S08195
 A'Molecule type: protein
 A'Residuals: 2-27, 'T', '29-30', 'SS', '33-44', 'IKE', '48-49', 'KO', '52-78', 'R', '80-111', 'P', '113-191 <VAN
 A>Note: the sequence from Fig. 5 is inconsistent with that from Fig. 4 in having 95-Arg
 C:Superfamily: histone H1
 C:Keywords: blocked amino end; chromosomal protein; DNA binding; nucleosome; nucleus
 F:2-191/Product: histone H1.2 #status predicted <MAT>
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu

Query Match 45.5%; Score 5; DB 2; Length 191;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 DB 18 APKAP 22

RESULT 43
 S73713
 MG319 homolog H08-orf193 - Mycoplasma pneumoniae (strain ATCC 29342)
 C:Species: Mycoplasma pneumoniae
 A:Variety: ATCC 29342
 C>Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
 C'Accession: S73713
 R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirl, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996
 A>Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumo*
 A'Reference number: S73327; MUID:97105885
 A'Accession: S73713
 A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A'Molecule type: DNA
 A'Residuals: 1-193 <HIM>
 A'Cross-references: EMBL:AE000037; GB:U00089; NID:g1674065; PIDN:AA896035.1; PID:g167
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C:Genetics:
 A:Genetic code: SGC3

Query Match 45.5%; Score 5; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
 |||||
 DB 68 TAPKA 72

RESULT 44
 S17244
 adenylylsulfate kinase (EC 2.7.1.25) - Yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: adenosine-5-phosphosulfate kinase; protein YKL001c
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
 C'Accession: S17244; S25323; S37811
 R:Korch, C.; Mountain, H.A.; Byström, A.S.
 Mol. Gen. Genet. 229, 96-108, 1991
 A>Title: Cloning, nucleotide sequence, and regulation of MET14, the gene encoding the
 A'Reference number: S17244; MUID:91375456
 A'Accession: S17244
 A'Molecule type: DNA
 A'Residuals: 1-202 <KOR>
 A'Cross-references: GB:S55315; NID:g235814; PIDN:AA819854.1; PID:g235815
 R:Duesterhoeft, A.; Philippson, P.
 Yeast 8, 749-759, 1992
 A>Title: DNA sequencing and analysis of a 24.7 kb segment encompassing centromere CEN
 A'Reference number: S25323; MUID:93070612
 A'Accession: S25323
 A>Status: nucleic acid sequence not shown
 A'Molecule type: DNA
 A'Residuals: 1-202 <DUP>
 A'Cross-references: EMBL:X65124; NID:g3517; PIDN:CAA46252.1; PID:g3529
 A'Experimental source: strain S288C
 R:Duesterhoeft, A.; Moestl, D.; Poehlmann, R.; Philippson, P.
 submitted to the Protein Sequence Database, March 1994
 A'Reference number: S37811
 A'Accession: S37811
 A'Molecule type: DNA
 A'Residuals: 1-202 <DU2>
 A'Cross-references: EMBL:Z28001; NID:g485972; PIDN:CAA81833.1; PID:g485973; GSPDB:GNO
 A'Experimental source: strain S288C
 C:Genetics:
 A:Gene: SCD:MET14; MIPS:YKL001c
 A'Cross-references: SCD:S0001484; MIPS:YKL001c
 A:Map position: 111
 C:Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
 C:Keywords: ATP; P-loop; phosphotransferase; purine nucleotide binding
 F:24-187/Domain: adenylylsulfate kinase homology <ASK>
 F:31-38/Region: nucleotide-binding motif A (P-loop)
 F:37/Binding site: ATP (Lys) #status predicted

Query Match 45.5%; Score 5; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 DB 166 APKAP 170

A:Molecule type: DNA
A:Residues: 1-174 <RAM>
A:Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA31056.1; PID:g3258373
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1929

Query Match 45.5%; Score 5; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
|1111
DB 23 APRAP 27

RESULT 37

A26882
pIL2 hypothetical protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Dec-1988 #sequence_rev15on 15-Dec-1988 #text_change 05-Nov-1999
C:Accession: A26882
R:Glaichenhaus, N.; Cuzin, F.
Cell 50, 1081-1089, 1987
A:Title: A role for ID repetitive sequences in growth and transformation-dependent regul
A:Reference number: A26882; MID:87301751
A:Accession: A26882
A:Molecule type: mRNA
A:Residues: 1-175 <GLA>
A:Cross-references: GB:M17412; NID:g207249; PIDN:AAA42232.1; PID:g207250
A:Experimental source: fibroblast
A>Note: the authors translated the codon TGG for residue 65 as Ser and GAA for residue 1

Query Match 45.5%; Score 5; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPT 10
|1111
DB 39 PKAPT 43

RESULT 38

T48699
hypothetical protein IAG.30 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C>Date: 05-May-2000 #sequence_rev15on 05-May-2000 #text_change 19-May-2000
C:Accession: T48699
R:Schulte, U.; Allyn, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24541
A:Accession: T48699
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-176 <SCH>
A:Cross-references: EMBL:AL353817; GSPDB:GN00112; NCSP:IAG.30
A:Experimental source: cosmid contig IAG; strain 74
C:Genetics:
A:Gene: NCSP:IAG.30
A:Map position: 2
C:Superfamily: Neurospora crassa hypothetical protein IAG.30

Query Match 45.5%; Score 5; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OQTAP 6
|1111
DB 153 OQTAP 157

RESULT 39

F70588
hypothetical protein Kv2843 - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_rev15on 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: F70588
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MID:9825987
A:Accession: F70588
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-181 <COL>
A:Cross-references: GB:Z95207; GB:AL123456; NID:g3261745; PIDN:CAB08447.1; PID:G31518
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Kv2843

Query Match 45.5%; Score 5; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
|1111
DB 41 APRAP 45

RESULT 40

T11906
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain N009 - Thermus aquaticus thermophil
N:Alternate names: NADH dehydrogenase I, subunit N009
C:Species: Thermus aquaticus thermophilus
C>Date: 16-Jul-1999 #sequence_rev15on 16-Jul-1999 #text_change 17-Mar-2000
C:Accession: T11906
R:Yano, T.; Chu, S.S.; Sled, V.S.; Ohnishi, T.; Yagi, T.
submitted to the EMBL Data Library, March 1996
A:Description: Cloning, sequencing, and expression studies of the proton-translocatin
A:Reference number: Z17372
A:Accession: T11906
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-182 <YAN>
A:Cross-references: EMBL:U52917; NID:g1279860; PID:g1279869; PIDN:AAA97946.1
A:Experimental source: strain HB-8
C:Genetics:
A:Gene: N009
C:Superfamily: unassigned ferredoxin 2(4Fe-4S)-related proteins; ferredoxin 2(4Fe-4S)
C:Keywords: NAD; oxidoreductase
F:46-116/Domain: ferredoxin 2(4Fe-4S) homology <FER>

Query Match 45.5%; Score 5; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 KAPTE 11
|1111
DB 174 KAPTE 178

RESULT 41

E75435
pyrimidine operon regulatory protein PyrR - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_rev15on 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: E75435

A;Experimental source: cv. Georgie
C;Superfamily: dehydrin-like proteins

Query Match	45.5%;	Score 5;	DB 2;	Length 139;
Best Local Similarity	100.0%;	Pred. No. 82;		
Matches	5;	Conservative	0;	Mismatches 0; Indels

Oy	1	QQQTA	5
Db	102	QQQTA	106

RESULT 32
C81214
comEA-related protein NMB0299 [imported] - *Neisseria meningitidis* (strain MC58 serogroup
C:Species: *Neisseria meningitidis*
C:Date: 31-Mar-2000 #sequence:revision 31-Mar-2000 #text-change 19-Jan-2001
C:Accession: C81214
R:Retelsin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Selzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Vamthanan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizzo, M.
Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappucci, R.; Ve
A:Title: Complete genome sequence of *Neisseria meningitidis* serotype B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: C81214
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <TE>
A:Cross-references: GB:AE002387; GB:AE002098; NID:g7225523; PIDN:AAF40750.1; PID:g722555
A:Experimental source: serogroup B, strain MC58
C:Genetics:
C:Gene: NMB0299

Query Match	45.5%	Score 5;	DB 2;	Length 148;
Best Local Similarity	100.0%	Pred. No. 87;		
Matches	5;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps

QY	5	APKAP	9
Db	134	APKAP	138

RESULT 33
F83464
Flagellar motor switch protein FILN PA1444 [Imported] - *Pseudomonas aeruginosa* (strain F83464)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83464
R:Stover, C.K.; Pham, X.O.; Ertvin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
N:ature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: AB2950, MUID:20437337
A:Accession: F83464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <STO>
A:Cross-references: GB:AE004574; GB:AE004091; NID:9947391; PIDN:AMG04833.1; GSPDB:GN0001
A:Experimental source: strain PA01
C:Genetics:
C:Gene: filN; PA1444

Query Match	45.5%	Score 5;	DB 2;	Length 157;
Best Local Similarity	100.0%	Pred. No. 91;		
Matches	5;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	6 PKAPT 10			

Db 62 PKAPT 66

RESULT 34

hypothetical protein NMA1867 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup C); Species: *Neisseria meningitidis*
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: F81813
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
: Holroyd, S.; Jajelski, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491
A:Reference number: A81775; MUID:20222536
A:Accession: F81813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-159 <PAR>
A:Cross-references: GB:AL162757; GB:AL157959; NTD:97380371; PIDN:CAB85090.1; PID:g7338
A:Experimental source: serogroup A, strain Z2491
A:Genetics:
A:Gene: NMA1867

Query Match	45.5%	Score 5;	DB 2;	Length 159;
Best Local Similarity	100.0%	Pred. No. 92;		
Matches	5;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY	3	QTAPK	7
Db	81	QTAPK	85

RESULT 35
I39546
hypothetical protein 2 - *Aeromonas hydrophila*
C:Species: *Aeromonas hydrophila*
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 08-Oct-1999
C:Accession: I39546
R:Thomas, S.R.; Trust, T.J.
J. Bacteriol. 177, 3932-3939, 1995
A:Title: A specific PiliD homolog is required for the secretion of paracrystalline sur-
A:Reference number: A57354; MUID:9532195
A:Accession: I39546
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <RES>
A:Cross-references: GB:I41662; NID:g950300; PIDN:AAA79321.1; PID:g1019922
A:Superfamily: *Aeromonas hydrophila* hypothetical protein 2

Query Match	45.5%	Score 5;	DB 2;	Length 166;
Best Local	100.0%;	Pred. NO. 95;		
Matches	5; Conservative	0; Mismatches	0; Indels	0; Gaps

QY	4	TAPKA	8
db	26	TAPKA	30

RESULT 36
A71208
hypothetical protein PH129 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: A71208
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: A71208
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Cross-references: DDBJ:D31702; NID:g496361; PIDN:BAA06511.1; PID:g496362
R;Shinkai, W.; Hase, T.; Yagi, T.; Matsubara, H.
J. Biochem. 87, 1747-1756, 1980
A;Title: Amino acid sequence of cytochrome c-3 from *Desulfovibrio vulgaris*, Miyazaki.
A;Reference number: A00125; M0ID:8029474
A;Accession: A00125
A;Molecule type: protein
A;Residues: 24-64, 'N', 66-130 <SH2>
R;Higuchi, Y.; Kusunoki, M.; Matsura, Y.; Yasuoka, N.; Kakudo, M.
J. Mol. Biol. 172, 109-139, 1984
A;Title: Refined structure of cytochrome c-3 at 1.8 angstrom resolution.
A;Reference number: A49705; M0ID:84114880
A;Contents: annotation; X-ray crystallography, 1.8 angstroms
R;Higuchi, Y.; Kusunoki, M.; Matsura, Y.; Yasuoka, N.; Kakudo, M.
submitted to the Brookhaven Protein Data Bank, November 1983
A;Reference number: A50415; PDB:2CDV
A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 24-64, 'N', 66-130
C;Function:
A;Description: accepts electrons from cytochrome-c3 hydrogenase (EC 1.12.2.1) and transfers
A;Pathway: sulfate respiration
C;Superfamily: cytochrome c3; cytochrome c3 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; sulfate respiration
F;43-129/Product: cytochrome c3 status experimental <MAT>
F;43-129/Domain: cytochrome c3 homology <CC3>
F;45-57/Binding site: heme iron (His) (axial ligands) #status experimental
F;48-106/Binding site: heme iron (His) (axial ligands) #status experimental
F;53-56/Binding site: heme (Cys) (covalent) #status experimental
F;58-75/Binding site: heme iron (His) (axial ligands) #status experimental
F;69-74/Binding site: heme (Cys) (covalent) #status experimental
F;93-129/Binding site: heme iron (His) (axial ligands) #status experimental
F;102-105/Binding site: heme (Cys) (covalent) #status experimental
F;123-128/Binding site: heme (Cys) (covalent) #status experimental

Query Match 45.5%; Score 5; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
|||||
Db 24 APRAP 28

RESULT 28
H82438
Large-conductance mechanosensitive channel VCA0612 [imported] - *Vibrio cholerae* (strain
C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82438
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; M0ID:20406833
A;Accession: H82438
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <HEI>
A;Cross-references: GB:AE004391; GB:AE003853; NID:g9658015; PIDN:AAF96513.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0612
A;Map position: 2
C;Superfamily: yhcC protein

Query Match 45.5%; Score 5; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
|||||

Db 109 APRAP 113

RESULT 29
S35752
dehydrin 7 - barley
C;Species: *Hordeum vulgare* (barley)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S35752
R;Robertson, M.; Close, T.J.; Cumling, A.C.
submitted to the EMBL Data Library, April 1993
A;Description: Sequence analysis of a dehydration-induced gene, dehydrin, from barley
A;Reference number: S35752
A;Accession: S35752
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <ROB>
A;Cross-references: EMBL:X71362; NID:g296197; PIDN:CAA50499.1; PID:g296198
C;Genetics:
A;Intons: 66/3
C;Superfamily: dehydrin-like protein

Query Match 45.5%; Score 5; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOQRA 5
|||||
Db 100 QOQRA 104

RESULT 30
S05544
dehydrin 8 - barley
N;Alternate names: dehydration-induced protein 8
C;Species: *Hordeum vulgare* (barley)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C;Accession: S05544
R;Close, T.J.; Kortt, A.A.; Chandler, P.M.
Plant Mol. Biol. 13, 95-108, 1989
A;Title: A cDNA-based comparison of dehydration-induced proteins (dehydrins) in barley
A;Reference number: S05543; M0ID:93357436
A;Accession: S05544
A;Molecule type: mRNA
A;Residues: 1-139 <CIO>
A;Cross-references: EMBL:X15288; NID:g18965; PIDN:CAA33362.1; PID:g18966
C;Superfamily: dehydrin-like protein

Query Match 45.5%; Score 5; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOQRA 5
|||||
Db 102 QOQRA 106

RESULT 31
T05715
dehydrin - barley
C;Species: *Hordeum vulgare* (barley)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 20-Jun-2000
C;Accession: T05715
R;Gull, M.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z15427
A;Accession: T05715
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-139 <GUL>
A;Cross-references: EMBL:X98326; PIDN:CAA66970.1

A:Molecule type: DNA
 A:Residues: 1-127 <CHS>
 A:Cross-references: EMBL:X17403; NID:959591; PIDN:CAA5348.1; PID:e27313; PID:g1780891
 A>Note: this sequence was submitted to the EMBL Data Library, December 1989
 A>Note: this reading frame between two stop codons and does not begin with a sta
 C:Superfamily: human cytomegalovirus hypothetical protein UL110

Query Match 45.5%; Score 5; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAP 6
 |||||
 DB 23 OOTAP 27

RESULT 24

A72468
 hypothetical protein APE2544 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 08-Sep-2000
 C:Accession: A72468
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
 A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A:Reference number: A72450; MUID:99310339
 A:Accession: A72468
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-127 <KAW>
 A:Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81561.1; PID:d1045347; PID:g510
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE2544
 C:Superfamily: Aeropyrum pernix hypothetical protein APE2544

Query Match 45.5%; Score 5; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
 |||||
 DB 80 TAPKA 84

RESULT 25

G64155
 yhcC protein - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
 C:Accession: G64155
 R:Flisbach, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.
 R:Flisbach, R.D.; Scott, J.; Shiley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, J.
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
 A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630
 A:Accession: G64155
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-128 <TIGR>
 A:Cross-references: GB:U02745; GB:I42023; NID:g1573617; PIDN:AAC22286.1; PID:g1573622; I
 C:Genetics:
 A:Gene: yhcC
 C:Superfamily: yhcC protein

Query Match 45.5%; Score 5; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 77;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 TAPKA 8
 |||||
 DB 110 TAPKA 114

RESULT 26

CCDV3
 cytochrome c3 precursor - Desulfovibrio vulgaris (strain Hildenborough)
 C:Species: Desulfovibrio vulgaris
 C>Date: 24-Apr-1984 #sequence_revision 17-Feb-1994 #text_change 03-Mar-2000
 C:Accession: A24799; A00124; D32427
 R:Voordouw, G.; Brenner, S.
 Eur. J. Biochem. 159, 347-351, 1986
 A>Title: Cloning and sequencing of the gene encoding cytochrome c3 from Desulfovibrio
 A:Reference number: A24799; MUID:87004646
 A:Accession: A24799
 A:Molecule type: DNA
 A:Residues: 1-129 <VOO>
 A:Cross-references: GB:X04304; NID:g40820; PIDN:CAA27847.1; PID:g40821
 R:Troun, E.B.; Campbell, L.L.
 J. Biol. Chem. 249, 386-393, 1974
 A>Title: Amino acid sequence of cytochrome c-3 from Desulfovibrio vulgaris.
 A:Reference number: A00124; MUID:74070664
 A:Accession: A00124
 A:Molecule type: protein
 A:Residues: 23-129 <TRO>
 A:Experimental source: strain Hildenborough, NCIB 8303
 R:Loutfi, M.; Guerlesquin, F.; Bianco, P.; Haladjian, J.; Brusch, M.
 Biochem. Biophys. Res. Commun. 159, 670-676, 1989
 A>Title: Comparative studies of polymeric cytochromes c isolated from Desulfovibrio v
 A:Reference number: A32427; MUID:89193654
 A:Accession: D32427
 A:Molecule type: protein
 A:Residues: 23-44 <LOU>
 C:Superfamily: cytochrome c3; cytochrome c3 homology
 C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; sulfate res
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-129/Product: cytochrome c3 #status experimental <KAW>
 F:44-128/Domain: cytochrome c3 homology <CC3>
 F:44,56/Binding site: heme iron (His) (axial ligands) #status predicted
 F:47,105/Binding site: heme iron (His) (axial ligands) #status predicted
 F:52,55/Binding site: heme (Cys) (covalent) #status predicted
 F:57,74/Binding site: heme iron (His) (axial ligands) #status predicted
 F:68,73/Binding site: heme (Cys) (covalent) #status predicted
 F:92,128/Binding site: heme iron (His) (axial ligands) #status predicted
 F:101,104/Binding site: heme (Cys) (covalent) #status predicted
 F:122,127/Binding site: heme (Cys) (covalent) #status predicted

Query Match 45.5%; Score 5; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 DB 23 APKAP 27

RESULT 27

CCDV3M
 cytochrome c3 precursor [validated] - Desulfovibrio vulgaris (strain Miyazaki)
 C:Species: Desulfovibrio vulgaris
 C>Date: 31-Oct-1980 #sequence_revision 10-Oct-1997 #text_change 15-Sep-2000
 C:Accession: S33874; A00125
 R:Kikimura, M.; Ozawa, K.; Kojima, S.; Kunagai, I.; Akutsu, H.; Miura, K.
 Protein Seq. Data Anal. 5, 193-196, 1993
 A>Title: The primary structure of pre-cytochrome c(3) from Desulfovibrio vulgaris (M
 A:Reference number: S33874
 A:Accession: S33874
 A:Molecule type: DNA
 A:Residues: 1-130 <KIT>

A:Cross-references: EMBL:X71782; NID:g417605; PIDN:CAA50667.1; PID:g417606

Query Match 45.5%; Score 5; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
DB 63 APKAP 67

RESULT 19

Hit family protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: G75374
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: G75374

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-118 <WHI>

A:Cross-references: GB:AE002005; GB:AE000513; NID:g6459377; PIDN:AAF11181.1; PID:g645938

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1621

A:Map position: 1

C:Superfamily: protein kinase C inhibitor; histidine triad homology

Query Match 45.5%; Score 5; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
DB 40 APKAP 44

RESULT 20

B49905

protein secretion operon exe protein I precursor - Aeromonas hydrophila

C:Species: Aeromonas hydrophila

C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 02-Sep-2000

C:Accession: B49905; S22912

R:Howard, S.P.; Critch, J.; Bedi, A.

J. Bacteriol. 175, 6695-6703, 1993

A:Title: Isolation and analysis of eight exe genes and their involvement in extracellular

A:Reference number: A49905; MUID:94012544

A:Accession: B49905

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-119 <HOW>

A:Cross-references: GB:X66504; NID:g551420; PIDN:CAA47130.1; PID:g38830

C:Genetics:

A:Gene: exeI

C:Superfamily: secretion protein xcpv

Query Match 45.5%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TAPKA 8
|||||
DB 102 TAPKA 106

RESULT 21

B81363

Hit-family protein Cj0898 [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 18-Aug-2000

C:Accession: B81363

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals

A:Reference number: A81250; MUID:20150912

A:Accession: B81363

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-121 <PAR>

A:Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73156.1; PID:g696

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj0898

C:Superfamily: protein kinase C inhibitor; histidine triad homology

Query Match 45.5%; Score 5; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
DB 33 APKAP 37

RESULT 22

S49484

histone H2B - sea cucumber (Holothuria tubulosa)

C:Species: Holothuria tubulosa

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S49484

R:Drabant, B.; Louroutziatis, A.; Pratz, E.; Cornudella, L.; Doenecke, D.

submitted to the EMBL Data Library, September 1994

A:Description: Structure of histone H2B and H4 genes of the sea cucumber Holothuria t

A:Reference number: S49484

A:Accession: S49484

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-123 <DRA>

A:Cross-references: EMBL:Z46225; NID:g559456; PIDN:CAA86297.1; PID:g559457

C:Superfamily: histone H2B

Query Match 45.5%; Score 5; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAP 9
|||||
DB 2 APKAP 6

RESULT 23

S09877

hypothetical protein UL110 - human cytomegalovirus (strain AD169)

C:Species: human cytomegalovirus, human herpesvirus 5

A:Note: host Homo sapiens (man)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000

C:Accession: S09877

R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohnl, R.; Brown, C.M.; Cerny, R.; Horsnell, T

M.; Barrall, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovi

A:Reference number: S09749; MUID:90269039

A:Accession: S09877

A>Status: nucleic acid sequence not shown; translation not shown

A:Reference number: A59233
A:Accession: A59233
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2121 <AND>
A:Cross-references: GB:AF233269; PIDN:AAF34810.1
C:Genetics:
A:Gene: Myo28B1
A:Cross-references: FlyBase:FBgn0040299
A:Map position: 2, 28B1
C:Superfamily: myosin motor domain homology
F:69-725/Domain: myosin motor domain homology <MMO>

Query Match 54.5%; Score 6; DB 2; Length 2121;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 APKAPT 10
|||||
Db 915 APKAPT 920

RESULT 14

S07073
arabinogalactan protein - Italian ryegrass (fragments)
C:Species: Lolium multiflorum (Italian ryegrass)
C:Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 05-Dec-1998
C:Accession: S07073
R:Gleeson, P.A.; McNamara, M.; Wattenhall, R.E.H.; Stone, B.A.; Fincher, G.B.
Biochem. J. 264, 857-862, 1989
A:Title: Characterization of the hydroxyproline-rich protein core of an arabinogalactan-
A:Reference number: S07073; MUID:90147544
A:Accession: S07073
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <GLE>
A:Note: 19-His and 23-Leu were also found
C:Keywords: hydroxyproline
F:6,7,9,11,14,16,18,20,26,30,34,36,39/Modified site: hydroxyproline (Pro) #status experi

Query Match 45.5%; Score 5; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 APKAP 9
|||||
Db 10 APKAP 14

RESULT 15

I47395
histone H1 I-1 (clone T31) - midge (Chironomus thummi) (fragment)
C:Species: Chironomus thummi thummi
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-May-1996
C:Accession: I47395
R:Schulze, E.; Trieschmann, L.; Schulze, B.; Schmidt, E.R.; Pitzel, S.; Zechel, K.; Gros
Proc. Natl. Acad. Sci. U.S.A. 90, 2481-2485, 1993
A:Title: Structural and functional differences between histone H1 sequence variants with
A:Reference number: A47395; MUID:93211985
A:Accession: I47395
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-67 <SCH>
A:Note: sequence extracted from NCBI backbone (NCBIP:128535)
C:Superfamily: histone H1

Query Match 45.5%; Score 5; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 APKAP 9
|||||
Db 27 APKAP 31

RESULT 16

A47395
histone H1 I-1 (N-terminal, clone L1234, globular domain) - midge (Chironomus thummi)
C:Species: Chironomus thummi
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-May-1996
C:Accession: A47395
R:Schulze, E.; Trieschmann, L.; Schulze, B.; Schmidt, E.R.; Pitzel, S.; Zechel, K.; G
Proc. Natl. Acad. Sci. U.S.A. 90, 2481-2485, 1993
A:Title: Structural and functional differences between histone H1 sequence variants w
A:Reference number: A47395; MUID:93211985
A:Accession: A47395
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-70 <SCH>
A:Experimental source: subsp. piger
A:Note: sequence extracted from NCBI backbone (NCBIP:128533)
C:Superfamily: histone H1

Query Match 45.5%; Score 5; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 APKAP 9
|||||
Db 27 APKAP 31

RESULT 17

A44465
sodium ion pump oxaloacetate decarboxylase subunit gamma - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: A44465
R:Woehlke, G.; Wifling, K.; Dimroth, P.
J. Biol. Chem. 267, 22798-22803, 1992
A:Title: Sequence of the sodium ion pump oxaloacetate decarboxylase from Salmonella t
A:Reference number: A44465; MUID:93054591
A:Accession: A44465
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-83 <WOE>
A:Experimental source: LT2
A:Note: sequence extracted from NCBI backbone (NCBIP:118071)
C:Keywords: transmembrane protein

Query Match 45.5%; Score 5; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 APKAP 9
|||||
Db 50 APKAP 54

RESULT 18

S36634
p112 protein - Antirrhinum sp.
C:Species: Antirrhinum sp.
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: S36634
R:Baldwin, T.C.; Coen, E.S.; Dickinson, H.G.
submitted to the EMBL Data Library, January 1993
A:Reference number: S36634
A:Accession: S36634
A:Molecule type: mRNA
A:Residues: 1-95 <BAL>

C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu homolog
C:Keywords: GTP binding; nucleotide binding; P-loop
F:496-609/Domain: translation elongation factor Tu homology <ETU>
F:502-609/Region: nucleotide-binding motif A (P-loop)
F:606-609/Region: GTP-binding NKXD motif
F:642-644/Region: GTP-binding SAK/L motif
F:508,509,529,606,607,609,642/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #

Query Match 54.5%; Score 6; DB 2; Length 1001;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAPT 10
|||||
Db 111 APKAPT 116

RESULT 10
T14343
zinc finger RNA binding protein, chromosome-associated - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14343
R:Meagher, M.J.; Schumacher, J.M.; Lee, K.; Holdcraft, R.W.; Edelhoff, S.; Distech, C.;
Gene 228, 197-211, 1999
A:Title: Identification of ZFR, an ancient and highly conserved murine chromosome-associated
A:Reference number: 217994; MUID:99173884
A:Accession: T14343
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1052 <MEA>
A:Cross-references: EMBL:AF071059; NID:g3293536; PID:g3293537; PIDN:AAC25762.1
A:Experimental source: testis
C:Genetics:
A:Gene: Zfr
A:Map position: 15A
C:Keywords: zinc finger

Query Match 54.5%; Score 6; DB 2; Length 1052;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTAPKA 8
|||||
Db 165 QTAPKA 170

RESULT 11
RRNGSM
RNA-directed RNA polymerase (EC 2.7.7.48) - strawberry mild yellow edge-associated virus
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
C:Species: strawberry mild yellow edge-associated virus
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 19-Jan-2001
C:Accession: JQ1426
R:Jelkmann, W.; Maiss, E.; Martin, R.R.
J. Gen. Virol. 73, 475-479, 1992
A:Title: The nucleotide sequence and genome organization of strawberry mild yellow edge-
A:Reference number: JQ1426; MUID:92166762
A:Accession: JQ1426
A:Molecule type: genomic RNA
A:Residues: 1-1323 <JEL>
A:Cross-references: GB:D12517; DBJ:D01227; NID:g222631; PIDN:BAA02082.1; PID:g222632
C:Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis; P
F:605-612/Region: nucleotide-binding motif A (P-loop)
F:668-673/Region: nucleotide-binding motif B
F:611/Binding site: ATP (Lys) #status predicted

Query Match 54.5%; Score 6; DB 1; Length 1323;
Best Local Similarity 100.0%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 APKAPT 10
|||||
Db 463 APKAPT 468

RESULT 12
T43214
ovt1 protein - nematode (Onchocerca volvulus)
N:Alternate names: myosin-like antigen
C:Species: Onchocerca volvulus
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
C:Accession: T43214; A44939; A54513; S27825
R:Triteeraprapab, S.; Richie, T.L.; Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert,
Mol. Biochem. Parasitol. 69, 161-171, 1995
A:Title: Molecular cloning of a gene expressed during early embryonic development in
A:Reference number: 222341; MUID:95287898
A:Accession: T43214
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2022 <TRI>
A:Cross-references: EMBL:U12681; NID:g530824; PID:g530825; PIDN:AAA80009.1
A:Experimental source: specific host Homo sapiens
R:Erondou, N.E.; Donelson, J.E.
Mol. Biochem. Parasitol. 40, 213-224, 1990
A:Title: Characterization of a myosin-like antigen from Onchocerca volvulus.
A:Reference number: A44939; MUID:90301142
A:Accession: A44939
A:Molecule type: mRNA
A:Residues: 733-874, 'E', 876-916, 'S', 918-1038, 1040-1047, 'S', 1049-1283, 'E', 1285-1363 <E
A:Cross-references: GB:M30398
A:Note: the sequence is revised in GenBank entry ONGANTML, release 115, (PIDN:AAA2941
R:Donelson, J.E.; Duke, B.O.L.; Moser, D.; Zeng, W.; Erondou, N.E.; Lucius, R.; Renz,
Mol. Biochem. Parasitol. 31, 241-250, 1988
A:Title: Construction of Onchocerca volvulus cDNA libraries and partial characterization
A:Reference number: A54513; MUID:89127417
A:Accession: A54513
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 733-866 <DON>
A:Cross-references: GB:J03995; NID:g159874; PIDN:AAA29412.1; PID:g159875
R:Ngozi, E.; Erondou, N.E.; Donelson, J.E.
submitted to the EMBL Data Library, April 1990
A:Description: Characterization of a myosin-like antigen from Onchocerca volvulus.
A:Reference number: S27825
A:Accession: S27825
A:Molecule type: mRNA
A:Residues: 733-874, 'E', 876-916, 'S', 918-1038, 1040-1047, 'S', 1049-1283, 'E', 1285-1347, 'E
A:Cross-references: EMBL:M30398; NID:g159876; PIDN:AAA29413.1; PID:g159877
C:Genetics:
A:Gene: ovt1
C:Keywords: leucine zipper

Query Match 54.5%; Score 6; DB 2; Length 2022;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAP 6
|||||
Db 302 QOOTAP 307

RESULT 13
AS9233
myosin VII-like protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 17-Nov-2000
C:Accession: A59233
R:Anderson, J.B.; Yamashita, R.A.; Sellers, J.R.
submitted to GenBank, February 2000
A:Description: Complete cDNA for an unconventional Myosin (Class VII) in Drosophila m

Db 4 TAPKAP 9

RESULT 5
G81384
succinate dehydrogenase (EC 1.3.99.1) flavoprotein Cj0409 [imported] - Campylobacter jejuni
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Sep-2000
C:Accession: G81384
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, R.; Whitehead, S.; Barrell, A.G.
C.W.: Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barral, P.; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, R.; Whitehead, S.; Barrell, A.G.
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyphomycetous ancestry
A:Reference number: AB1250; MUID:20150912
A:Accession: G81384
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-663 <PAR>
A:Cross-references: GB:AL139075; GB:AL111168; NID:g9697817; PIDN:CAB74245.1; PID:g6967818
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: fda; Cj0409
C:Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology; fda
C:Keywords: oxidoreductase

Query Match 54.5%; Score 6; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTAPKA 8
|||||
Db 91 QTAPKA 96

RESULT 6
H83012
periplasmic glucans biosynthesis protein MdoH PA5077 [imported] - Pseudomonas aeruginosa
C:Species: pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83012
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, L.S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Science 287, 1230-1233, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337
A:Accession: H83012
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-861 <SPO>
A:Cross-references: GB:AE004920; GB:AE004091; NID:g9951358; PIDN:AAG08462.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: mdoH; PA5077

Query Match 54.5%; Score 6; DB 2; Length 861;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTAPKA 8
|||||
Db 376 QTAPKA 381

RESULT 7
A48753
NFAT transcription factor phosphoprotein - mouse (fragment)
N:Alternate names: nuclear factor of activated T cells, phosphoprotein chain
C:Species: Mus musculus (house mouse)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C:Accession: A48753


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979 4 36.4 220 2 JC5954 ribosomal protein
980 4 36.4 220 2 T18982 hypothetical prote
981 4 36.4 221 2 S49482 histone H1 - mouse
982 4 36.4 221 2 S33219 histone H1.C - Afr
983 4 36.4 221 2 S58685 hypothetical prote
984 4 36.4 221 2 T45044 hypothetical prote
985 4 36.4 221 2 T36514 hypothetical prote
986 4 36.4 221 2 T34554 hypothetical prote
987 4 36.4 222 2 JC1384 beta-casein precu
988 4 36.4 222 2 A32879 beta-casein precu
989 4 36.4 222 2 T16731 hypothetical prote
990 4 36.4 222 2 S66832 hypothetical prote
991 4 36.4 223 1 TJBPII tail assembly prot
992 4 36.4 223 2 A96622 conserved hypotet
993 4 36.4 223 2 T36952 conserved hypotet
994 4 36.4 224 1 KBR0A2 beta-casein precu
995 4 36.4 224 2 C86571 L4 ribosomal prote
996 4 36.4 224 2 H72055 ribosomal protein
997 4 36.4 224 2 T24802 hypothetical prote
998 4 36.4 224 2 B70327 ABC transporter -
999 4 36.4 225 2 F85718 probable tail comp
1000 4 36.4 225 2 C85475 hypothetical prote

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ALIGNMENTS

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RESULT 1
A41487
protein p60 precursor - Listeria monocytogenes
N:Alternate names: Invasion-associated protein
C:Species: Listeria monocytogenes
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1996
C:Accession: A41487 B41487
R:Koehler, S.; Delmester-Waechter, M.; Chakraborty, T.; Lottspeich, F.; Goebel, W.
Intect. Immun. 58, 1943-1950, 1990
A:Title: The gene coding for protein p60 of Listeria monocytogenes and its use as a spec
A:Reference number: A41487; PMID:90256283
A:Accession: A41487
A:Molecule type: DNA
A:Residues: 1484 <KOE>
A:Cross-references: GB:X52268
A:Accession: B41487
A:Molecule type: protein
A:Residues: 28-49 <KO2>
C:Genetics:
A:Gene: lap
F:1.27/Domain: signal sequence #status predicted <SIG>
F:28-484/Product: protein 60 #status predicted <MAT>

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Query Match 100.0%; Score 11; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 6; 9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 QOQAPKAPTE 11
    |||||
Db 291 QOQAPKAPTE 301

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RESULT 2
T29819
hypothetical protein F25E2.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T29819
R:Minx, P.; Le, T.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid F25E2.
A:Reference number: Z20691
A:Accession: T29819
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

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A:Residues: 1-343 <MIN>
A:Cross-references: EMBL:U50197; PIDD:AAA91256.1; CESP:F25E2.3
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F25E2.3
A:Insertions: 9/3; 48/2; 66/3; 96/1; 176/3; 245/1; 311/1
C:Superfamily: acyl-CoA thioesterase II

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```

Query Match 54.5%; Score 6; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 6 PKAPTE 11
    |||||
Db 4 PKAPTE 9

```

```

RESULT 3
T22894
hypothetical protein F58B3.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22894
R:Harris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19633
A:Accession: T22894
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <NLI>
A:Cross-references: EMBL:Z73427; PIDD:CAA97799.1; GSPDB:GN00022; CESP:F58B3.7
A:Experimental source: clone F58B3
C:Genetics:
A:Gene: CESP:F58B3.7
A:Map position: 4
A:Insertions: 19/1; 46/3; 317/3

```

```

Query Match 54.5%; Score 6; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 5 APKAPT 10
    |||||
Db 255 APKAPT 260

```

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RESULT 4
T37217
probable ATP/GTP binding protein - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37217
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21615
A:Accession: T37217
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-606 <OL1>
A:Cross-references: EMBL:AL031514; PIDD:CAA20595.1; GSPDB:GN00070; SCOEDB:SC2H4.01
C:Genetics:
A:Gene: SCOEDB:SC2H4.01

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Query Match 54.5%; Score 6; DB 2; Length 606;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4 TAPKAP 9
    |||||

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833	4	36.4	195	2	S52221	906	4	36.4	208	2	S14700	hypothetical 23k p
834	4	36.4	195	2	T03522	907	4	36.4	208	2	T07732	tuberculosis-relat
835	4	36.4	195	2	B69927	908	4	36.4	209	2	G69694	ribosomal protein
836	4	36.4	195	2	T39603	909	4	36.4	209	2	T44383	ribosomal protein
837	4	36.4	196	2	D69278	910	4	36.4	209	2	A59068	beta-casein varian
838	4	36.4	196	2	S43436	911	4	36.4	209	2	I40307	outer surface prot
839	4	36.4	196	2	C86858	912	4	36.4	209	2	C70630	hypothetical prote
840	4	36.4	197	2	A53126	913	4	36.4	210	2	A47733	gfp-binding protei
841	4	36.4	197	2	C70519	914	4	36.4	210	2	S36297	T-cell receptor ga
842	4	36.4	198	1	B64842	915	4	36.4	210	2	A64161	hypothetical prote
843	4	36.4	198	1	A35851	916	4	36.4	210	2	T19239	hypothetical prote
844	4	36.4	198	2	G81675	917	4	36.4	210	2	T28002	hypothetical prote
845	4	36.4	198	2	S45188	918	4	36.4	210	2	T43338	adenovirus E1B int
846	4	36.4	198	2	JC5613	919	4	36.4	211	2	S34729	gfp-binding protei
847	4	36.4	198	2	JC1457	920	4	36.4	211	2	G75533	ribosomal protein
848	4	36.4	198	2	T07280	921	4	36.4	211	2	A42261	heparan sulfate pr
849	4	36.4	198	2	I52655	922	4	36.4	211	2	D65011	hypothetical prote
850	4	36.4	198	2	S70515	923	4	36.4	211	2	A65880	hypothetical prote
851	4	36.4	198	2	P00034	924	4	36.4	211	2	T10072	periplasmic protei
852	4	36.4	198	2	S48994	925	4	36.4	211	2	E81382	hypothetical prote
853	4	36.4	198	2	T19385	926	4	36.4	211	2	S28046	TUB8 protein - pot
854	4	36.4	199	2	J50430	927	4	36.4	212	2	T51629	endoplasmatic reti
855	4	36.4	199	2	A82360	928	4	36.4	212	2	A83521	conserved hypotnet
856	4	36.4	199	2	S23379	929	4	36.4	213	1	HSRBI3	histone H1.3 - rab
857	4	36.4	199	2	A82721	930	4	36.4	213	1	S24363	ribosomal protein
858	4	36.4	199	2	S15164	931	4	36.4	213	2	JE0247	Ig lambda chain NI
859	4	36.4	199	2	S72728	932	4	36.4	213	2	S21066	Ig lambda chain V
860	4	36.4	199	2	S05509	933	4	36.4	213	2	S75886	hypothetical prote
861	4	36.4	199	2	S77228	934	4	36.4	213	2	E83979	hypothetical prote
862	4	36.4	199	2	T18879	935	4	36.4	213	2	G85673	hypothetical prote
863	4	36.4	199	2	T29151	936	4	36.4	213	2	F64854	ycfM protein precu
864	4	36.4	199	2	D83773	937	4	36.4	213	2	F70946	probable regulato
865	4	36.4	200	1	MORT3V	938	4	36.4	213	2	E82698	conserved hypotnet
866	4	36.4	200	2	G75550	939	4	36.4	214	1	JC4808	ribosomal protein
867	4	36.4	201	2	UC5337	940	4	36.4	214	2	C82255	adenylate kinase V
868	4	36.4	201	2	D70619	941	4	36.4	214	2	S39831	hypothetical prote
869	4	36.4	201	2	S37847	942	4	36.4	214	2	S17807	hypothetical prote
870	4	36.4	201	2	A47742	943	4	36.4	214	2	H85359	hypothetical prote
871	4	36.4	202	2	T46523	944	4	36.4	215	2	C85584	probable tail comp
872	4	36.4	202	2	I53137	945	4	36.4	215	2	A86437	hypothetical prote
873	4	36.4	202	2	A42410	946	4	36.4	215	2	H82483	probable hexulose-
874	4	36.4	202	2	S06882	947	4	36.4	215	2	S73929	ribosomal protein
875	4	36.4	202	2	D83578	948	4	36.4	215	2	H86774	hypothetical prote
876	4	36.4	202	2	T48709	949	4	36.4	215	2	B70622	probable ribosomal
877	4	36.4	202	2	S64051	950	4	36.4	215	2	T22446	hypothetical prote
878	4	36.4	203	1	T31684	951	4	36.4	216	2	PC4355	connectin - chicke
879	4	36.4	203	2	H65052	952	4	36.4	216	2	JE0245	Ig lambda chain NI
880	4	36.4	203	2	T12808	953	4	36.4	216	2	A42193	Ig lambda chain (B
881	4	36.4	203	2	H86713	954	4	36.4	216	2	S03401	Ig lambda chain (K
882	4	36.4	203	2	F96694	955	4	36.4	216	2	S29258	Ig lambda chain V
883	4	36.4	203	2	C85921	956	4	36.4	216	2	S69130	Ig lambda chain (D
884	4	36.4	203	2	B83166	957	4	36.4	216	2	S36288	T-cell receptor ga
885	4	36.4	203	2	T18679	958	4	36.4	216	2	T33964	hypothetical prote
886	4	36.4	204	1	D70111	959	4	36.4	216	2	T00121	hypothetical prote
887	4	36.4	204	2	G75307	960	4	36.4	217	2	JE0246	Ig lambda chain NI
888	4	36.4	204	2	S44829	961	4	36.4	217	2	T37859	probable transcrip
889	4	36.4	204	2	G82468	962	4	36.4	217	2	T30805	hypothetical prote
890	4	36.4	204	2	A82216	963	4	36.4	217	2	F82612	hypothetical prote
891	4	36.4	205	2	T32959	964	4	36.4	217	2	S45446	hypothetical prote
892	4	36.4	205	2	T02662	965	4	36.4	218	2	S34359	ornithine carbamoy
893	4	36.4	205	2	B82237	966	4	36.4	218	2	G70550	butyrate--acetace
894	4	36.4	205	2	H85072	967	4	36.4	218	2	A71304	hypothetical prote
895	4	36.4	206	1	HSTR1R	968	4	36.4	218	2	B72116	hypothetical prote
896	4	36.4	206	2	G70307	969	4	36.4	218	2	T30000	hypothetical prote
897	4	36.4	206	2	UC5491	970	4	36.4	219	1	HSXLIB	histone H1B - Afri
898	4	36.4	206	2	B81819	971	4	36.4	219	2	T08083	H+-transporting AT
899	4	36.4	206	2	T34979	972	4	36.4	219	2	E75025	1-Isospartyl prot
900	4	36.4	206	2	G86279	973	4	36.4	219	2	T26632	hypothetical prote
901	4	36.4	206	2	T32854	974	4	36.4	219	2	A86649	hypothetical prote
902	4	36.4	207	2	F69609	975	4	36.4	219	2	S42674	adhesive protein -
903	4	36.4	208	2	B49444	976	4	36.4	220	2	DB3390	carbonate dehydrat
904	4	36.4	208	2	I70195	977	4	36.4	220	2	I51447	histone H1B - Afri
905	4	36.4	208	2	B86887	978	4	36.4	220	2	A46597	acidic calmodulin-

687	4	36.4	160	2	S18658	variant surface an
688	4	36.4	160	2	H69015	ribosomal protein
689	4	36.4	160	2	F84350	hypothetical prote
690	4	36.4	160	2	A82733	conserved hypotet
691	4	36.4	161	2	J00352	heat shock protein
692	4	36.4	161	2	A29557	calcium-binding pr
693	4	36.4	161	2	S05547	dehydrin 17 - barl
694	4	36.4	161	2	B84366	hypothetical prote
695	4	36.4	162	2	JC7157	calcium vector pro
696	4	36.4	162	2	T50504	DRI-like protein -
697	4	36.4	162	2	S28122	gas-vesicle operon
698	4	36.4	162	2	T40004	hypothetical prote
699	4	36.4	162	2	S74418	hypothetical prote
700	4	36.4	163	2	F83059	acetylactate synth
701	4	36.4	163	2	H81066	acetylactate synth
702	4	36.4	163	2	F49905	protein secretion
703	4	36.4	163	2	B44813	probable molybdenu
704	4	36.4	163	2	E75416	hypothetical prote
705	4	36.4	163	2	T33130	hypothetical prote
706	4	36.4	164	1	S74345	protein-tyrosine-p
707	4	36.4	164	2	T37174	hypothetical prote
708	4	36.4	164	2	D85928	hypothetical prote
709	4	36.4	165	1	S70213	hypothetical prote
710	4	36.4	165	2	D96758	hypothetical prote
711	4	36.4	165	2	A60611	18K microfilariar
712	4	36.4	165	2	S55766	transcription init
713	4	36.4	165	2	H83918	hypothetical prote
714	4	36.4	166	2	B76526	hypothetical prote
715	4	36.4	167	1	S37878	IgE-dependent hist
716	4	36.4	167	2	S50808	hypothetical prote
717	4	36.4	167	2	E83743	4-hydroxybenzoyl-C
718	4	36.4	167	2	H72579	hypothetical prote
719	4	36.4	168	2	JN0073	glycophorin A - mo
720	4	36.4	168	2	E75257	molybdenum cofact
721	4	36.4	168	2	T02036	early light-induce
722	4	36.4	168	2	S65242	hypothetical prote
723	4	36.4	168	2	T20606	hypothetical prote
724	4	36.4	169	2	D81180	16S rRNA processin
725	4	36.4	169	2	B81924	probable 16S rRNA
726	4	36.4	169	2	S47066	finger protein HZF
727	4	36.4	170	2	E81662	Holliday junction
728	4	36.4	170	2	JT0588	hypothetical 20K p
729	4	36.4	171	2	E83140	phosphatidylglycer
730	4	36.4	171	2	H81029	lipoprotein NMB189
731	4	36.4	171	2	E81974	lipoprotein NMA055
732	4	36.4	171	2	S40769	hypothetical prote
733	4	36.4	172	1	F1883F	translation initia
734	4	36.4	172	2	B64320	acetylactate synth
735	4	36.4	172	2	S77842	probable asparagin
736	4	36.4	172	2	A45637	microcolte surface
737	4	36.4	172	2	F82309	autoinducer-2 prod
738	4	36.4	172	2	T36713	hypothetical prote
739	4	36.4	172	2	I40349	ribosomal protein
740	4	36.4	173	2	S69519	hypothetical prote
741	4	36.4	174	2	H83481	hypothetical prote
742	4	36.4	174	2	T51542	hypothetical prote
743	4	36.4	175	2	E83777	O6-methylguanine D
744	4	36.4	175	2	S70915	major oleosin nap-
745	4	36.4	175	2	B86767	hypothetical prote
746	4	36.4	176	2	G70658	probable aroK prot
747	4	36.4	176	2	A73624	hypothetical prote
748	4	36.4	176	2	T35459	hypothetical prote
749	4	36.4	177	2	F84782	60S ribosomal prot
750	4	36.4	177	2	S53952	protease 2 precu
751	4	36.4	177	2	D82638	hypothetical prote
752	4	36.4	177	2	D83135	hypothetical prote
753	4	36.4	178	1	A39070	endothelin 2 precu
754	4	36.4	178	2	S74564	hypothetical prote
755	4	36.4	178	2	T49712	hypothetical prote
756	4	36.4	178	2	E75340	conserved hypotet
757	4	36.4	178	2	H85816	hypothetical prote
758	4	36.4	179	2	F71854	probable outer mem
759	4	36.4	179	2	E64660	peptidoglycan asso
760	4	36.4	179	2	H85429	ribosomal protein
761	4	36.4	179	2	T48372	hypothetical prote
762	4	36.4	180	1	J00986	lipid body-associ
763	4	36.4	180	2	S72923	hypothetical prote
764	4	36.4	180	2	F83797	hypothetical prote
765	4	36.4	180	2	G83985	hypothetical prote
766	4	36.4	181	2	D85630	hypothetical prote
767	4	36.4	182	2	E72630	hypothetical prote
768	4	36.4	182	2	F69387	hypothetical prote
769	4	36.4	182	2	T23828	hypothetical prote
770	4	36.4	183	2	F82882	ribosome releasing
771	4	36.4	183	2	S59091	conserved hypotet
772	4	36.4	183	2	E69388	hypothetical prote
773	4	36.4	183	2	E96582	hypothetical prote
774	4	36.4	183	2	B64547	hypothetical prote
775	4	36.4	183	2	T28711	hypothetical prote
776	4	36.4	184	2	A82013	tdDP-4-dehydrotham
777	4	36.4	184	2	A45281	transcription fact
778	4	36.4	184	2	H72070	heat shock protein
779	4	36.4	184	2	B86553	HSP-70 cofactor [1
780	4	36.4	184	2	A69525	hypothetical prote
781	4	36.4	184	2	E96594	unknown protein, 6
782	4	36.4	184	2	A82631	hypothetical prote
783	4	36.4	184	2	S73868	lipoprotein signal
784	4	36.4	184	2	S25815	hypothetical prote
785	4	36.4	185	2	S59560	histone H1.41 - ga
786	4	36.4	185	2	S38959	ribosomal protein
787	4	36.4	185	2	H82799	fibrinillin XFO487
788	4	36.4	185	2	D84456	hypothetical prote
789	4	36.4	186	1	R5BY8E	ribosomal protein
790	4	36.4	187	2	S77483	adenylate kinase (
791	4	36.4	188	2	S25979	ribosomal protein
792	4	36.4	188	2	T26939	hypothetical prote
793	4	36.4	188	2	E65207	hypothetical 20.4
794	4	36.4	188	2	C86092	hypothetical prote
795	4	36.4	188	2	D82240	conserved hypotet
796	4	36.4	189	2	S71465	fibrinectin - chic
797	4	36.4	189	2	G75349	conserved hypotet
798	4	36.4	189	2	T43766	hypothetical prote
799	4	36.4	189	2	T21254	hypothetical prote
800	4	36.4	190	2	A82015	tdDP-4-dehydrotham
801	4	36.4	190	2	S25740	Ig lambda chain -
802	4	36.4	190	2	S66981	ribosomal protein
803	4	36.4	190	2	E64775	probable lipoprote
804	4	36.4	190	2	G85542	glycoprotein/polyv
805	4	36.4	190	2	T43013	conserved hypotet
806	4	36.4	190	2	T25462	hypothetical prote
807	4	36.4	191	2	S56012	XS-2 protein (homo
808	4	36.4	191	2	S40177	Exoi protein - Rhl
809	4	36.4	191	2	H81444	probable cytochrom
810	4	36.4	191	2	T35508	hypothetical prote
811	4	36.4	192	2	S42963	viral infectivity
812	4	36.4	192	2	T09382	vif protein - huma
813	4	36.4	192	2	A48353	genome polyprotein
814	4	36.4	192	2	B48353	genome polyprotein
815	4	36.4	192	2	A83798	transcriptional re
816	4	36.4	192	2	F72805	gp49 protein - Myc
817	4	36.4	193	2	B69178	hypothetical prote
818	4	36.4	193	2	T44106	hypothetical prote
819	4	36.4	193	2	G64356	hypothetical prote
820	4	36.4	194	1	C75206	L-fucose-phospha
821	4	36.4	194	1	HSTR1	histone H1 - trout
822	4	36.4	194	1	HSU10	histone H1.0 - hum
823	4	36.4	194	2	A82072	conserved hypotet
824	4	36.4	194	2	E69899	hypothetical prote
825	4	36.4	194	2	S72877	hypothetical prote
826	4	36.4	194	2	T44862	transcription regu
827	4	36.4	194	2	B64159	hypothetical prote
828	4	36.4	194	2	T14746	hypothetical prote
829	4	36.4	195	1	MOHU3V	myosin alkali. ligh
830	4	36.4	195	1	WCICA	coaglogen precurs
831	4	36.4	195	2	S24228	BHV-1 protein homo
832	4	36.4	195	2	E70555	hypothetical prote

541	4	36.4	130	2	S46702	hypothetical prote
542	4	36.4	131	1	RDEB15	funarate reductase
543	4	36.4	131	2	S56380	succinate dehydrog
544	4	36.4	131	2	E86111	hypothetical prote
545	4	36.4	131	2	E30552	T-cell activation
546	4	36.4	131	2	H75323	hypothetical prote
547	4	36.4	132	1	RWMSAV	T-cell receptor al
548	4	36.4	132	1	G69256	conserved hypoteth
549	4	36.4	132	2	T48278	hypothetical prote
550	4	36.4	133	2	S61662	dolichyl-diphospho
551	4	36.4	134	1	AMHUB	natriuretic peptid
552	4	36.4	134	2	G82411	conserved hypoteth
553	4	36.4	134	2	JC6091	kinetoplast DNA-as
554	4	36.4	134	2	D64744	exopolysaccharide
555	4	36.4	134	2	F85504	hypothetical prote
556	4	36.4	134	2	B72737	hypothetical prote
557	4	36.4	134	2	D81096	hypothetical prote
558	4	36.4	135	2	S56687	histone H2B153 - w
559	4	36.4	135	2	C70890	hypothetical prote
560	4	36.4	136	2	S56684	histone H2B-6 - wh
561	4	36.4	136	2	S76416	hypothetical prote
562	4	36.4	136	2	T07975	probable arabinoga
563	4	36.4	136	2	T07945	probable arabinoga
564	4	36.4	136	2	C72575	hypothetical prote
565	4	36.4	137	2	T02035	histone H2B - maiz
566	4	36.4	137	2	T22308	hypothetical prote
567	4	36.4	138	2	C27577	T-cell receptor al
568	4	36.4	138	2	S56685	histone H2B-8 - wh
569	4	36.4	138	2	B84793	probable histone H
570	4	36.4	138	2	T45905	histone H2B-like p
571	4	36.4	138	2	T39504	hypothetical prote
572	4	36.4	138	2	F86117	probable transposa
573	4	36.4	139	2	E65036	hypothetical prote
574	4	36.4	139	2	T06389	histone H2B-2 - to
575	4	36.4	139	2	G85904	probable chlorodex
576	4	36.4	140	2	PH0134	Ig Lambda chain pr
577	4	36.4	140	2	JC4607	hydrophobin 1 prec
578	4	36.4	140	2	C69269	hypothetical prote
579	4	36.4	140	2	G65090	hypothetical prote
580	4	36.4	140	2	H85963	probable enzyme yq
581	4	36.4	141	2	G69904	capsular polysacch
582	4	36.4	141	2	A27482	vasotocin / neurop
583	4	36.4	141	2	H70698	hypothetical prote
584	4	36.4	141	2	H75583	probable copper re
585	4	36.4	141	2	PC1294	triphosphite surfac
586	4	36.4	141	2	T46380	hypothetical prote
587	4	36.4	141	2	C72606	hypothetical prote
588	4	36.4	142	2	T06393	histone H2B - toma
589	4	36.4	142	2	T10078	hypothetical prote
590	4	36.4	142	2	G84201	diadenosine tetrap
591	4	36.4	143	1	GPYF-	leghemoglobin I -
592	4	36.4	143	2	I48406	histone H2A.X - mo
593	4	36.4	143	2	S07631	histone H2A.X - hu
594	4	36.4	143	2	C86061	hypothetical prote
595	4	36.4	143	2	S10208	hypothetical 16.5K
596	4	36.4	143	2	F86168	hypothetical prote
597	4	36.4	143	2	E30338	DNA transport mach
598	4	36.4	143	2	A83431	type III export pr
599	4	36.4	144	2	C69889	hypothetical prote
600	4	36.4	144	2	T25028	hypothetical prote
601	4	36.4	144	2	A86795	hypothetical prote
602	4	36.4	144	2	T01476	hypothetical prote
603	4	36.4	145	2	T08063	histone H2B - pepp
604	4	36.4	145	2	H72544	hypothetical prote
605	4	36.4	145	2	F83834	hypothetical prote
606	4	36.4	145	2	T01424	pectinesterase hom
607	4	36.4	145	2	F82133	hypothetical prote
608	4	36.4	145	2	F96766	protein actin F2P9
609	4	36.4	146	2	T12137	leghemoglobin K -
610	4	36.4	146	2	S47771	hypothetical 17.1k
611	4	36.4	146	2	B64053	ferric uptake regu
612	4	36.4	146	2	T07125	plastid-lipid-asso
613	4	36.4	146	2	B83700	hypothetical prote
614	4	36.4	146	2	G86029	hypothetical prote
615	4	36.4	147	2	T18577	peptidylprolyl iso
616	4	36.4	147	2	T09722	histone H2B1 - upl
617	4	36.4	147	2	A70977	probable ribosomal
618	4	36.4	147	2	S72991	ribosomal protein
619	4	36.4	147	2	S00848	fibronectin, trans
620	4	36.4	147	2	T30616	hypothetical prote
621	4	36.4	147	2	G72626	probable GTP cyclo
622	4	36.4	147	2	S32015	flagellum-associat
623	4	36.4	147	2	T13202	hypothetical prote
624	4	36.4	148	2	T37532	ubiquitin-conjugat
625	4	36.4	148	2	B45637	merozoite surfact
626	4	36.4	148	2	E81788	conserved hypoteth
627	4	36.4	148	2	T22508	hypothetical prote
628	4	36.4	149	2	S23626	Ig lambda chain V
629	4	36.4	149	2	D82178	hypothetical prote
630	4	36.4	150	1	WMVZR2	I7K protein - vacc
631	4	36.4	150	2	S28049	histone H2B - maiz
632	4	36.4	150	2	F72163	AIL protein - vari
633	4	36.4	150	2	C42517	AIL protein - vacc
634	4	36.4	150	2	B36848	AIL protein - vari
635	4	36.4	150	2	T28542	hypothetical prote
636	4	36.4	150	2	T37387	VLRF-2, late gene
637	4	36.4	150	2	T24956	hypothetical prote
638	4	36.4	150	2	T37513	probable acetyltra
639	4	36.4	150	2	S58172	mithramycin polyke
640	4	36.4	150	2	T52587	probable arabinoga
641	4	36.4	150	2	T48611	ag86 protein - Ara
642	4	36.4	150	2	E83057	hypothetical prote
643	4	36.4	150	2	T17314	hypothetical prote
644	4	36.4	151	1	MUBPA7	N-acetylmuramoyl-L
645	4	36.4	151	2	S07506	L-N-acetylmuramoyl-L
646	4	36.4	151	2	S28048	histone H2B - maiz
647	4	36.4	151	2	D84688	probable histone H
648	4	36.4	151	2	E65178	high affinity ribo
649	4	36.4	152	1	DABP73	adenosylmethionine
650	4	36.4	152	2	S14236	Ig gamma-1 chain C
651	4	36.4	152	2	S22323	histone H2B - whea
652	4	36.4	152	2	T17873	hypothetical prote
653	4	36.4	153	2	T44263	tRNA-pseudouridine
654	4	36.4	153	2	A64674	hypothetical prote
655	4	36.4	153	2	F71841	hypothetical prote
656	4	36.4	153	2	D64364	formate hydrogeny
657	4	36.4	154	1	DFSECM	aspartate carbamoyl
658	4	36.4	154	2	T02077	histone H2B - maiz
659	4	36.4	154	2	T08308	hypothetical prote
660	4	36.4	154	2	B83444	conserved hypoteth
661	4	36.4	154	2	E72485	hypothetical prote
662	4	36.4	155	2	T05169	Ls61 protein homol
663	4	36.4	155	2	S56258	hypothetical prote
664	4	36.4	155	2	G83774	hypothetical prote
665	4	36.4	155	2	E69482	hypothetical prote
666	4	36.4	155	2	T16855	hypothetical prote
667	4	36.4	155	2	T00134	ribosomal protein
668	4	36.4	156	1	R3KRT3A	conserved hypoteth
669	4	36.4	156	2	A81015	conserved hypoteth
670	4	36.4	156	2	G83199	conserved hypoteth
671	4	36.4	156	2	T02806	probable membrane
672	4	36.4	156	2	S74733	hypothetical prote
673	4	36.4	157	1	JC2444	ribosomal protein
674	4	36.4	157	2	JN0549	ribosomal protein
675	4	36.4	157	2	S57603	hypothetical prote
676	4	36.4	157	2	T23000	hypothetical prote
677	4	36.4	157	2	T50859	hypothetical prote
678	4	36.4	158	2	E84956	response regulator
679	4	36.4	158	2	D81820	acetoacetate synth
680	4	36.4	158	2	C71406	hypothetical prote
681	4	36.4	158	2	S74730	hypothetical prote
682	4	36.4	159	2	T06768	disease resistance
683	4	36.4	159	2	H75391	hypothetical prote
684	4	36.4	159	2	J00136	hypothetical 17.8k
685	4	36.4	160	1	S17194	endothelin 2 precu
686	4	36.4	160	2	C69526	histidine triad pr

395	4	36.4	104	2	F85359	hypothetical prote
396	4	36.4	104	2	B39435	hypothetical prote
397	4	36.4	105	1	L2HU	Ig lambda chain C
398	4	36.4	105	1	ASLJGR2	vpr protein - huma
399	4	36.4	105	1	ASLJGR	vpr protein - huma
400	4	36.4	105	1	S12156	vpr protein - huma
401	4	36.4	105	2	S53095	hypothetical prote
402	4	36.4	105	2	E64550	apolipoprotein 1 p
403	4	36.4	105	2	A26602	probable membrane
404	4	36.4	105	2	S48425	hypothetical IS110
405	4	36.4	105	2	E81798	hypothetical prote
406	4	36.4	106	1	A70701	thioredoxin - Rhod
407	4	36.4	106	1	A35135	conserved hypotet
408	4	36.4	106	2	F69055	probable periplasm
409	4	36.4	106	2	H72547	hypothetical prote
410	4	36.4	106	2	E72461	protein disulfide
411	4	36.4	107	2	T17951	subtilisin-trypsin
412	4	36.4	107	2	JX0361	Ig lambda chain V-
413	4	36.4	107	2	B46516	T-cell receptor V-
414	4	36.4	107	2	S40133	hypothetical prote
415	4	36.4	107	2	T31471	hypothetical prote
416	4	36.4	107	2	T27713	Ig kappa chain V-I
417	4	36.4	108	1	K1H0WE	thioredoxin [valid
418	4	36.4	109	1	TXEC	thioredoxin - Salm
419	4	36.4	109	1	S35497	Ig lambda chain V-
420	4	36.4	109	2	L1HUEP	hypothetical prote
421	4	36.4	109	2	S77093	NADH dehydrogenase
422	4	36.4	110	2	S15107	Ig lambda chain V-
423	4	36.4	110	2	S57408	Ig lambda chain V-
424	4	36.4	110	2	S57428	Ig light chain V-J
425	4	36.4	110	2	A49056	T-cell receptor al
426	4	36.4	110	2	T48830	hypothetical prote
427	4	36.4	110	2	E82745	hypothetical prote
428	4	36.4	110	2	T02713	50S ribosomal prot
429	4	36.4	111	1	L1H0NM	Ig lambda chain V-
430	4	36.4	111	1	L1H0NG	Ig lambda chain V-
431	4	36.4	111	1	L2H0VL	Ig lambda chain V-
432	4	36.4	111	2	S47009	Ig lambda chain VI
433	4	36.4	111	2	S47185	Ig lambda chain -
434	4	36.4	111	2	S22899	T-cell receptor al
435	4	36.4	111	2	T06418	pathogenesis-relat
436	4	36.4	111	2	E56556	fork head homolog
437	4	36.4	112	1	L1H0HA	Ig lambda chain V-
438	4	36.4	112	1	L1H0MM	Ig lambda chain V-
439	4	36.4	112	2	D44151	Ig lambda chain V
440	4	36.4	112	2	S51148	antibody light cha
441	4	36.4	112	2	C44151	Ig lambda chain V
442	4	36.4	112	2	S03503	T-cell receptor al
443	4	36.4	112	2	S40284	protein-tyrosine-p
444	4	36.4	112	2	A46717	collipase precursor
445	4	36.4	112	2	F75628	hypothetical prote
446	4	36.4	112	2	A84369	hypothetical prote
447	4	36.4	112	2	G81802	insertion element
448	4	36.4	113	1	KVMS75	Ig kappa chain V r
449	4	36.4	113	2	S42571	subtilisin inhibit
450	4	36.4	113	2	T36670	probable anti-sigm
451	4	36.4	114	2	C86362	cytochrome C [lipo
452	4	36.4	114	2	E84971	hypothetical prote
453	4	36.4	115	2	T07233	ribosomal protein
454	4	36.4	115	2	T48602	hypothetical prote
455	4	36.4	115	2	D84501	hypothetical prote
456	4	36.4	116	2	S62681	ribosomal protein
457	4	36.4	116	2	S24989	ribosomal protein
458	4	36.4	116	2	B40617	transcription repr
459	4	36.4	116	2	E72509	probable non speci
460	4	36.4	117	2	S04525	Ig lambda chain pr
461	4	36.4	117	2	S23627	Ig lambda chain pr
462	4	36.4	117	2	B44253	alveolar macrophag
463	4	36.4	117	2	S31130	hypothetical prote
464	4	36.4	117	2	T30740	hypothetical prote
465	4	36.4	117	2	A83312	conserved hypotet
466	4	36.4	117	2	JH0658	histone H1-like pr
467	4	36.4	118	1	R7MCML	ribosomal protein
468	4	36.4	118	2	S47077	Wnt-B protein - F1
469	4	36.4	118	2	S12627	Ig lambda chain pr
470	4	36.4	118	2	S21918	T-cell receptor al
471	4	36.4	118	2	S12440	Ig lambda chain (M
472	4	36.4	118	2	S12441	Ig lambda chain (K
473	4	36.4	118	2	S12442	Ig lambda chain (K
474	4	36.4	118	2	T07177	probable oleoyl-la
475	4	36.4	118	2	S49913	crotopogenin - Phy
476	4	36.4	118	2	S49905	acidic elicitin A1
477	4	36.4	118	2	G64544	hypothetical prote
478	4	36.4	118	2	F71964	hypothetical prote
479	4	36.4	118	2	E33958	hypothetical 14k p
480	4	36.4	118	2	B85686	unknown protein en
481	4	36.4	118	2	T05520	geranylgeranylated
482	4	36.4	119	1	PSOXA	phospholipase A2 (
483	4	36.4	119	2	T14396	lipid transfer pro
484	4	36.4	119	2	T07984	lipid transfer pro
485	4	36.4	119	2	T06007	ribosomal protein
486	4	36.4	119	2	S76276	hypothetical prote
487	4	36.4	119	2	E64940	hypothetical prote
488	4	36.4	119	2	F85790	hypothetical prote
489	4	36.4	119	2	B72526	hypothetical prote
490	4	36.4	119	2	B84451	probable nitrilase
491	4	36.4	120	2	A61301	histone H2B - Tet
492	4	36.4	120	2	F86395	histone H2B - Tet
493	4	36.4	120	2	G65009	60S ribosomal prot
494	4	36.4	120	2	S56686	histone H2B.2 - w
495	4	36.4	121	2	B82946	histone H2B123 - w
496	4	36.4	121	2	S11671	ribosomal protein
497	4	36.4	121	2	D71527	hypothetical prote
498	4	36.4	121	2	S75660	hypothetical prote
499	4	36.4	122	2	A27097	histone H2B.1 - Te
500	4	36.4	122	2	B27097	histone H2B.2 - Te
501	4	36.4	122	2	S77492	ribosomal protein
502	4	36.4	123	2	F72630	hypothetical prote
503	4	36.4	123	2	E64418	conserved hypotet
504	4	36.4	123	2	S49906	HA6 (highly acidic
505	4	36.4	123	2	B75546	hypothetical prote
506	4	36.4	123	2	D86755	prophage p12 prote
507	4	36.4	123	2	A64525	hypothetical prote
508	4	36.4	124	2	I40348	ribosomal protein
509	4	36.4	124	2	I40350	ribosomal protein
510	4	36.4	124	2	E70148	ribosomal protein
511	4	36.4	124	2	S72681	probable membrane
512	4	36.4	124	2	S38476	lys protein - pha
513	4	36.4	125	1	F1SP4	photosystem I chal
514	4	36.4	125	1	H64637	probable translati
515	4	36.4	125	2	A81310	30S ribosomal prot
516	4	36.4	125	2	E70332	conserved hypotet
517	4	36.4	125	2	A71878	hypothetical prote
518	4	36.4	125	2	T43414	DNA-directed RNA p
519	4	36.4	125	2	S74966	hypothetical prote
520	4	36.4	125	2	T00706	hypothetical prote
521	4	36.4	125	2	C72471	hypothetical prote
522	4	36.4	126	2	S53545	probable membrane
523	4	36.4	126	2	S09919	hypothetical prote
524	4	36.4	126	2	S75837	hypothetical prote
525	4	36.4	127	2	C86064	thioredoxin 1 [limp
526	4	36.4	127	2	T36833	ribosomal protein
527	4	36.4	127	2	C84502	En/Spm-like transp
528	4	36.4	127	2	F82405	glyoxylase I fam11
529	4	36.4	128	2	A60215	myelin basic prote
530	4	36.4	128	2	A72404	hypothetical prote
531	4	36.4	128	2	T40344	hypothetical zinc
532	4	36.4	128	2	PE0006	histidinol dehydro
533	4	36.4	129	1	K1H0DI	Ig kappa chain pre
534	4	36.4	129	2	S78058	Ig lambda chain pr
535	4	36.4	129	2	D49094	methylnalonyl-CoA
536	4	36.4	130	1	L1H0BL	Ig lambda chain pr
537	4	36.4	130	2	S09712	Ig lambda chain V
538	4	36.4	130	2	S78057	Ig lambda chain pr
539	4	36.4	130	2	A75010	hypothetical prote
540	4	36.4	130	2	E70353	hypothetical prote

249	5	45.5	1929	2	T21559	hypothetical prote
250	5	45.5	1994	2	D86452	protein F6N18.13 [
251	5	45.5	2187	2	T30826	nascent polypeptid
252	5	45.5	2212	2	T28157	erythrocyte membra
253	5	45.5	2278	1	S56274	FAB1 protein - yea
254	5	45.5	2647	2	T28161	hypothetical prote
255	5	45.5	2756	2	T30183	hypothetical prote
256	5	45.5	6805	2	S20901	titlin - rabbit (fr
257	5	45.5	138344	1	I38344	titlin, cardiac mus
258	4	36.4	26926	9	PC7078	unidentified 48.7k
259	4	36.4	9	2	PN0115	insulin-like growt
260	4	36.4	20	2	E41299	T-cell receptor al
261	4	36.4	21	2	D47256	kinetoplast DNA-as
262	4	36.4	22	2	PC1272	subtilisin inhibit
263	4	36.4	34	2	S55417	pyruvate synthase
264	4	36.4	35	2	S69599	potassium channel
265	4	36.4	36	2	A82208	hypothetical prote
266	4	36.4	38	2	S23173	photosystem I chaf
267	4	36.4	40	2	S32045	Ig gamma-1 chain C
268	4	36.4	42	2	T36238	hypothetical prote
269	4	36.4	45	1	HPBO	haptoglobin precu
270	4	36.4	47	2	FA7395	histone H1 II-1 (c
271	4	36.4	47	2	S43964	hypothetical prote
272	4	36.4	48	2	S74261	tiopronin T3f, fast
273	4	36.4	51	2	I39691	cytochrome-c3 hydr
274	4	36.4	51	2	I39691	orf 3' of Idh - lac
275	4	36.4	52	2	HA7395	histone H1 II-1 (c
276	4	36.4	52	2	S01945	myosin catalytic I
277	4	36.4	53	2	F47395	histone H1 II-1 (c
278	4	36.4	53	2	B47395	histone H1 II-1 (c
279	4	36.4	53	2	C47395	histone H1 II-1 (c
280	4	36.4	53	2	D47395	histone H1 II-1 (c
281	4	36.4	53	2	GA7395	histone H1 II-2 (c
282	4	36.4	56	2	S74259	tiopronin T 3, fast
283	4	36.4	56	2	B72804	gp36 protein - Myc
284	4	36.4	56	2	F81824	hypothetical prote
285	4	36.4	57	2	S62889	non-histone protei
286	4	36.4	59	2	S74260	tiopronin T1f, fast
287	4	36.4	60	2	A30160	H+-transporting AT
288	4	36.4	60	2	D85758	hypothetical prote
289	4	36.4	60	2	C82812	hypothetical prote
290	4	36.4	61	2	F81844	hypothetical prote
291	4	36.4	61	2	T19658	hypothetical prote
292	4	36.4	62	2	T30977	hypothetical prote
293	4	36.4	62	2	T10302	hypothetical prote
294	4	36.4	64	2	F83334	hypothetical prote
295	4	36.4	64	2	D82032	hypothetical prote
296	4	36.4	64	2	E81008	hypothetical prote
297	4	36.4	66	2	H81813	hypothetical prote
298	4	36.4	67	2	S48660	troponin T 1, fast
299	4	36.4	67	2	A85736	hypothetical prote
300	4	36.4	67	2	B55855	tall protein - pha
301	4	36.4	67	2	D64894	hypothetical prote
302	4	36.4	68	2	T45155	hypothetical prote
303	4	36.4	69	2	C84275	hypothetical prote
304	4	36.4	69	2	S51861	hypothetical prote
305	4	36.4	70	2	S25190	hypothetical prote
306	4	36.4	70	2	T46343	plin precursor -
307	4	36.4	71	2	A60325	hypothetical prote
308	4	36.4	71	2	E75316	cytochrome-c oxida
309	4	36.4	71	2	D82541	hypothetical prote
310	4	36.4	72	2	T17585	hypothetical prote
311	4	36.4	73	2	T68536	hypothetical prote
312	4	36.4	73	2	A36260	pepsinogen - huma
313	4	36.4	73	2	B86279	alpha-2-macroglobu
314	4	36.4	74	2	S42233	hypothetical prote
315	4	36.4	74	2	E69871	fixg protein - Azo
316	4	36.4	74	2	H70070	hypothetical prote
317	4	36.4	75	2	B64988	hypothetical prote
318	4	36.4	75	2	A85858	hypothetical prote
319	4	36.4	76	2	H70576	hypothetical prote
320	4	36.4	76	2	T03810	hypothetical prote
321	4	36.4	77	2	C86842	30S ribosomal prot
322	4	36.4	77	2	B75454	hypothetical prote
323	4	36.4	79	2	T44149	hypothetical prote
324	4	36.4	79	2	T26118	hypothetical prote
325	4	36.4	81	2	D69082	ribosomal protein
326	4	36.4	81	2	S28041	hemp protein - yer
327	4	36.4	83	2	S66246	nuclear factor int
328	4	36.4	83	2	A46348	hypothetical prote
329	4	36.4	83	2	A33854	outer membrane lip
330	4	36.4	84	1	MMBPMB	gene p protein - p
331	4	36.4	84	1	T27174	hypothetical prote
332	4	36.4	85	2	T4165	hypothetical prote
333	4	36.4	86	1	OCB07	cytochrome-c oxida
334	4	36.4	86	2	T07204	hypothetical prote
335	4	36.4	87	1	D45345	trans-activating t
336	4	36.4	87	2	S44877	zC21.5 protein - C
337	4	36.4	88	2	T36450	hypothetical prote
338	4	36.4	89	2	S15467	hypothetical prote
339	4	36.4	89	2	E84167	LI protein - bovin
340	4	36.4	89	2	D72581	hypothetical prote
341	4	36.4	90	1	OOBECF	hypothetical prote
342	4	36.4	90	2	C85516	legument protein -
343	4	36.4	90	2	T33692	probable activator
344	4	36.4	91	1	W4WL58	hypothetical prote
345	4	36.4	91	2	D64066	E4 protein - human
346	4	36.4	91	2	D86503	host factor I - Ha
347	4	36.4	91	2	T30512	hypothetical prote
348	4	36.4	91	2	B75623	hypothetical prote
349	4	36.4	91	2	C72119	hypothetical prote
350	4	36.4	93	2	T06803	probable dehydrin
351	4	36.4	94	2	T06417	pathogenesis-relat
352	4	36.4	94	2	JO1164	Tat protein - Maed
353	4	36.4	94	2	S67047	SMC1 protein - yea
354	4	36.4	95	2	SA9571	Ig lambda chain pr
355	4	36.4	95	2	G30603	T-cell receptor al
356	4	36.4	95	2	UC4760	SM73 protein - hum
357	4	36.4	95	2	T45315	hypothetical prote
358	4	36.4	96	2	B41898	dextranucrase (EC
359	4	36.4	97	2	H96743	probable Dnaa prot
360	4	36.4	97	2	S30990	gene 45 protein -
361	4	36.4	98	1	OCB06A	cytochrome-c oxida
362	4	36.4	98	2	S36068	Ig lambda chain -
363	4	36.4	98	2	S36047	Ig lambda chain -
364	4	36.4	98	2	S36048	Ig lambda chain -
365	4	36.4	98	2	S36050	Ig lambda chain -
366	4	36.4	98	2	SA9414	major carboxysome
367	4	36.4	98	2	S05527	capsicain - Phycop
368	4	36.4	98	2	S06671	cinamomnin - Phyto
369	4	36.4	99	2	S36051	Ig lambda chain -
370	4	36.4	99	2	S36052	Ig lambda chain -
371	4	36.4	99	2	S36053	Ig lambda chain -
372	4	36.4	99	2	S36054	Ig lambda chain -
373	4	36.4	99	2	S36058	Ig lambda chain -
374	4	36.4	99	2	S03525	T-cell receptor al
375	4	36.4	99	2	S42360	capsicain - Phycop
376	4	36.4	99	2	B86580	CTF656 hypothetical
377	4	36.4	99	2	E72043	conserved hypothet
378	4	36.4	100	1	MMWGN3	11k protein - narc
379	4	36.4	101	2	A36869	probable export pr
380	4	36.4	101	2	C69930	hypothetical prote
381	4	36.4	101	2	S30970	gene 25 protein -
382	4	36.4	101	2	G72802	grp25 protein - Myc
383	4	36.4	101	2	F85812	flagellar biosynthe
384	4	36.4	102	2	B48360	orly upstream of m
385	4	36.4	103	1	LIH0NM	Ig lambda chain V-
386	4	36.4	103	2	A38923	Al type amyloid fl
387	4	36.4	103	2	S62052	hypothetical prote
388	4	36.4	103	2	A71197	hypothetical prote
389	4	36.4	103	2	T40081	very hypothetical
390	4	36.4	103	2	T49368	hypothetical prote
391	4	36.4	103	2	D82165	hypothetical prote
392	4	36.4	103	2	G81399	2-oxoglutarate syn
393	4	36.4	104	1	ASLJCY	vpr protein - huma
394	4	36.4	104	1	ASLJCY	vpr protein - huma

103	5	45.5	343	2	A45073	Gal beta 1,3galNac
104	5	45.5	344	1	S35140	probable ketol-act
105	5	45.5	352	2	T36719	probable integral
106	5	45.5	354	2	S65687	(A+T)-stretch-bind
107	5	45.5	357	2	F70898	probable gfp-bind1
108	5	45.5	363	2	I64150	probable gfp-bind1
109	5	45.5	373	2	T451747	GDP-D-mannose-4,6-
110	5	45.5	373	2	E82570	chorismate mutase
111	5	45.5	375	2	F75467	probable lipoprote
112	5	45.5	378	2	A47300	cell adhesion prot
113	5	45.5	380	2	S51797	vasodilator-stimul
114	5	45.5	382	2	T14336	RAD23 protein, iso
115	5	45.5	385	2	T29315	hypothetical prote
116	5	45.5	388	2	T26372	hypothetical prote
117	5	45.5	398	2	S50507	excision repair pr
118	5	45.5	408	2	C70379	hypothetical prote
119	5	45.5	412	2	A48702	2-methyl-branched-
120	5	45.5	412	2	C72548	probable dihydrol
121	5	45.5	412	2	S17758	tubulin beta chain
122	5	45.5	414	1	JN0826	granulatin polyket
123	5	45.5	415	1	S05394	hypothetical prote
124	5	45.5	416	2	T34279	hypothetical prote
125	5	45.5	431	2	G75017	histidyl-tRNA synt
126	5	45.5	443	2	F83881	hypothetical prote
127	5	45.5	445	2	E70360	glucose inhibited
128	5	45.5	447	2	S37048	cysteine proteinas
129	5	45.5	448	2	T27955	hypothetical prote
130	5	45.5	448	2	S39348	26S ATP/ubiquitin-
131	5	45.5	448	2	T01570	hypothetical prote
132	5	45.5	451	2	D47691	UDP-N-acetylmuram
133	5	45.5	451	2	A81206	sugar transporter,
134	5	45.5	451	2	E81781	probable integral
135	5	45.5	456	2	T46986	hypothetical prote
136	5	45.5	457	2	T24962	odr-7 protein - Ca
137	5	45.5	459	1	KIXFV	major capsid prote
138	5	45.5	470	2	S50854	DAX-1 protein - hu
139	5	45.5	471	2	T48743	probable 26S ATP/u
140	5	45.5	476	2	B44997	merozoite surface
141	5	45.5	479	2	A38578	protein kinase 2 (
142	5	45.5	479	2	G83259	hypothetical prote
143	5	45.5	480	2	G96723	hypothetical prote
144	5	45.5	485	2	F83593	outer membrane pro
145	5	45.5	489	2	T04596	hypothetical prote
146	5	45.5	500	2	T19525	hypothetical prote
147	5	45.5	504	2	T13475	hypothetical prote
148	5	45.5	508	1	A30007	dolichyl-diphospho
149	5	45.5	508	1	ISRSSS	protein disulfide-
150	5	45.5	508	1	ISHUSS	protein disulfide-
151	5	45.5	509	1	ISMSSS	protein disulfide-
152	5	45.5	509	1	A38362	protein disulfide-
153	5	45.5	510	1	ISBOSS	protein disulfide-
154	5	45.5	510	2	A54798	Vg-1-related prote
155	5	45.5	513	2	F83162	nitrate reductase
156	5	45.5	515	1	ISCHSS	protein disulfide-
157	5	45.5	520	2	T04591	ferulate-5'-hydroxy
158	5	45.5	527	2	T07607	phosphate transpor
159	5	45.5	528	2	T05724	probable inorganic
160	5	45.5	533	2	S69336	arylsulfatase (EC
161	5	45.5	536	2	D84325	HttR1 transducer (
162	5	45.5	540	2	T00646	hypothetical prote
163	5	45.5	545	2	PM0005	chaperonine 60K al
164	5	45.5	545	2	I48951	oncotelet antigen
165	5	45.5	553	1	H70786	probable dihydrol
166	5	45.5	554	2	S46775	hypothetical prote
167	5	45.5	576	2	G69880	hypothetical prote
168	5	45.5	576	2	T46385	hypothetical prote
169	5	45.5	578	2	T40984	transcription fact
170	5	45.5	581	2	E75383	conserved hypochet
171	5	45.5	583	2	S10712	acetylcholinestera
172	5	45.5	583	2	T16007	hypothetical prote
173	5	45.5	584	2	S55106	probable membrane
174	5	45.5	587	1	A36936	nitrogenase (EC 1.
175	5	45.5	597	2	S40998	hypothetical prote
176	5	45.5	610	2	T17775	protein kinase hom
177	5	45.5	613	2	S48557	hypothetical prote
178	5	45.5	613	2	T42671	hypothetical prote
179	5	45.5	624	2	JC5471	regulatory protein
180	5	45.5	638	1	TOECDK	dnak-type molecula
181	5	45.5	638	2	F85481	hypothetical prote
182	5	45.5	638	2	C64156	hypothetical prote
183	5	45.5	638	2	T44660	nitrous-oxide redu
184	5	45.5	650	2	T36419	hypothetical prote
185	5	45.5	656	1	B44954	fumurate reductase
186	5	45.5	656	2	B86033	hypothetical prote
187	5	45.5	659	2	E86313	hypothetical prote
188	5	45.5	667	2	A48579	trophozoite surfac
189	5	45.5	681	2	S36534	el protein - human
190	5	45.5	701	2	S72722	protein secretion
191	5	45.5	714	2	G71963	hypothetical prote
192	5	45.5	714	2	H64543	hypothetical prote
193	5	45.5	718	2	A81122	hypothetical prote
194	5	45.5	728	2	T26607	hypothetical prote
195	5	45.5	733	2	G84668	hypothetical prote
196	5	45.5	768	2	F83060	hypothetical prote
197	5	45.5	770	2	G02228	DOC-2 - human
198	5	45.5	787	2	A44452	translation initia
199	5	45.5	800	2	S37387	internalin A precu
200	5	45.5	820	2	T51510	hypothetical prote
201	5	45.5	824	2	T23923	hypothetical prote
202	5	45.5	837	2	A57542	p96 protein - mous
203	5	45.5	863	2	T38016	importin beta-1 su
204	5	45.5	876	2	S20531	hypothetical prote
205	5	45.5	891	2	H83218	heme acquisition p
206	5	45.5	894	2	D85569	histidine kinase k
207	5	45.5	894	2	B42372	hypothetical prote
208	5	45.5	927	2	T24031	hypothetical prote
209	5	45.5	941	2	A86404	probable protein A
210	5	45.5	943	2	JC4081	sucrase/fructanase
211	5	45.5	971	2	T33907	hypothetical prote
212	5	45.5	986	2	B81675	polymorphic membra
213	5	45.5	1012	2	I53172	RAE-28 - mouse
214	5	45.5	1027	2	A56533	chromatin remodel1
215	5	45.5	1040	1	T46931	alpha-mannosidase
216	5	45.5	1040	1	A38306	alpha-mannosidase
217	5	45.5	1041	2	A81960	probable DNA helic
218	5	45.5	1049	2	T30525	alpha-mannosidase
219	5	45.5	1051	1	JW0051	serine/threonine-s
220	5	45.5	1061	1	S27311	ribonuclease E (EC
221	5	45.5	1061	2	B85671	hypothetical prote
222	5	45.5	1070	2	S19686	alpha-glucosidase
223	5	45.5	1098	2	B70232	hypothetical prote
224	5	45.5	1151	2	T18535	high molecular mas
225	5	45.5	1151	2	T30936	reverse transcript
226	5	45.5	1161	2	G81915	hypothetical prote
227	5	45.5	1177	2	T16594	hypothetical prote
228	5	45.5	1218	2	J50069	hypothetical pi op
229	5	45.5	1224	2	T14007	microtubule-associ
230	5	45.5	1237	2	A54080	protein-tyrosine-p
231	5	45.5	1301	1	A41622	protein-tyrosine-p
232	5	45.5	1329	2	A84525	probable retroelem
233	5	45.5	1336	2	T16718	hypothetical prote
234	5	45.5	1403	2	S24548	homeotic protein p
235	5	45.5	1409	2	T37188	presynaptic activi
236	5	45.5	1416	2	T20823	hypothetical prote
237	5	45.5	1520	2	B82274	conserved hypochet
238	5	45.5	1612	2	S59969	DNA topoisomerase
239	5	45.5	1621	2	A82255	hypothetical prote
240	5	45.5	1640	2	D86798	prophage pi3 prote
241	5	45.5	1785	2	A45546	major merozoite su
242	5	45.5	1785	2	T21558	hypothetical prote
243	5	45.5	1825	2	T52521	related to SEN1 pr
244	5	45.5	1870	2	S37671	MHC class III hist
245	5	45.5	1872	2	S36152	MHC class III hist
246	5	45.5	1876	2	T13801	phosphoinositide 3
247	5	45.5	1899	2	T32732	PAM C-terminal int
248	5	45.5	1919	2	T42098	PAM interacting pr

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OM protein - protein search, using sw model

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24.739 Million cell updates/sec

Title: US-09-372-036-29
Perfect score: 11
Sequence: 1 OOOOAPKAPTE 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	484	2 A41487	protein p60 precu
2	6	54.5	343	2 T29819	hypothetical prote
3	6	54.5	371	2 T22894	hypothetical prote
4	6	54.5	606	2 T37217	probable ATP/GTP b
5	6	54.5	663	2 G81384	succinate dehydrog
6	6	54.5	861	2 H83012	periplasmic glucan
7	6	54.5	890	2 A48753	NPAT transcription
8	6	54.5	995	2 T22942	hypothetical prote
9	6	54.5	1001	2 S74544	translational initia
10	6	54.5	1052	2 T14343	zinc finger RNA bi
11	6	54.5	1323	1 RRMGSW	RNA-directed RNA p
12	6	54.5	2022	2 T43214	ovrl protein - nem
13	6	54.5	2121	2 A59233	myosin VII-like pr
14	5	45.5	46	2 S07073	arabinogalactan pr
15	5	45.5	67	2 I47395	histone H1 I-1 (cl
16	5	45.5	70	2 A44395	histone H1 I-1 (N-
17	5	45.5	83	2 A44465	sodium ion pump ox
18	5	45.5	95	2 S36634	ptl2 protein - Ant
19	5	45.5	95	2 G75374	hit family protein
20	5	45.5	118	2 B49905	protein secretion
21	5	45.5	121	2 B81363	Hit-family protein
22	5	45.5	123	2 S49484	histone H2B - sea
23	5	45.5	127	2 S09877	hypothetical prote
24	5	45.5	127	2 A72488	hypothetical prote
25	5	45.5	128	2 G64155	YHc protein - Hae
26	5	45.5	129	1 CCDV3	cytochrome c3 prec
27	5	45.5	130	1 CCDV3M	large-conductance
28	5	45.5	136	2 H82438	dehydrin 7 - barle
29	5	45.5	137	2 S35752	

30	5	45.5	139	2 S05544	dehydrin 8 - barle
31	5	45.5	139	2 T05715	dehydrin - barley
32	5	45.5	138	2 C81214	comE-related prot
33	5	45.5	157	2 F83464	flagellar motor sw
34	5	45.5	159	2 F81813	hypothetical prote
35	5	45.5	166	2 I39546	hypothetical prote
36	5	45.5	174	2 A71208	hypothetical prote
37	5	45.5	175	2 A26882	ptl2 hypothetical
38	5	45.5	176	2 T48699	hypothetical prote
39	5	45.5	181	2 F70588	hypothetical prote
40	5	45.5	182	2 T11906	NADH dehydrogenase
41	5	45.5	183	2 E75435	pyrimidine operon
42	5	45.5	191	2 T42232	histone H1.2 - Cae
43	5	45.5	193	2 S73713	MG319 homolog H08
44	5	45.5	202	1 S17244	adenylylsulfate ki
45	5	45.5	205	2 H81057	comE operon protei
46	5	45.5	207	2 T49218	hypothetical prote
47	5	45.5	207	2 D83944	SOS regulon transc
48	5	45.5	212	2 H75317	translational initia
49	5	45.5	214	2 S70734	adenylylate kinase (
50	5	45.5	216	2 T38907	hypothetical prote
51	5	45.5	218	2 H82758	hypothetical prote
52	5	45.5	223	2 T16654	hypothetical prote
53	5	45.5	224	2 T43331	clathrin light cha
54	5	45.5	225	2 T15228	probable histone B
55	5	45.5	229	2 T40789	clathrin light cha
56	5	45.5	231	2 C64990	ferredoxin-type pr
57	5	45.5	231	2 H85859	ferredoxin-type pr
58	5	45.5	236	2 S22322	histone H1 - wheat
59	5	45.5	239	2 S28630	opacity protein op
60	5	45.5	241	2 F42600	probable octopine
61	5	45.5	244	2 S40436	histone H1 - midge
62	5	45.5	252	1 F70647	NADH dehydrogenase
63	5	45.5	261	2 JN0747	histone H1-I - Vol
64	5	45.5	262	2 T31468	hypothetical prote
65	5	45.5	266	2 S16616	opacity protein op
66	5	45.5	269	2 D82060	conserved hypothet
67	5	45.5	270	2 S75051	lactose transport
68	5	45.5	270	2 B83927	hypothetical prote
69	5	45.5	279	1 S08717	thermolase (EC 3.4
70	5	45.5	280	2 T09576	lbpX transcription
71	5	45.5	283	2 S25769	lbpX protein - Pse
72	5	45.5	288	2 C83289	lipase modulator p
73	5	45.5	289	2 T17957	hypothetical prote
74	5	45.5	292	2 B42822	cyclin D3 - human
75	5	45.5	296	2 A56943	sensory/motor neur
76	5	45.5	296	2 T20005	hypothetical prote
77	5	45.5	298	1 C37841	probable site-spec
78	5	45.5	299	2 G86649	drpP-L-rhamnose sy
79	5	45.5	301	2 C85049	hypothetical prote
80	5	45.5	303	2 C75289	hypothetical prote
81	5	45.5	304	2 A81128	probable lysR-famI
82	5	45.5	307	2 F84502	En/Spm transposon
83	5	45.5	313	2 E45509	desiccation-relate
84	5	45.5	315	2 T29525	hypothetical prote
85	5	45.5	320	2 S78604	taurin-binding pro
86	5	45.5	320	2 G85531	taurine transport
87	5	45.5	320	2 S61586	probable membrane
88	5	45.5	321	2 D70833	hypothetical prote
89	5	45.5	321	2 C71463	probable p-loop AT
90	5	45.5	323	2 I39867	microbial serine p
91	5	45.5	327	2 D83674	phenylacetic acid
92	5	45.5	330	2 T25169	hypothetical prote
93	5	45.5	330	2 T42947	hypothetical prote
94	5	45.5	331	2 B85830	spherulin 4 precu
95	5	45.5	332	2 S03871	hypothetical prote
96	5	45.5	333	2 A85620	probable nitrate t
97	5	45.5	333	2 G64833	ketol-acid reducto
98	5	45.5	338	2 E83059	ketol-acid reducto
99	5	45.5	339	2 S24161	ketol-acid reducto
100	5	45.5	340	2 B86778	ketol-acid reducto
101	5	45.5	340	2 G81411	p3 protein - grape
102	5	45.5	341	1 P3VVC	

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TAPKA 8
 |||||
 Db 92 tapka 96

RESULT 50
 AAR54838
 ID AAR54838 standard; Protein: 279 AA.
 XX
 AC AAR54838;
 XX
 DT 11-JAN-1995 (first entry)
 XX
 DE Thermilase (P229X).
 XX
 KW Subtilisin; mutant; variant; enzyme; protease; substrate;
 KM thermilase.
 XX
 OS Thermoterranomyces vulgaris.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 229
 FT /label= Ala, Leu, Met, Gln, Val, Ser
 FT /note= "pref. Ala"
 XX
 PN US5316941-A.
 XX
 PD 31-MAY-1994.
 XX
 PF 06-JAN-1989; 89US-0294340.
 XX
 PR 06-JAN-1988; 89US-0294340.
 PR 29-APR-1992; 92US-0876818.
 XX
 PA (GENV) GENENCOR INC.
 XX
 PI Bott RR, Caldwell RM, Estell DA, Graycar TP;
 XX
 DR WPI; 1994-176274/21.
 XX
 PT New DNA encoding subtilisin mutated at position 225 - producing
 PT protease with altered substrate specificity and reactivity
 XX
 PS Disclosure; Fig 3b; 13pp; English.
 XX
 CC DNA encoding subtilisin in which the amino acid equiv. to Pro(225)
 CC of B. amyloliquefaciens subtilisin has been replaced by Ala, Leu,
 CC Met, Gln, Val or Ser (pref. Ala) is claimed. Compared with wild-
 CC type subtilisin, the variants have different catalytic and/or
 CC Michaelis constants, i.e. different substrate reactivity and/or
 CC specificity, partic. at least a 2-fold increase or decrease in the
 CC kcat/Km ratio. Changing Pro to Ala gives a mutant enzyme with
 CC greater activity for ester as opposed to anilide substrates.
 XX
 SQ Sequence 279 AA;

Query Match 45.5%; Score 5; DB 15; Length 279;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TAPKA 8
 |||||
 Db 92 tapka 96

Search completed: August 15, 2001, 12:35:42
 Job time: 167 sec

PT isolated from culture medium of fungus *Tritirachium album* or
 PT produced by recombinant DNA techniques
 XX
 PS ; Fig 9a-9c; 74pp; English.
 CC Fig. 9 represents a comparison of the AA sequences of protease TW3 with
 CC those of proteinase K, subtilisin novo, subtilisin Carlsberg, subtilisin
 CC DY and thermolase. The AA sequence of the mature TW3 protein
 CC as determined from the nucleotide sequence has approximately 90%
 CC homology with that of proteinase K. There are certain positions where
 CC the TW3 AA sequence resembles that in subtilisins, but not to proteinase
 CC K. For example, at positions 143, a methionine residue occurs in all
 CC subtilisins as well as in protease TW3, while a leucine residue is
 CC present at that position in proteinase K. Similarly at position 219, an
 CC alanine residue is present in protease TW3 and subtilisins, but not in
 CC proteinase K. In addition, the AA fragment, Ser-Thr-, is absent from
 CC AAP80851) at position 226 and 227. Purified serine protease (SP),
 CC can be used in detergents and cleansers or spot removers, as a depilatory
 CC in tanning and also in the food industry for the prepn. of protein
 CC hydrolysates and in serology for the detection of incomplete antibodies.
 XX
 SQ Sequence 278 AA;
 Query Match 45.5%; Score 5; DB 9; Length 278;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 TAPKA 8
 |||||
 Db 92 tapka 96
 RESULT 48
 AAR90544 standard; protein: 278 AA.
 XX
 AC AAR90544;
 XX
 DT 08-AUG-1996 (first entry)
 XX
 DE pUG4-5-CDK-BP clone #125 derived CDK4 binding protein.
 XX
 KM Cell cycle; CDK4; regulation; G1 phase; proliferation; tumorigenesis;
 KM cyclin dependent kinase; differentiation; CDK4 inhibitor; agonist;
 KM antagonist.
 XX
 OS Synthetic.
 OS
 PN MO9533819-A2.
 XX
 PD 14-DEC-1995.
 XX
 PF 02-JUN-1995; 95WO-US07113.
 XX
 PR 02-JUN-1994; 94US-0253155.
 XX
 PA (MITO-) MITOTIX INC.
 XX
 PI Draetta G, Gyuris J;
 XX
 DR WPI; 1996-040227/04.
 DR N-PSDB; AAT12173.
 XX
 PT Cyclin-dependent kinase-4 binding protein - used in the isolation of
 PT (ant)agonists of cell cycle regulation.
 XX
 PS Claim 1; Page 81-82; 115pp; English.
 XX
 CC AAR90533-R90556 are cyclin dependent kinase 4 (CDK4) binding proteins.
 CC encoded by clones of the plasmid pUG4-5-CDKBP. CDK4 binding proteins
 CC (CDK4-BP) may be used in an assay for screening test compounds as

CC inhibitors of CDK/CDK4-BP interaction. The complexes formed by CDK4
 CC and D-type cyclins are strongly implicated in the control of the early
 CC G1 phase of the cell cycle and are strong candidates for controlling
 CC and/or preventing tumorigenesis and the onset of cancer. Nucleic acids
 CC encoding CDK4-BP or fragments of these may be used as probes/primers
 CC to diagnose the presence or absence of genetic lesions in a gene
 CC encoding 1 of the 24 CDK4-BP, and hence to diagnose the risk for a
 CC subject of developing a cell-proliferation associated disorder (e.g.
 CC cancer).
 XX
 SQ Sequence 278 AA;
 Query Match 45.5%; Score 5; DB 17; Length 278;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 TAPKA 8
 |||||
 Db 57 tapka 61
 RESULT 49
 AAP80274 standard; protein: 279 AA.
 XX
 AC AAP80274;
 XX
 DT 10-SEP-1990 (first entry)
 XX
 DE Amino acid sequence of *Bacillus thermilase* subtilisin.
 XX
 KM Enzyme mutant; catalytic function; *Bacillus thermilase* subtilisin.
 XX
 OS *Bacillus thermilase*.
 OS
 PN WO8807578-A.
 XX
 PD 06-OCT-1988.
 XX
 PF 30-MAR-1988; 88WO-US01078.
 XX
 PR 02-APR-1987; 87US-0034085.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wells JA, Carter PJ;
 XX
 DR WPI; 1988-292862/41.
 XX
 PT Enzyme mutants with modified catalytic functional gp. -
 PT react with modified substrates which contain moiety to
 PT complement catalytic functionality
 XX
 PS Disclosure; Fig 3b; 90pp; English.
 XX
 CC The patent is for a novel enzyme mutant (EM), not found in nature,
 CC derived by the replacement or modification, in a precursor enzyme, of at
 CC least one catalytic gp. of an amino acid residue which when in contact
 CC with a selected region of a polypeptide substrate, functions
 CC catalytically. The precursor enzyme may be, eg oxido-reductases,
 CC transferases, hydrolases, lyases, isomerases or ligases. EM have a
 CC catalytic preference for substrates which provide the replaced or
 CC modified functional gp. or its equivalent such that the substrate
 CC together with the enzyme mutant assists in its own catalysis.
 CC In Fig 3b B. amyloliquefaciens subtilisin and thermilase are aligned to
 CC compare conserved residues.
 XX
 SQ Sequence 279 AA;
 Query Match 45.5%; Score 5; DB 9; Length 279;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;

FT	Misc-difference	/note= "unidentified amino acid"
FT	16	/note= "unidentified amino acid"
XX		
PV	MO9709994-A1.	
PD	20-MAR-1997.	
XX		
XX	16-SEP-1996;	96WO-US14819.
XX		
PR	15-SEP-1995;	95US-0529055.
XX		
PA	(UABR-) UAB RES FOUND.	
PI	Briles DE, Brooks-Walter A, Crain MJ, Hollingshead S;	
PI	McDaniel LS, Swiatlo E, Tart R, Yochter J;	
XX		
DR	WPI. 1997-202002/18.	
XX		
PT	Streptococcus pneumoniae surface protein PspC and truncated Pspa -	
PT	used in vaccines for protecting animals against S.pneumoniae	
PT	Infection	
PS	Example 6; Fig 13; 296pp; English.	
XX		
CC	This sequence shows the central portion, including the C-terminus	
CC	of the alpha-helix region and some of the proline-rich region, of	
CC	pneumococcal surface protein A (Pspa) of Streptococcus pneumoniae	
CC	strain ATCC6303. Comparison of the N-terminal and central regions	
CC	(AAM1433-57 and AAM14562-91) of Pspa polypeptides from different	
CC	pneumococcal strains can be used to divide the strains into several	
CC	families based on sequence homologies. Pspa polypeptides, or	
CC	fragments of them, can be used in vaccines to protect animals	
CC	against S. pneumoniae infection and hence for the prevention of	
CC	diseases such as otitis media, meningitis, bacteraemia and pneumonia.	
CC	The sequence of the 3' half of the Pspa alpha-helical region and the	
CC	immediate 5' tip of the coding sequence are likely to be the critical	
CC	sequences for predicting Pspa cross-reactions and vaccine	
CC	composition.	
XX		
SQ	Sequence	215 AA:
OY	Query Match	45.5%; Score 5; DB 18; Length 215;
	Best Local Similarity	100.0%; Pred. No. 2.5e+02;
	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	4 TAPKA 8	
DB	125 tapka 129	
RESULT 46		
AAM80691		
ID	AAM80691 standard; Protein; 243 AA.	
XX		
AC	AAM80691;	
DT	24-DEC-1998 (first entry)	
DE	S. pneumoniae protein of unknown function.	
XX		
KW	Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;	
KW	vaccine; antibody; infection; detection; treatment; hypothetical;	
KW	cell wall biosynthetic, external target; minimal gene set protein.	
XX		
OS	Streptococcus pneumoniae.	
XX		
PN	MO9826072-A1.	
XX		
PD	18-JUN-1998.	
PF	09-DEC-1997;	97WO-US22578.

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XX 13-DEC-1996; 96US-0036281.
PR
PA (ELIL ) LILLY & CO ELI.
XX
XX Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR,
PI Mills BJ, Norris FH, Peery RB, Rosteck PR,
PI Skarud PL, Smith MC, Solenberg PJ, Treadway PJ,
PI Young Bellido ML;
XX
XX WPI; 1998-348529/30.
DR N-PSDB; AAV65255.
XX
XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
PT for evaluating gene expression, and identification of virulence
XX genes
XX
XX Claim 3; Pages 279-280; 333pp; English.
XX
XX This sequence represents a Streptococcus pneumoniae protein of unknown
CC function. The invention provides DNA sequences (AAV65201 to AAV65304)
CC from the Streptococcus pneumoniae genome and corresponding protein
CC sequences (AAW80605 to AAW80728). The protein sequences are classified as
CC hypothetical, cell wall biosynthetic, external target, or minimal gene
CC set proteins. A recombinant host containing a vector comprising any of
CC the above nucleic acids can be used for the recombinant expression of the
CC proteins. The invention also provides a DNA chip having arrayed on it at
CC least 15 base pair fragment of any one or more of these DNA sequences.
CC The DNA chip can be used methods for evaluating gene expression in S.
CC pneumoniae and for identifying virulence genes in S. pneumoniae.
CC Antibodies that selectively bind to the above proteins or peptide
CC fragments can be used to treat S. pneumoniae infection. The antibodies
CC can also be used to detect S. pneumoniae cells.
XX
XX Sequence 243 AA:
SQ
XX
XX Query Match 45.5%; Score 5; DB 19; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 2,7e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 KAPTE 11 .
XX |||||
DB 120 Kapte 124
XX
XX RESULT 47
XX AAP80850
XX ID AAP80850 standard: protein; 278 AA.
XX
XX AAP80850;
XX
XX 10-SEP-1990 (first entry)
XX
XX Sequence of subtilisin thermilase.
XX
XX Serine protease TW3; proteinase K; subtilisin thermilase.
XX
XX MO8807581-A.
XX
XX 06-OCT-1988.
XX
XX 28-MAR-1988; 88WO-US01040.
XX
XX 03-MAR-1987; 87US-0035816.
XX
XX (AMGE ) AMGEN INC.
XX
XX Samal BB, Stabinsky Y;
XX
XX WPI; 1988-292865/41.
XX
XX New purified serine protease -
PT

```

XX PN WO200006736-A2.
 XX XX 10-FEB-2000.
 PD XX
 PF 27-JUL-1999; 99WO-G802444.
 XX XX
 PR 27-JUL-1998; 98GB-0016335.
 PR 19-MAR-1999; 99US-0125163.
 XX XX
 PA (MICR-) MICROBIAL TECHNIQS LTD.
 PI Le Page RWF, Wells JM, Hanniffy SB;
 DR WPI: 2000-195299/17.
 XX
 PT New Group B Streptococcus protein, useful as vaccine, for diagnosis of
 PT Streptococcal infections and for screening of antibodies or affibodies
 XX
 PS Claim 1; Fig 1: 123pp; English.
 XX
 CC AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given
 CC in AA91375 to AA91343) isolated from Group B Streptococcus (GBS), also
 CC known as Streptococcus agalactiae. The GBS polynucleotides and
 CC polypeptides have antibacterial activity. Immunogenic compositions
 CC comprising GBS polynucleotides or polypeptides can be used as vaccines
 CC and for the treatment or prophylaxis of GBS infection. The
 CC polynucleotides and polypeptides can also be used in the detection of GBS
 CC and for screening DNA encoding bacterial cell envelope associated or
 CC secreted antigens in gram positive bacteria. AAA05873 to AAA05941
 CC represent primers used in the exemplification of the present invention.
 XX
 SQ Sequence 206 AA;
 OY 6 PKAPT 10
 Db 144 pkapt 148
 DE
 RESULT 44
 AAB42897
 ID AAB42897 standard; Protein: 209 AA.
 AC AAB42897;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF2661 polypeptide sequence SEQ ID NO:5332.
 XX
 KW Human: open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoxic; antiparkinsonian; noctropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antihypertoid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX

PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shimkets RA, Leach M;
 DR WPI: 2000-602362/57.
 DR N-PSDB: AAC77106.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 11; Page 4497-4498; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoxic; antiparkinsonian; noctropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antihypertoid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 209 AA;
 OY 7 KAPTE 11
 Db 195 kapte 199
 DE
 RESULT 45
 AAAM14563
 ID AAAM14563 standard; Protein: 215 AA.
 XX
 AC AAAM14563;
 XX
 DT 28-OCT-1997 (first entry)
 XX
 DE Streptococcus pneumoniae PspA central region.
 XX
 KW PspA; pneumococcal surface protein; vaccine; otitis media;
 KW meningitis; bacteraemia; pneumonia.
 XX
 OS Streptococcus pneumoniae strain ATCC 6303.
 XX
 PN Key Location/Qualifiers
 FT Misc-difference 4

CC chemicals, for modulating fine chemical production in *C. glutamicum* or
 CC related bacteria (e.g. *Brevibacterium lactofermentum*), the typing or
 CC identification of *C. glutamicum* or related bacteria, as reference points
 CC for mapping *C. glutamicum* genome, and as markers for transformation.
 CC AAF68082 and AAF68082 represent sequencing primers which are used in an
 CC example from the present invention.

XX Sequence 189 AA;

Query Match 45.5%; Score 5; DB 22; Length 189;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
 |||||
 Db 20 tapka 24

RESULT 41

AA82664

ID AAR82664 standard; Protein: 190 AA.

XX AAR82664;

DT 27-JAN-1996 (first entry)

DE E. coli RNase E.

KW RNase E; antiviral; transgenic plant.

OS Escherichia coli.

PN W09522245-A.

PD 24-AUG-1995.

PF 16-FEB-1995; 95WO-US02058.

PR 18-FEB-1994; 94US-0198973.

PA (CLEV-) CLEVELAND CLINIC FOUND.

PI Sengupta DN, Silverman RH;

DR WPI: 1995-302493/39.

PT New transgenic plants resistant to viral infection contg. 2-5A-dependent

PT RNase - useful in developing products useful in gene therapy against

PS viral disease and cancer.

PS Disclosure: Page 110; 196pp; English.

XX The novel 2-5A dependent RNase of the invention has a mol. wt. of

CC about 84 kDa. Analysis of the AA sequence has revealed several

CC characteristics unique to the 2-5A-dependent RNases.

CC There is limited homology with RNase E, encoded by the altered

CC mRNA stability (ams)/rne gene of *E. coli*.

XX Sequence 190 AA;

OY 1 00QTA 5
 |||||
 Db 41 qgqta 45

RESULT 42

AAW94681

ID AAW94681 standard; Protein: 190 AA.

XX AAW94681;

DT 04-MAY-1999 (first entry)

DE Escherichia coli RNase E.

KW 2-5A-dependent RNase; endoribonuclease; interferon; insect cell;

KW 5'-phosphorylated 2',5'-linked oligoadenylate; recombinant protein.

OS Escherichia coli.

PN US5877019-A.

PD 02-MAR-1999.

PF 21-AUG-1996; 96US-0701005.

PR 22-OCT-1993; 93US-0141304.

PR 08-MAR-1993; 93US-0028086.

PR 21-AUG-1996; 96US-0701005.

PA (CLEV-) CLEVELAND CLINIC FOUND.

PI Hassel BA, Silverman RH, Zhou A;

DR WPI: 1999-189652/16.

PT Insect cells expressing 2-5A-dependent RNase enzymes - useful for

PT producing recombinant enzymes

PS Disclosure: Fig 9A; 62pp; English.

XX The present invention describes an insect cell capable of expressing

CC human or mouse 2-5A-dependent RNase (an endoribonuclease that requires

CC 5'-phosphorylated 2',5'-linked oligoadenylates) at levels at least two

CC orders of magnitude higher than those obtained from mammalian cells,

CC where the insect cell includes a recombinant baculovirus expression

CC vector that contains cDNA encoding a 2-5A-dependent RNase. The insect

CC cell can be used to produce recombinant 2-5A-dependent RNase (in amounts

CC of tens of milligrams), allowing meaningful biophysical studies to be

CC conducted on 2-5A-dependent RNase. The present sequence represents

CC Escherichia coli RNase E which has homology with human and mouse

CC 2-5A-dependent RNase.

XX Sequence 190 AA;

OY 1 00QTA 5
 |||||
 Db 41 qgqta 45

Query Match 45.5%; Score 5; DB 20; Length 190;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

RESULT 43
 AAY91339
 ID AAY91339 standard; Protein: 206 AA.
 XX AAY91339;
 DT 30-MAY-2000 (first entry)
 DE Group B Streptococcus protein sequence SEQ ID NO:72.
 KW Group B Streptococcus; Streptococcus agalactiae; protein antigen;
 KW vaccine; screening; immunogen; detection; diagnosis; infection;
 KW antibody; antibody; antibacterial.
 OS Streptococcus agalactiae.

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPT 10
|1111
Db 148 pkapt 152

RESULT 39
AAB63253
ID AAB63253 standard; Protein: 188 AA.

AC AAB63253;
XX
DT 26-MAR-2001 (first entry)
XX

DE Human breast cancer associated antigen protein sequence SEQ ID NO:615.

KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW cancer associated antigen; cytostatic; cancer vaccine.

OS Homo sapiens.

PN W0200073801-A2.

PD 07-DEC-2000.

PF 26-MAY-2000; 2000WO-US14749.

PR 28-MAY-1999; 99US-0136526.

PR 10-SEP-1999; 99US-0153454.

PA (LUDW-) LUDWIG INST CANCER RES.

XX
PI Obata Y;

DR WPI: 2001-025274/03.

PT Nucleic acids encoding breast, gastric and prostate cancer associated

PT antigen precursors, useful for diagnosing and treating a condition

PT characterized by expression of an abnormal amount of a protein, e.g.

PT cancer -

XX Example 1; Page 483-484; 799pp; English.

XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014

CC represent nucleotide sequences encoding human breast, gastric and

CC prostate cancer associated antigen precursors (CAAP) respectively.

CC AAB6332 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970

CC represent human breast, gastric and prostate CAAP protein sequence

CC respectively. CAAPs have cytostatic activity and can be used in the

CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic

CC acids or anti-CAAP antibodies are useful for diagnosing and treating a

CC condition characterized by expression of an abnormal amount of a protein,

XX e.g. cancer.

XX Sequence 188 AA;

XX

XX

XX

XX

XX

XX 11-APR-2001 (first entry)

DE Corynebacterium glutamicum MCT protein SEQ ID NO:240.

XX Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;

KW membrane construction and membrane transport protein; petroleum spill;

KW hydrocarbon degradation; gram positive aerobic bacterium; marker;

KW identification; microorganism; fine chemical production; transformation;

XX genome mapping; genetic engineering.

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XX

SQ Sequence 177 AA;

Query Match 45.5%; Score 5; DB 16; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPT 10
 |||||
 Db 148 pkapt 152

RESULT 37
 AAY50043
 ID AAY50043 standard; protein; 177 AA.
 XX
 AC AAY50043;
 XX
 DT 19-JAN-2000 (first entry)
 XX
 DE Pseudomonas syringae translation initiation factor IF3.
 XX
 KM Translation initiation factor; IF3; bacterial; screening;
 KM antibacterial; antibiotic; drug target; initiation codon; recognition;
 KM ubiquitous; conserved; broad spectrum; infection; contamination;
 XX sterilisation.
 XX
 OS Pseudomonas syringae.
 XX
 PN WO9952357-A1.
 PD 21-OCT-1999.
 XX
 PF 14-APR-1999; 99WO-US08134.
 XX
 PR 14-APR-1998; 98US-0081736.
 XX
 PA (RIBO-) RIBOGENE INC.
 XX
 PI Dammel GS, Watson JC, Hernandez VJ;
 XX
 DR WPI: 1999-620242/53.
 XX
 PT Assays for inhibitors of bacterial translation initiation factor 3 -
 XX
 PS Disclosure: Fig 1; 66pp; English.

This sequence represents Pseudomonas syringae translation initiation factor IF3. IF3 is an essential factor, acting to prevent association of ribosomal subunits and to recognise the correct initiation codon. IF3 can be used as a drug target for potential antibiotics. The invention relates to methods for screening for test compounds that inhibit the activity of IF3 which comprise using a reporter gene system in whole cells and detecting the ability of IF3 to discriminate against translation initiation at an atypical start codon of the reporter gene. IF3 is apparently ubiquitous and conserved throughout the bacterial kingdom. It is therefore likely that any compounds which are effective at inhibiting IF3 of one bacterial species will have an inhibitory effect on the IF3 of its functional equivalents in a wide range of bacteria. Importantly, IF3 has no functional homologue in mammalian cells. As a result, the potential toxicity of IF3 inhibitors is likely to be low. Compounds identified by the method that inhibit bacterial IF3 are useful for inhibiting the growth of bacteria, especially for treating an infectious disease in a human or a companion or livestock animal. The compound may be adjunctionally administered with a second antibacterial compound. IF3 inhibitors identified by the method are also useful for sterilising bacteria-contaminated objects or material. The compounds identified can penetrate and specifically kill the pathogenic bacterial cell, or arrest its growth without also adversely affecting its human, animal or plant host. This is because the target is highly selective as no homologous mammalian counterpart exists. The high-throughput primary screen allows for the easy visible identification of positive hits.

XX Sequence 177 AA;

Query Match 45.5%; Score 5; DB 20; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 8 apkap 12

RESULT 38
 AAB09006
 ID AAB09006 standard; Protein; 177 AA.
 XX
 AC AAB09006;
 XX
 DT 30-AUG-2000 (first entry)
 XX
 DE Hepatitis GB virus protein sequence SEQ ID NO:49.
 XX
 KM Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic;
 KM infection; detection; characterisation; hepatitis.
 XX
 OS Hepatitis GB virus.
 XX
 PN US6051374-A.
 PD 18-APR-2000.
 XX
 PF 07-JUN-1995; 95US-0488445.
 XX
 PR 14-FEB-1994; 94US-0196030.
 PR 13-MAY-1994; 94US-0242654.
 PR 29-JUL-1994; 94US-0283314.
 PR 23-NOV-1994; 94US-0344185.
 PR 23-NOV-1994; 94US-0344190.
 PR 30-JAN-1995; 95US-0377557.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buljk SL;
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GC;
 XX
 DR WPI: 2000-338307/29.
 XX
 PT Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the
 PT HGBV polynucleotide probe and detecting the complex that contains
 PT target HGBV -
 XX
 PS Example 5; Column 171-172; 369pp; English.

The present invention describe a method for detecting target hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of containing HGBV. The method involves reacting (T) with a HGBV polynucleotide probe (I) containing 15 contiguous nucleotides, and which selectively hybridises to the HGBV genome or its full complement, and detecting the complex that contains THN, indicating the presence of target HGBV. The method is used for detecting target HGBV nucleic acid in the test sample suspected of containing HGBV and for characterisation of newly ascertained etiological agent of non-A, non-B, non-C, non-D and non-E hepatitis causing agents collectively termed as hepatitis GB viruses. AAY55270 to AAY54489 and AAB08985 to AAB09480 represent nucleotide and protein sequences used in the exemplification of the present invention.

SQ Sequence 177 AA;

Query Match 45.5%; Score 5; DB 21; Length 177;

CC frames in the complete genome (see AAX91990) of *Chlamydia pneumoniae*.
 CC *C. pneumoniae* causes respiratory disease such as pneumonia and
 CC bronchitis and is thought to be a contributing factor in heart
 CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the *C. pneumoniae* genome (see AAY34584-Y35879) can be used in
 CC immunogenic compositions as vaccines. Vectors containing *C. pneumoniae*
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of *C. pneumoniae*.
 XX
 SQ Sequence 132 AA;
 XX
 Query Match 45.5%; Score 5; DB 20; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 KAPTE 11
 11111
 DB 94 kapte 98
 XX
 RESULT 33
 AAY13180
 ID AAY13180 standard; Protein; 135 AA.
 XX
 AC AAY13180;
 XX
 DT 22-JUN-1999 (first entry)
 XX
 DE Human secreted protein encoded by 5' EST SEQ ID NO: 194.
 XX
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition.
 XX
 OS Homo sapiens.
 OS
 PN WO9906552-A2.
 PN
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-IB01236.
 XX
 PR 01-AUG-1997; 97US-0905223.
 XX
 PA (GEST) GENSET.
 XX
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;
 FI N-PSDB; AAX51980.
 DR WPI; 1999-153782/13.
 XX
 PT New isolated brain-derived nucleic acids - used to develop products
 PT which may have cytokine, immune, regulatory, haematopoiesis
 PT regulating, anti-inflammatory or tumour inhibition activity
 XX
 PS Claim 34; Page 556; 577pp; English.
 XX
 CC AAX51787 to AAX52019 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12987 to
 CC AAY13219, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and

CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell.
 XX
 SQ Sequence 135 AA;
 XX
 Query Match 45.5%; Score 5; DB 20; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 QTRPK 7
 11111
 DB 8 qtrpk 12
 XX
 RESULT 34
 AAG02253
 ID AAG02253 standard; Protein; 157 AA.
 XX
 AC AAG02253;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 6334.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 OS
 PN EP103401-A2.
 PN
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC02259.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 13; SEQ ID 6334; 71pp + CD-ROM; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX
 SQ Sequence 157 AA;

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RESULT 30
AAV39038
ID AAV39038 standard; Protein: 113 AA.
XX
AC AAV39038;
XX
DT 05-NOV-1999 (first entry)
XX
DE M. tuberculosis recombinant antigen protein MO-9.
XX
KM Antigen; diagnosis; detection; infection; antibody; immunisation;
KW vaccine; immunity.
XX
OS Mycobacterium tuberculosis.
XX
PN MO9942118-A2.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99MO-US03265.
XX
PR 05-MAY-1998; 98US-0072596.
XX
PR 18-FEB-1998; 98US-0024753.
XX
PA (CORI-) CORIXA CORP.
XX
PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R.
PI Lodes MJ, Reed SG, Skelky YAW, Twardzik DR, Vedyick TS;
XX
DR WPI; 1999-527416/44.
XX
PT New polypeptide comprising antigenic portions of M. tuberculosis
PS Example 5; Page 260; 323pp; English.
XX
CC This invention describes novel recombinant antigens and their encoding
CC nucleic acids derived from Mycobacterium tuberculosis. The novel
CC polypeptides are useful for detecting M. tuberculosis infection in a
CC biological sample by detecting antibodies which bind with the
CC polypeptides, and are useful as vaccines for immunizing against
CC M. tuberculosis infection. The new detection methods are needed as
CC current vaccination strategies do not provide 100% immunity.
XX
SQ Sequence 113 AA;

Query Match 45.5%; Score 5; DB 20; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
DB 103 apkap 107

RESULT 31
AAW46291
ID AAW46291 standard; protein: 119 AA.
XX
AC AAW46291;
XX
DT 29-JUL-1998 (first entry)
XX
DE Pneumococcal surface protein As (PspAs) from clade 5 strain ATCC6303.
XX
KM Streptococcus pneumoniae; vaccine; pneumococcal surface protein As;
KW infection; protection; PspAs.
XX
OS Streptococcus pneumoniae.
XX
PN MO9811915-A1.
XX

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PD 26-MAR-1998.
XX
PF 22-SEP-1997; 97MO-US16761.
XX
PR 20-SEP-1996; 96US-0710749.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Becker RS, Briles DE, Hollingshead S;
XX
DR WPI; 1998-217031/19.
XX
PT New vaccines for protection against pneumococcal infection -
PT comprising at least 2 pneumococcal surface protein As, each
PT selected from a different family
XX
PS Example 3; Fig 7; 57pp; English.
XX
CC This is the sequence of a pneumococcal surface protein As (PspAs) from
CC strain ATCC6303, a representative strain of clade 5. This can be used in
CC the preparation of a vaccine composition comprising at least 2 PspAs,
CC each of which is selected from a different family. The vaccines can
CC provide for broad range protection against infection by different
CC Streptococcus pneumoniae strains.
XX
SQ Sequence 119 AA;

Query Match 45.5%; Score 5; DB 19; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKA 8
DB 99 tapka 103

RESULT 32
AAV35711
ID AAV35711 standard; Protein: 132 AA.
XX
AC AAV35711;
XX
DT 13-SEP-1999 (first entry)
XX
DE Chlamydia pneumoniae protein not found in C. trachomatis.
XX
KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX
OS Chlamydia pneumoniae.
XX
PN MO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98MO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
XX
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST ) GENSET.
XX
PI Griffiths R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Page 1416-1417; Disclosure: 1912pp; English.
XX
AAV34584-Y35879 represent the proteins encoded by all the open reading
CC

```

DR WPI: 2000-056500/05.
DR N-PSDB; AA240359.
XX
XX
PT A mutant cytochrome c3 and a microbe having the mutant cytochrome c3 -
PT useful for improving the electron transfer reaction velocity of the heme
PT protein of a sulphate-reducing microbe and a photosynthetic microbe
XX
XX
PS Example 4; Page 7; 11pp; Japanese.
XX
XX This sequence is the wild type cytochrome c3 of *Desulfovibrio vulgaris*
CC Miyazaki F IAM2604. The invention relates to mutant cytochrome c3
CC proteins that are mutated near the heme 3 region, and is structurally
CC changed by gene manipulation so that the extent a specific amino acid
CC structural part controlling the electron transfer velocity of heme
CC protein covers heme 3 is lowered. By mutating this region of cytochrome
CC c3, the electron transfer reaction velocity of the heme protein of a
CC sulphate-reducing microbe and a photosynthetic microbe can be improved.
XX
XX
SQ Sequence 107 AA;

Query Match 45.5%; Score 5; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APPAP 9
11111
DB 1 apkap 5

RESULT 28
AAV55100
ID AAV55100 standard; peptide; 107 AA.
XX
XX AAV55100;
AC
XX
XX 02-MAR-2000 (first entry)
DT
XX
XX

DE Mutant cytochrome c3 peptide #5.

XX Cytochrome c3; muteln; heme 3 region; electron transfer velocity;
KW heme protein; sulphate-reducing microbe; photosynthetic microbe.
XX
XX
XX

OS *Desulfovibrio vulgaris*.
OS Synthetic.
OS
XX
XX
XX

PM JP11290081-A.

XX 26-OCT-1999.
PD

XX 15-APR-1998; 96UP-0104667.
PF

XX 15-APR-1998; 96UP-0104667.
PR

XX (MITO) MITSUBISHI JUKOGYO KK.
PA

XX WPI: 2000-056500/05.
DR

XX A mutant cytochrome c3 and a microbe having the mutant cytochrome c3 -
PT useful for improving the electron transfer reaction velocity of the heme
PT protein of a sulphate-reducing microbe and a photosynthetic microbe
XX
XX
PS Example 5; Page 9; 11pp; Japanese.

XX This sequence represents a mutant cytochrome c3 of the invention. It is
CC a mutant of the *Desulfovibrio vulgaris* Hildenborough ATCC29579 sequence.
CC The protein is mutated near the heme 3 region, and is structurally
CC changed by gene manipulation so that the extent a specific amino acid
CC structural part controlling the electron transfer velocity of heme
CC protein covers heme 3 is lowered. By mutating this region of cytochrome
CC c3, the electron transfer reaction velocity of the heme protein of a
CC sulphate-reducing microbe and a photosynthetic microbe can be improved.
XX

SQ Sequence 107 AA;

Query Match 45.5%; Score 5; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APPAP 9
11111
DB 1 apkap 5

RESULT 29
AAV39181
ID AAV39181 standard; Protein; 113 AA.
XX
XX
XX AAV39181;
AC
XX
XX

XX 05-NOV-1999 (first entry)
DT
XX
XX

DE M. tuberculosis antigen 5' MO-9 amino acid sequence.

XX Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
KW immunotherapy; diagnosis; immunisation; vaccine; infection;
KW immune response; skin test.
XX
XX

OS Mycobacterium tuberculosis.
OS
XX
XX

PN WO9942076-A2.

XX 26-AUG-1999.
PD

XX 17-FEB-1999; 99WO-US03268.
PF

XX 05-MAY-1998; 98US-0072967.
PR

XX 18-FEB-1998; 98US-0025197.
PR

XX (CORI-) CORIXA CORP.
PA

XX Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
XX

XX WPI: 1999-527409/44.
DR

XX N-PSDB; AA219373.
DR

XX New antigens from Mycobacterium tuberculosis useful in diagnostic
PT skin tests and protective or therapeutic vaccines or compositions
XX
XX
PS Example 5; Page 215; 299pp; English.

XX The present invention describes polypeptides comprising an immunogenic
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described
CC are vaccines and fusion protein containing M. tuberculosis Ag's.
CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and
CC other polypeptides fragments, can be used in pharmaceutical compositions
CC or vaccines to generate a protective or therapeutic immune response to
CC M. tuberculosis and as reagents in skin tests for diagnosis of
CC tuberculosis. Ag can induce proliferation of, or cytokine secretion
CC by, T, B or natural killer cells and/or macrophages in
CC tuberculosis-immune subjects. AA219249 to AA219460 and AAV39083 to
CC AAV39225 are used in the exemplification of the present invention.
XX

SQ Sequence 113 AA;

Query Match 45.5%; Score 5; DB 20; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APPAP 9
11111
DB 103 apkap 107

Query Match 45.5%: Score 5; DB 21; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
| | | | |
Db 1 apkap 5

RESULT 25

AAV55097 ID AAV55097 standard; peptide; 107 AA.

XX AAV55097;

DT 02-MAR-2000 (first entry)

DE Mutant cytochrome c3 peptide #3.

XX Cytochrome c3; mutcin; heme 3 region; electron transfer velocity;

KM heme protein; sulphate-reducing microbe; photosynthetic microbe.

XX Desulfovibrio vulgaris.

OS Synthetic.

PN JP11290081-A.

PD 26-OCT-1999.

PF 15-APR-1998; 98JP-0104667.

PR 15-APR-1998; 98JP-0104667.

PA (MITO) MITSUBISHI JUKOGYO KK.

DR WPI; 2000-056500/05.

PT A mutant cytochrome c3 and a microbe having the mutant cytochrome c3 -

PT useful for improving the electron transfer reaction velocity of the heme

PS protein of a sulphate-reducing microbe and a photosynthetic microbe

XX Claim 5; Page 9; 11pp; Japanese.

CC This sequence represents a mutant cytochrome c3 of the invention. It is

CC a mutant of the Desulfovibrio vulgaris Hildenborough ATCC29579 sequence.

CC The protein is mutated near the heme 3 region, and is structurally

CC changed by gene manipulation so that the extent a specific amino acid

CC structural part controlling the electron transfer velocity of heme

CC protein covers heme 3 is lowered. By mutating this region of cytochrome

CC c3, the electron transfer reaction velocity of the heme protein of a

CC sulphate-reducing microbe and a photosynthetic microbe can be improved.

XX Sequence 107 AA;

OY 5 APKAP 9
| | | | |
Db 1 apkap 5

RESULT 26

AAV55098 ID AAV55098 standard; peptide; 107 AA.

XX AAV55098;

DT 02-MAR-2000 (first entry)

XX Mutant cytochrome c3 peptide #4.

DE Cytochrome c3; mutcin; heme 3 region; electron transfer velocity;

KM heme protein; sulphate-reducing microbe; photosynthetic microbe.

XX Desulfovibrio vulgaris.

OS Synthetic.

PN JP11290081-A.

PD 26-OCT-1999.

PF 15-APR-1998; 98JP-0104667.

PR 15-APR-1998; 98JP-0104667.

PA (MITO) MITSUBISHI JUKOGYO KK.

DR WPI; 2000-056500/05.

PT A mutant cytochrome c3 and a microbe having the mutant cytochrome c3 -

PT useful for improving the electron transfer reaction velocity of the heme

PS protein of a sulphate-reducing microbe and a photosynthetic microbe

XX Claim 6; Page 9-10; 11pp; Japanese.

CC This sequence represents a mutant cytochrome c3 of the invention. It is

CC a mutant of the Desulfovibrio vulgaris Hildenborough ATCC29579 sequence.

CC The protein is mutated near the heme 3 region, and is structurally

CC changed by gene manipulation so that the extent a specific amino acid

CC structural part controlling the electron transfer velocity of heme

CC protein covers heme 3 is lowered. By mutating this region of cytochrome

CC c3, the electron transfer reaction velocity of the heme protein of a

CC sulphate-reducing microbe and a photosynthetic microbe can be improved.

XX Sequence 107 AA;

OY 5 APKAP 9
| | | | |
Db 1 apkap 5

RESULT 27

AAV55099 ID AAV55099 standard; Protein; 107 AA.

XX AAV55099;

DT 02-MAR-2000 (first entry)

DE Wild type cytochrome c3 protein sequence.

XX Cytochrome c3; mutcin; heme 3 region; electron transfer velocity;

KM heme protein; sulphate-reducing microbe; photosynthetic microbe.

XX Desulfovibrio vulgaris.

PN JP11290081-A.

PD 26-OCT-1999.

PF 15-APR-1998; 98JP-0104667.

PR 15-APR-1998; 98JP-0104667.

PA (MITO) MITSUBISHI JUKOGYO KK.

XX

KW Cytochrome c3; sulfate-reducing microbe; mutant; bio-element;
 KW molecular wire; organic semiconductor; commutator element.
 OS Desulfovibrio vulgaris.
 XX JP2000217577-A.
 PN 08-AUG-2000.
 PD 28-JAN-1999; 99JP-0020018.
 PF 28-JAN-1999; 99JP-0020018.
 PR (MITO) MITSUBISHI JUKOGYO KK.
 PA
 XX MPI: 2000-605045/58.
 DR N-PSDB: AAA98362.
 DR
 XX Production of mutant cytochrome C3, useful as a material for a bio
 PT element such as an organic semiconductor, by point-mutating wild type
 PT cytochrome C3 from a sulfate reducing microbe -
 PS Claim 1; Page 8; 9pp; Japanese.
 XX
 CC This invention describes the novel production of a mutant cytochrome C3
 CC comprising a sequence (A) of 107 amino acids (fully defined in the
 CC specification), by point-mutating a wild type cytochrome C3 derived from
 CC a sulfate reducing microbe. The new method includes the following steps:
 CC (1) a plasmid carrying a gene of the mutant cytochrome C3 is introduced
 CC to an aerobic microbe to transform the aerobic microbe; (2) culturing
 CC aerobically the transformed aerobic microbe to grow it; and (3)
 CC collecting the mutant cytochrome C3 produced by the transformed aerobic
 CC microbe. Cytochrome C3 can be used as a material for a bio element such
 CC as a molecular wire, organic semiconductor and a commutator element.
 CC
 SQ Sequence 107 AA:

Query Match 45.5%; Score 5; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APPAP 9
 I I I I I
 DB 1 apkap 5

RESULT 23
 AAY55095
 ID AAY55095 standard; peptide; 107 AA.
 XX
 AC AAY55095;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Mutant cytochrome c3 peptide #1.
 XX
 KW Cytochrome c3; muteln; heme 3 region; electron transfer velocity;
 KW heme protein; sulphate-reducing microbe; photosynthetic microbe.
 XX
 OS Desulfovibrio vulgaris.
 OS Synthetic.
 XX
 PN JP11290081-A.
 PD 26-OCT-1999.
 PF 15-APR-1998; 98JP-0104667.
 PR 15-APR-1998; 98JP-0104667.
 XX
 PA (MITO) MITSUBISHI JUKOGYO KK.
 XX

DR MPI: 2000-056500/05.
 XX
 PT A mutant cytochrome c3 and a microbe having the mutant cytochrome c3 -
 PT useful for improving the electron transfer reaction velocity of the heme
 PT protein of a sulphate-reducing microbe and a photosynthetic microbe
 XX
 XX Claim 2; Page 8; 11pp; Japanese.
 PS
 CC This sequence represents a mutant cytochrome c3 of the invention. It is
 CC a mutant of the Desulfovibrio vulgaris Miyazaki F IAM2604 sequence.
 CC The protein is mutated near the heme 3 region, and is structurally
 CC changed by gene manipulation so that the extent a specific amino acid
 CC structural part controlling the electron transfer velocity of heme
 CC protein covers heme 3 is lowered. By mutating this region of cytochrome
 CC c3, the electron transfer reaction velocity of the heme protein of a
 CC sulphate-reducing microbe and a photosynthetic microbe can be improved.
 CC
 SQ Sequence 107 AA:

Query Match 45.5%; Score 5; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APPAP 9
 I I I I I
 DB 1 apkap 5

RESULT 24
 AAY55096
 ID AAY55096 standard; peptide; 107 AA.
 XX
 AC AAY55096;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Mutant cytochrome c3 peptide #2.
 XX
 KW Cytochrome c3; muteln; heme 3 region; electron transfer velocity;
 KW heme protein; sulphate-reducing microbe; photosynthetic microbe.
 XX
 OS Desulfovibrio vulgaris.
 OS Synthetic.
 XX
 PN JP11290081-A.
 PD 26-OCT-1999.
 PF 15-APR-1998; 98JP-0104667.
 PR 15-APR-1998; 98JP-0104667.
 XX
 PA (MITO) MITSUBISHI JUKOGYO KK.
 XX
 DR MPI: 2000-056500/05.
 DR
 PT A mutant cytochrome c3 and a microbe having the mutant cytochrome c3 -
 PT useful for improving the electron transfer reaction velocity of the heme
 PT protein of a sulphate-reducing microbe and a photosynthetic microbe
 XX
 XX Claim 3; Page 8; 11pp; Japanese.
 PS
 CC This sequence represents a mutant cytochrome c3 of the invention. It is
 CC a mutant of the Desulfovibrio vulgaris Miyazaki F IAM2604 sequence.
 CC The protein is mutated near the heme 3 region, and is structurally
 CC changed by gene manipulation so that the extent a specific amino acid
 CC structural part controlling the electron transfer velocity of heme
 CC protein covers heme 3 is lowered. By mutating this region of cytochrome
 CC c3, the electron transfer reaction velocity of the heme protein of a
 CC sulphate-reducing microbe and a photosynthetic microbe can be improved.
 CC
 SQ Sequence 107 AA:

XX The present sequence represents a cytochrome c3 protein used in an
 CC example of the present invention. A new method has been developed
 CC for improving electron moving velocity (EMV) of haem protein. The
 CC method comprises controlling in the specific aa structure EMV of
 CC haem protein around the haem 3 of cytochrome c3, where the degree of
 CC the aa structure covering haem 3 is lowered. Also described in the
 CC present invention is a method for improving the reaction velocity of
 CC redox reaction of a sulphate reducing microorganism having cytochrome c3
 CC performed analogically to the method above. The velocity and the yield
 CC of bioreaction can efficiently be improved.
 XX
 SQ Sequence 107 AA;

Query Match 45.5%; Score 5; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 1 apkap 5

RESULT 20
 AAM57221
 ID AAM57221 standard; Protein: 107 AA.

XX AAM57221:
 XX
 XX 04-AUG-1998 (first entry)

DE Cytochrome c3 protein SEQ ID NO:5 from Desulfovibrio vulgaris.

KM Desulfovibrio vulgaris Miyazaki F IAM2604; haem 3; cytochrome c3;
 KM electron moving velocity; haem protein; heme.

OS Desulfovibrio vulgaris.

XX JP10113182-A.

XX 06-MAY-1998.

XX 11-OCT-1996; 96JP-0269698.

XX 11-OCT-1996; 96JP-0269698.

XX (MITO) MITSUBISHI JUKOGYO KK.

XX WPI: 1998-315472/28.

PT Improvement of electron moving velocity of haem protein - by
 PT controlling degree of amino acid structure covering haem protein

XX Example 5; Page 8; 11pp; Japanese.

CC The present sequence represents a cytochrome c3 protein used in an
 CC example of the present invention. A new method has been developed
 CC for improving electron moving velocity (EMV) of haem protein. The
 CC method comprises controlling in the specific aa structure EMV of
 CC haem protein around the haem 3 of cytochrome c3, where the degree of
 CC the aa structure covering haem 3 is lowered. Also described in the
 CC present invention is a method for improving the reaction velocity of
 CC redox reaction of a sulphate reducing microorganism having cytochrome c3
 CC performed analogically to the method above. The velocity and the yield
 CC of bioreaction can efficiently be improved.
 XX
 SQ Sequence 107 AA;

Query Match 45.5%; Score 5; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 1 apkap 5

RESULT 21
 AAB10915
 ID AAB10915 standard; Protein: 107 AA.

XX AAB10915;

XX 01-FEB-2001 (first entry)

DE D. vulgaris cytochrome C3 protein.

XX Cytochrome C3; sulfate-reducing microbe; mutant; bio-element;
 KW molecular wire; organic semiconductor; commutator element.

OS Desulfovibrio vulgaris.

XX JP2000217577-A.

XX 08-AUG-2000.

XX 28-JAN-1999; 99JP-0020018.

XX 28-JAN-1999; 99JP-0020018.

XX (MITO) MITSUBISHI JUKOGYO KK.

XX WPI: 2000-605045/58.

DR N-PSDB: AAA98361.

PT Production of mutant cytochrome C3, useful as a material for a bio
 PT element such as an organic semiconductor, by point-mutating wild type
 PT cytochrome C3 from a sulfate reducing microbe -

XX Disclosure; Page 6; 9pp; Japanese.

CC This invention describes the novel production of a mutant cytochrome C3
 CC comprising a sequence (A) of 107 amino acids (fully defined in the
 CC specification), by point-mutating a wild type cytochrome C3 derived from
 CC a sulfate reducing microbe. The new method includes the following steps:
 CC (1) a plasmid carrying a gene of the mutant cytochrome C3 is introduced
 CC to an aerobic microbe to transform the aerobic microbe; (2) culturing
 CC aerobically the transformed aerobic microbe to grow it; and (3)
 CC collecting the mutant cytochrome C3 produced by the transformed aerobic
 CC microbe. Cytochrome C3 can be used as a material for a bio element such
 CC as a molecular wire, organic semiconductor and a commutator element.
 XX

SQ Sequence 107 AA;

Query Match 45.5%; Score 5; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
 |||||
 Db 1 apkap 5

RESULT 22

AAB10916
 ID AAB10916 standard; Protein: 107 AA.

XX AAB10916;

XX 01-FEB-2001 (first entry)

DE D. vulgaris cytochrome C3 mutant protein.

XX

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RESULT 17
AAW57218
ID AAW57218 standard; Protein; 107 AA.
XX
AC AAW57218;
XX
DT 04-AUG-1998 (first entry)
XX
DE Desulfovibrio vulgaris Miyazaki F IAM2604 haem 3 of cytochrome c3.
XX
KM Desulfovibrio vulgaris Miyazaki F IAM2604; haem 3; cytochrome c3;
XX electron moving velocity; haem protein; heme.
XX
OS Desulfovibrio vulgaris.
XX
PN JP10113182-A.
XX
PD 06-MAY-1998.
XX
PF 11-OCT-1996; 96JP-0269698.
XX
PR 11-OCT-1996; 96JP-0269698.
XX
PA (MITO ) MITSUBISHI JUKOGYO KK.
XX
DR WPI; 1998-315472/28.
XX N-PSDB; AAV28847.
XX
PT Improvement of electron moving velocity of haem protein - by
PS controlling degree of amino acid structure covering haem protein
XX
PS Claim 3; Page 6; 11pp; Japanese.
XX
CC The present sequence represents haem 3 from cytochrome c3 of
CC Desulfovibrio vulgaris Miyazaki F IAM2604. A new method has been
CC developed for improving electron moving velocity (EMV) of haem protein.
CC The method comprises controlling in the specific aa structure EMV of
CC haem protein around the haem 3 of cytochrome c3, where the degree of
CC the aa structure covering haem 3 is lowered. Also described in the
CC present invention is a method for improving the reaction velocity of
CC redox reaction of a sulphate reducing microorganism having cytochrome c3
CC performed analogically to the method above. The velocity and the yield
CC of bioreaction can efficiently be improved.
XX
SQ Sequence 107 AA;

Query Match 45.5%; Score 5; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
DB 1 apkap 5

RESULT 18
AAW57219
ID AAW57219 standard; Protein; 107 AA.
XX
AC AAW57219;
XX
DT 04-AUG-1998 (first entry)
XX
DE Cytochrome c3 protein SEQ ID NO:3 from J10113182 Example 1.
XX
KM Desulfovibrio vulgaris Miyazaki F IAM2604; haem 3; cytochrome c3;
XX electron moving velocity; haem protein; heme.
XX
OS Synthetic.
XX
DE Desulfovibrio vulgaris.

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XX
PN JP10113182-A.
XX
PD 06-MAY-1998.
XX
PF 11-OCT-1996; 96JP-0269698.
XX
PR 11-OCT-1996; 96JP-0269698.
XX
PA (MITO ) MITSUBISHI JUKOGYO KK.
XX
DR WPI; 1998-315472/28.
XX
PT Improvement of electron moving velocity of haem protein - by
PS controlling degree of amino acid structure covering haem protein
XX
PS Example 1; Page 7; 11pp; Japanese.
XX
CC The present sequence represents a cytochrome c3 protein used in an
CC example of the present invention. A new method has been developed
CC for improving electron moving velocity (EMV) of haem protein. The
CC method comprises controlling in the specific aa structure EMV of
CC haem protein around the haem 3 of cytochrome c3, where the degree of
CC the aa structure covering haem 3 is lowered. Also described in the
CC present invention is a method for improving the reaction velocity of
CC redox reaction of a sulphate reducing microorganism having cytochrome c3
CC performed analogically to the method above. The velocity and the yield
CC of bioreaction can efficiently be improved.
XX
SQ Sequence 107 AA;

Query Match 45.5%; Score 5; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APKAP 9
DB 1 apkap 5

RESULT 19
AAW57220
ID AAW57220 standard; Protein; 107 AA.
XX
AC AAW57220;
XX
DT 04-AUG-1998 (first entry)
XX
DE Cytochrome c3 protein SEQ ID NO:4 from J10113182 Example 1.
XX
KM Desulfovibrio vulgaris Miyazaki F IAM2604; haem 3; cytochrome c3;
XX electron moving velocity; haem protein; heme.
XX
OS Synthetic.
XX
DE Desulfovibrio vulgaris.
XX
PN JP10113182-A.
XX
PD 06-MAY-1998.
XX
PF 11-OCT-1996; 96JP-0269698.
XX
PR 11-OCT-1996; 96JP-0269698.
XX
PA (MITO ) MITSUBISHI JUKOGYO KK.
XX
DR WPI; 1998-315472/28.
XX
PT Improvement of electron moving velocity of haem protein - by
PS controlling degree of amino acid structure covering haem protein
XX
PS Example 1; Page 7-8; 11pp; Japanese.

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CC tumour specific polynucleotides and polypeptides can be used in

Db 36 p_{kapt} 40

CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 CC
 XX

SQ Sequence 25 AA;

Query Match 45.5%; Score 5; DB 14; Length 25;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QOTAP 6
 |||||
 Db 14 qqtap 18

RESULT 13

AA94958
 ID AAY94958 standard; Protein; 54 AA.

AC AAY94958;

DT 16-JUN-2000 (first entry)

DE Human secreted protein clone LB9_3 protein sequence SEQ ID NO:122.

XX Human; secreted protein; immunostimulant; immunosuppressant; vitruclide;
 XX antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
 XX antidiabetic; antiaesthetic; antirheumatic; antiparasitic; antiparasitic;
 XX antihypertensive; immune deficiency; severe combined immunodeficiency; SCID;
 XX infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
 XX connective tissue disease; multiple sclerosis; erythematosis;
 XX rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
 XX Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
 XX insulin dependent diabetes mellitus; graft-versus-host-disease;
 XX autoimmune inflammatory eye disease; allergy.

OS Homo sapiens.

PN WO200009552-A1.

PD 24-FEB-2000.

PF 13-AUG-1999; 99WO-US18298.

PR 14-AUG-1998; 98US-0096622.

PR 17-AUG-1998; 98US-0096815.

PR 04-SEP-1998; 98US-0099229.

PR 23-OCT-1998; 98US-0105368.

PR 08-JAN-1999; 99US-0115234.

PR 12-FEB-1999; 99US-0119931.

PR 18-FEB-1999; 99US-0120575.

PR 30-APR-1999; 99US-0132020.

PR 11-AUG-1999; 99US-0096622.

XX (GENY) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallee ER, Collins-Racie LA, Evans C;
 PI Werberg D, Treacy M, Agostino MO, Steinfinger RJ, Spaulding V;
 PI Wong GG, Clark HF, Fechtel K;

XX MPI: 2000-205979/18.

XX New polynucleotides encoding secreted proteins, which may have e.g.
 XX nutritional, chemokine, immune stimulating or suppressing,
 XX hemopoietic, tissue growth, activin/inhibin
 XX antiinflammatory or tumor inhibition activity

PS Claim 131; Page 581; 641pp; English.
 XX AAA16618 to AAA16697 encode the human secreted proteins given in
 CC AAY94898 to AAY94980, isolated from human adult brain, adult thyroid,

CC adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,
 CC adult placenta, adult testis, whole embryo, adult cartilage, kidney,
 CC foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,
 CC and adult bladder. cDNA libraries. The polynucleotides and proteins are
 CC predicted to have biological activities which would make them suitable
 CC for treating, preventing or ameliorating medical conditions in humans
 CC and animals. The polynucleotides can be used as markers for tissues in
 CC which the protein is preferentially expressed, as molecular weight
 CC markers on Southern gels, and as chromosome markers or tags to identify
 CC chromosomes or to map gene positions. The proteins can be used in the
 CC treatment of immune deficiencies and disorders, such as severe combined
 CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
 CC infections. These infections include human immunodeficiency virus (HIV),
 CC hepatitis, herpesviruses, mycobacteria, *Leishmania* spp., malaria and
 CC candidiasis. The proteins can be used to treat autoimmune disorders such
 CC as connective tissue disease, multiple sclerosis, systemic lupus
 CC erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation,
 CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
 CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
 CC autoimmune inflammatory eye disease. The proteins can also be used to
 CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent
 CC probes for the human secreted proteins from the present invention.
 CC
 XX

SQ Sequence 54 AA;

Query Match 45.5%; Score 5; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TAPKA 8
 |||||
 Db 45 tapka 49

RESULT 14

AA60235
 ID AAY60235 standard; Protein; 95 AA.

AC AAY60235;

DT 31-JAN-2000 (first entry)

DE Human endometrium tumour EST encoded protein 295.

XX Endometrium; human; tumour; cancer; antineoplastic; cytostatic; EST;
 XX treatment; uterine; gene therapy; expressed sequence tag.

XX Homo sapiens.

PN DE19817948-A1.

PD 21-OCT-1999.

PF 17-APR-1998; 98DE-1017948.

PR 17-APR-1998; 98DE-1017948.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pflarsky C, Dahl E;
 PI N-PSDB; AA242076.

XX MPI: 1999-591957/51.

XX New nucleic acid sequences expressed in uterine cancer tissues, and
 XX derived polypeptides, for treatment of uterine and endometrial cancer
 XX and identification of therapeutic agents

PS Claim 23; Page 392; 444pp; German.

XX This invention describes novel human nucleic acid (cDNA) sequences (A),
 CC that are highly expressed in uterine tumour tissue and which have

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XX 16-JUN-1994 (first entry)
XX Listeria p60 peptide epitope.
DE Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX Synthetic.
XX DE4318450-A.
XX 16-DEC-1993.
XX 03-JUN-1993; 93DE-4318450.
XX 11-JUN-1992; 92DE-4219111.
XX 25-NOV-1992; 92DE-4239567.
XX (MERE ) MERCK PATENT GMBH.
XX PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
XX PI Hofmann G, Bubert A, Goebel W, Koehler S;
XX WPI: 1993-406956/51.
XX New primers for PCR detection of Listeria - including individual
XX species, also new peptide(s) for raising antibodies for
XX immunochemical detection
XX PS Disclosure; Page 3; 19pp; German.
XX CC The sequence is that of a Listeria p60 peptide epitope which
XX CC which may be used in the prodn. of antibodies for the detection
XX CC of Listeria by immunoassay (partic. ELISA). It may be used as
XX CC part of a method that allows determination of individual Listeria
XX CC species, esp. L. monocytogenes.
XX SQ Sequence 11 AA;

Query Match 45.58; Score 5; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOTAP 6
DB 7 qctap 11

RESULT 11
AAR54625
ID AAR54625 standard; Protein; 13 AA.
XX AC AAR54625;
XX DT 16-JUN-1994 (first entry)
XX DE Listeria innocua p60 peptide epitope.
XX KW Antibodies; immunoassay; conjugate.
XX OS Synthetic.
XX PN DE4318450-A.
XX PD 16-DEC-1993.
XX PF 03-JUN-1993; 93DE-4318450.
XX PR 11-JUN-1992; 92DE-4219111.
XX PR 25-NOV-1992; 92DE-4239567.
XX PA (MERE ) MERCK PATENT GMBH.

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XX Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
XX PI Hofmann G, Bubert A, Goebel W, Koehler S;
XX WPI: 1993-406956/51.
XX New primers for PCR detection of Listeria - including individual
XX species, also new peptide(s) for raising antibodies for
XX immunochemical detection
XX PS Disclosure; Fig 5; 19pp; German.
XX CC The sequence is that of a Listeria innocua p60 peptide epitope which
XX CC which may be used in the prodn. of antibodies for the detection
XX CC of Listeria by immunoassay (partic. ELISA). It may be used as
XX CC part of a method that allows determination of individual Listeria
XX CC species.
XX SQ Sequence 13 AA;

Query Match 45.58; Score 5; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOTAP 6
DB 8 qctap 12

RESULT 12
AAR45165
ID AAR45165 standard; Protein; 25 AA.
XX AC AAR45165;
XX DT 16-JUN-1994 (first entry)
XX DE Listeria p60 peptide epitope.
XX KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Region 1..7 /note="opt. 0-7 amino acid residues"
XX FT Region 19..25 /note="opt. 0-7 amino acid residues"
XX PN DE4318450-A.
XX PD 16-DEC-1993.
XX PF 03-JUN-1993; 93DE-4318450.
XX PR 11-JUN-1992; 92DE-4219111.
XX PR 25-NOV-1992; 92DE-4239567.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
XX PI Hofmann G, Bubert A, Goebel W, Koehler S;
XX WPI: 1993-406956/51.
XX New primers for PCR detection of Listeria - including individual
XX species, also new peptide(s) for raising antibodies for
XX immunochemical detection
XX PS Claim 3; Page 4; 19pp; German.
XX CC The sequence is that of a Listeria p60 peptide epitope which

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Query Match 63.6%; Score 7; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOTAPKA 8
 1111111
 Db 1 qqlapka 7

RESULT 8

AAV26181
 ID AAV26181 standard; Protein; 150 AA.

AC AAV26181;

XX 22-OCT-1999 (first entry)

DE Rice acetohydroxyacid reductoisomerase.

KW Acetohydroxyacid reductoisomerase; rlr24.pk0087.e7 clone; rice; BCABE;
 KW branched chain biosynthetic enzyme; herbicide; immunological screening;
 KW probe; inhibitor; plant breeding; gene mapping.

OS Oryza sativa.

XX Key Location/Qualifiers

FT Misc-difference 14 /note= "encoded by MACC"

FT Misc-difference 16 /note= "encoded by NCC"

FT Misc-difference 86 /note= "encoded by GAN"

FT Misc-difference 108 /note= "encoded by AAN"

FT Misc-difference 118 /note= "encoded by CAN"

PN WO928446-A2.

XX 10-JUN-1999.

XX 18-NOV-1998; 98WO-US24615.

XX 02-DEC-1997; 97US-0067388.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Allen SM, Falco SC, Hiltz WD;

XX WPI: 1999-385378/32.

XX N-PSDB: AAX80619.

XX New isolated branched chain amino acid biosynthetic genes

PS Claim 6; Page 48-49; 69pp; English.

CC The present sequence is a portion of a rice acetohydroxyacid
 CC reductoisomerase, which is a branched chain amino acid biosynthetic
 CC enzyme (BCABE). The enzyme is encoded by a partial cDNA insert in clone
 CC rlr24.pk0087.e7. The clone is derived from rice leaf 15 days after
 CC germination, 24 hours after infection of Magaporthe grisea 4360-R-62
 CC strain. Host cells, transformed by a chimeric gene comprising the
 CC nucleic acid fragment, are used for the production of BCABE. The enzyme
 CC is involved in biosynthesis and utilization of branched chain amino
 CC acids, such as valine, isoleucine, and leucine. The products can be
 CC used for altering the levels of branched chain aminoacids in plants.
 CC They can also be used as targets to facilitate identification and/or
 CC design of inhibitors of those enzymes that may be useful as herbicides.
 CC The nucleic acid fragments can also be used as probes for mapping the
 CC genes that they are a part of, and as markers for traits linked to those
 CC genes. Such information may be useful in plant breeding in order to
 CC develop lines with desired phenotypes.

XX SQ Sequence 150 AA;

Query Match 54.5%; Score 6; DB 20; Length 150;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRKAPT 10
 1111111
 Db 22 apkapt 27

RESULT 9

AAAR60252
 ID AAR60252 standard; Protein; 890 AA.

AC AAR60252;

XX 15-FEB-1995 (first entry)

DE NF-ATP.

KW NF-AT; NF-ATP; preexisting nuclear factor of activated T-cell protein;
 KW T-lymphocyte; immunosuppressive.

OS Mus sp.

PN WO9415964-A.

PD 21-JUL-1994.

PF 18-JAN-1994; 94WO-US00545.

PR 15-JAN-1993; 93US-0006067.

PR 11-FEB-1993; 93US-0017052.

PR 29-OCT-1993; 93US-0145006.

XX (DAND) DANA FARBER CANCER INST INC.

XX (HARD) HARVARD COLLEGE.

XX Hogan PG, Jain J, Mccaffrey P, Rao A;

XX WPI: 1994-249140/30.

XX Purified nuclear factor of activated T cell protein - useful for
 PT detecting protein expression and screening potential

XX immunosuppressants

XX Disclosure; Page 58-61; 100pp; English.

XX A cDNA clone, mNF-ATPQ1A1/A, of mouse preexisting nuclear factor
 CC of activated T-cell protein (NF-ATP) was isolated from a T-cell
 CC library. The open reading frame encoded the protein given in
 CC AAR60252.

XX Sequence 890 AA;

Query Match 54.5%; Score 6; DB 15; Length 890;
 Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OOOTAP 6
 1111111
 Db 695 qqlap 700

RESULT 10

AAAR54621
 ID AAR54621 standard; Protein; 11 AA.

AC AAR54621;

PF 03-JUN-1993: 93DE-4318450.
 XX
 PR 11-JUN-1992: 92DE-4219111.
 PR 25-NOV-1992: 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 PI Schubert P, Neumann S, Pawelzik W, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of *Listeria* - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PS
 PS Disclosure; Page 3; 19pp; German.
 XX
 CC The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 CC
 SQ Sequence 9 AA:

Query Match 81.8%; Score 9; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QQTAPKAPT 10
 |||||
 Db 1 qqtapkept 9

RESULT 6
 AAR45162
 ID AAR45162 standard; Protein; 23 AA.
 XX
 AC AAR45162;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE *Listeria* p60 peptide epitope.
 XX
 KW *Listeria* monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..7
 FT /note= "opt. 0-7 amino acid residues"
 FT Region 17..23
 FT /note= "opt. 0-7 amino acid residues"
 XX
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993: 93DE-4318450.
 XX
 PR 11-JUN-1992: 92DE-4219111.
 PR 25-NOV-1992: 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 PI Schubert P, Neumann S, Pawelzik W, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of *Listeria* - including individual

PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Claim 3; Page 4; 19pp; German.
 XX
 CC The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 CC
 SQ Sequence 23 AA:

Query Match 81.8%; Score 9; DB 14; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.0023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QQTAPKAPT 10
 |||||
 Db 8 qqtapkept 16

RESULT 7
 AAR73906
 ID AAR73906 standard; peptide; 7 AA.
 XX
 AC AAR73906;
 XX
 DT 05-DEC-1995 (first entry)
 XX
 DE *Listeria* monocytogenes protein p60 precursor peptide 292-298.
 XX
 KW *Listeria* monocytogenes; protein p60 precursor; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KW viral; peptide 292-298.
 XX
 OS *Listeria* monocytogenes.
 XX
 PN W09509232-A.
 XX
 PD 06-APR-1995.
 XX
 PF 28-SEP-1994: 94WO-CA00516.
 XX
 PR 28-SEP-1993: 93US-0127499.
 XX
 PA (SHAR//) SHARMA L R.
 PA (VALS//) VAN ALSTYNE D.
 XX
 PI Sharma LR, Van Alstyne D;
 XX
 DR WPI: 1995-147431/19.
 XX
 PT New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 PS
 PS Claim 35; Page 77; 98pp; English.
 XX
 CC AAR73913 is the *Listeria* monocytogenes protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 CC
 SQ Sequence 7 AA:

961	4	36.4	179	21	AA606292	Arabidopsis thalia
962	4	36.4	179	21	AA641095	Zea mays protein f
963	4	36.4	179	21	AA58630	Protein regulating
964	4	36.4	179	22	AA846316	H. pylori HPS144 p
965	4	36.4	179	22	AA836630	Human FLEXHR-52 pr
966	4	36.4	180	14	AA833883	C-terminal portion
967	4	36.4	180	14	AA843884	Human clone 34 pro
968	4	36.4	180	17	AA805400	Arabidopsis thalia
969	4	36.4	180	21	AA620206	Human GRP-binding
970	4	36.4	181	19	AA857883	Arabidopsis thalia
971	4	36.4	181	21	AA628367	S. thermophilus fl
972	4	36.4	182	19	AA856799	Neisseria meningit
973	4	36.4	182	20	AA858894	Zea mays protein f
974	4	36.4	183	10	AA633229	Amino acid sequenc
975	4	36.4	183	10	AA893649	MG-4 antigen. AA
976	4	36.4	183	11	AA806439	Human secreted pro
977	4	36.4	183	20	AA807984	Arabidopsis thalia
978	4	36.4	183	21	AA606111	Arabidopsis thalia
979	4	36.4	183	21	AA619925	L. lactis fl portl
980	4	36.4	184	19	AA856796	C. pneumoniae prot
981	4	36.4	184	20	AA855124	Plant SPF encoded
982	4	36.4	184	21	AA824729	Eucalyptus grandis
983	4	36.4	184	21	AA816320	Arabidopsis thalia
984	4	36.4	184	21	AA607341	Arabidopsis thalia
985	4	36.4	184	21	AA613308	Arabidopsis thalia
986	4	36.4	184	21	AA639660	Arabidopsis thalia
987	4	36.4	184	21	AA650665	Arabidopsis thalia
988	4	36.4	185	21	AA642098	Arabidopsis thalia
989	4	36.4	185	21	AA658323	Arabidopsis thalia
990	4	36.4	186	21	AA630971	Arabidopsis thalia
991	4	36.4	186	21	AA850008	Neisseria gonorrhe
992	4	36.4	186	21	AA875009	Neisseria meningit
993	4	36.4	186	21	AA875010	Human gene 3 encod
994	4	36.4	186	22	AA887419	H. pylori outer me
995	4	36.4	187	18	AA820795	Pinus radiata tran
996	4	36.4	187	21	AA833058	Arabidopsis thalia
997	4	36.4	187	21	AA640385	Human regulatory m
998	4	36.4	188	20	AA893946	Amino acid sequenc
999	4	36.4	188	21	AA807997	Arabidopsis thalia
1000	4	36.4	188	21	AA659574	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AA845171

ID AAR45171 standard; Protein: 11 AA.

XX AAR45171:

XX

DT 16-JUN-1994 (first entry)

XX

DE Listeria p60 peptide epitope.

XX

KM Listeria monocytogenes; antibodies; immunosassay; conjugate.

XX

OS Synthetic.

XX

PN DE4318450-A.

XX

PD 16-DEC-1993.

XX

PF 03-JUN-1993; 93DE-4318450.

XX

PR 11-JUN-1992; 92DE-4219111.

PR 25-NOV-1992; 92DE-4239567.

XX

PA (MERE) MERCK PATENT GMBH.

XX

PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;

XX

PI Hofmann G, Bubert A, Goebel W, Koehler S;

XX

DR WPI: 1993-406956/51.

XX

PT New primers for PCR detection of Listeria - including individual

PT species, also new peptide(s) for raising antibodies for

PT immunochemical detection

XX

PS Disclosure; Fig 2; 19pp; German.

XX

CC The sequence is that of a Listeria p60 peptide epitope which

CC which may be used in the prodn. of antibodies for the detection

CC of Listeria by Immunoassay (partic. ELISA). It may be used as

CC part of a method that allows determination of individual Listeria

CC species, esp. L. monocytogenes.

XX

SQ Sequence 11 AA:

Query Match 100.0%; Score 11; DB 14; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 OOOTAPKAPTE 11

Db 1 qqrtaapkapte 11

RESULT 2

AA873894

ID AAR73894 standard; peptide: 21 AA.

XX AAR73894:

AC

XX

DT 05-DEC-1995 (first entry)

XX

DE Listeria monocytogenes protein P60 precursor peptide 285-305.

XX

KM Listeria monocytogenes; protein P60 precursor; vaccine;

KM meningitis related homologous antigenic sequence; MRHAS; RV-1;

KW immunosassay; diagnosis; treatment; prophylactic; bacterial;

KW viral; peptide 285-305.

XX

OS Listeria monocytogenes.

XX

PN WO9509232-A.

XX

PD 06-APR-1995.

XX

PF 28-SEP-1994; 94WO-CA00516.

XX

PR 28-SEP-1993; 93US-0127499.

XX

PA (SHAR/) SHARMA L R.

PA (VALS/) VAN ALSTYNE D.

XX

PI Sharma LR, Van Alstyne D;

XX

DR WPI: 1995-147431/19.

XX

PT New peptide(s) and corresp. antibodies for the treatment of

PT meningitis - the peptide(s) corresp. to homologous antigenic

PT sites on bacterial and viral agents and on chemokine(s), used for

PT detecting and preventing meningitis

XX

PS Claim 34; Page 74; 98pp; English.

XX

CC AAR73913 is the Listeria monocytogenes protein P60 precursor. It

CC contains the meningitis related antigenic sequences (MRHAS) claimed

CC in AAR73891-873894 and AAR73903-873906, which are recognised by a

CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The

CC claimed MRHAS peptides may be used in immunoassays to diagnose the

CC presence of bacterial and/or viral meningitis agents in a sample,

CC or in prophylactic and therapeutic meningitis treatments. The

CC peptides may also be used as vaccines against meningitis.

815	4	36.4	147	21	AAAG14003	Arabidopsis thalia
816	4	36.4	147	21	AAAG41096	zea mays protein f
817	4	36.4	147	21	AAAG45002	zea mays protein f
818	4	36.4	148	16	AAAM12693	Human cystatin B.
819	4	36.4	148	20	AAAY41588	Fragment of human
820	4	36.4	148	21	AAAB54088	Human pancreatic c
821	4	36.4	149	21	AAAG40950	zea mays protein f
822	4	36.4	149	21	AAAG49988	Arabidopsis thalia
823	4	36.4	149	21	AAAG54635	zea mays protein f
824	4	36.4	149	22	AAAT72673	Polylutamine trac
825	4	36.4	150	20	AAAT28887	Lactobacillus brev
826	4	36.4	150	21	AAAG25512	Arabidopsis thalia
827	4	36.4	150	21	AAAG41597	Arabidopsis thalia
828	4	36.4	151	18	AAAM27857	Amino acid sequenc
829	4	36.4	151	18	AAAM25527	Staphylococcus aur
830	4	36.4	151	21	AAAG26405	Arabidopsis thalia
831	4	36.4	151	21	AAAG33230	zea mays protein f
832	4	36.4	151	21	AAAG33786	Arabidopsis thalia
833	4	36.4	151	21	AAAG35418	zea mays protein f
834	4	36.4	151	21	AAAG40734	zea mays protein f
835	4	36.4	152	12	AAAR12520	Adometase encoded
836	4	36.4	152	12	AAAR74824	Bacteriophage T3 S
837	4	36.4	152	16	AAAR75212	Bacteriophage T3 S
838	4	36.4	152	17	AAAR88606	S-adenosylmethioni
839	4	36.4	152	17	AAAR88611	S-adenosylmethioni
840	4	36.4	152	17	AAAR88601	S-adenosylmethioni
841	4	36.4	152	17	AAAR88603	Adometase (12V) SA
842	4	36.4	152	18	AAAM29147	S-adenosylmethioni
843	4	36.4	152	18	AAAM11594	Adometase. Bacter
844	4	36.4	152	20	AAAY48291	Human prostate can
845	4	36.4	152	20	AAAM30603	Tomato E4 promoter
846	4	36.4	152	20	AAAM30604	S-adenosylmethioni
847	4	36.4	152	21	AAAG44025	Arabidopsis thalia
848	4	36.4	152	21	AAAG54637	zea mays protein f
849	4	36.4	153	20	AAAT74188	Human prostate tum
850	4	36.4	153	21	AAAY53589	Human preproinsuli
851	4	36.4	154	21	AAAG40970	zea mays protein f
852	4	36.4	154	21	AAAG44024	Arabidopsis thalia
853	4	36.4	154	22	AAAB30324	Helicobacter pylori
854	4	36.4	155	19	AAAM72382	Arabidopsis pathog
855	4	36.4	155	22	AAAB49660	S. cerevisiae YFR0
856	4	36.4	156	20	AAAY60068	Human endometrium
857	4	36.4	156	20	AAAM90885	Non-B. non-C. non-
858	4	36.4	156	21	AAAG18865	zea mays protein f
859	4	36.4	156	21	AAAG23571	zea mays protein f
860	4	36.4	156	21	AAAG54607	Human breast cance
861	4	36.4	156	22	AAAB63350	Human breast cance
862	4	36.4	157	19	AAAM58594	Mouse protein L256
863	4	36.4	157	21	AAAM93818	Maize CIP1 protein
864	4	36.4	157	21	AAAB10276	Murine adult thymu
865	4	36.4	157	21	AAAB11620	Arabidopsis thalia
866	4	36.4	157	21	AAAG27172	zea mays protein f
867	4	36.4	158	20	AAAT08804	Yeast NUP2 protein
868	4	36.4	158	20	AAAY08832	Yeast NUP2 protein
869	4	36.4	158	21	AAAB33212	Pinus radiata tran
870	4	36.4	158	21	AAAG04324	Arabidopsis thalia
871	4	36.4	158	21	AAAG45297	Arabidopsis thalia
872	4	36.4	159	20	AAAY00318	Human secreted pro
873	4	36.4	159	21	AAAG08936	Arabidopsis thalia
874	4	36.4	159	21	AAAG10210	Arabidopsis thalia
875	4	36.4	159	21	AAAG11619	Arabidopsis thalia
876	4	36.4	159	21	AAAG40733	zea mays protein f
877	4	36.4	159	21	AAAG48761	Arabidopsis thalia
878	4	36.4	159	21	AAAG53229	Arabidopsis thalia
879	4	36.4	160	15	AAAR60319	Pre-pro-vasoactive
880	4	36.4	160	15	AAAR60320	Pre-pro-vasoactive
881	4	36.4	160	21	AAAB53652	Human colon cancer
882	4	36.4	160	21	AAAB15419	Protein A-proinsul
883	4	36.4	160	21	AAAG08107	Arabidopsis thalia
884	4	36.4	160	21	AAAG19894	Arabidopsis thalia
885	4	36.4	160	21	AAAG43222	Arabidopsis thalia
886	4	36.4	160	21	AAAG54875	Arabidopsis thalia
887	4	36.4	161	21	AAAB54206	Human pancreatic c
888	4	36.4	161	21	AAAG04244	Arabidopsis thalia
889	4	36.4	161	21	AAAG06112	Arabidopsis thalia
890	4	36.4	161	21	AAAG45945	Arabidopsis thalia
891	4	36.4	162	20	AAAY50046	Bacillus stearothe
892	4	36.4	162	20	AAAY70241	Human RNA-associat
893	4	36.4	163	18	AAAM55291	H. pylori ORF 14ce
894	4	36.4	163	20	AAAY41231	H. Influenzae Yigu
895	4	36.4	163	21	AAAB43807	Human cancer assoc
896	4	36.4	163	21	AAAG08106	Arabidopsis thalia
897	4	36.4	164	10	AAAP94787	Protein G variant.
898	4	36.4	164	11	AAAR07011	Protein G variant.
899	4	36.4	164	12	AAAR10015	Type 9 Gx7809 prot
900	4	36.4	164	15	AAAS53299	IgG-binding Strept
901	4	36.4	164	21	AAAB24872	Plant SPD encoded
902	4	36.4	165	21	AAAG11618	Arabidopsis thalia
903	4	36.4	165	21	AAAG15310	Arabidopsis thalia
904	4	36.4	165	21	AAAG54557	zea mays protein f
905	4	36.4	165	21	AAAB57273	Human gene 72-enco
906	4	36.4	166	21	AAAB58526	Human prostate can
907	4	36.4	166	21	AAAG07157	Arabidopsis thalia
908	4	36.4	166	21	AAAG33328	zea mays protein f
909	4	36.4	166	21	AAAG48809	Arabidopsis thalia
910	4	36.4	167	21	AAAG58554	Arabidopsis thalia
911	4	36.4	168	20	AAAY50050	Mycobacterium tube
912	4	36.4	168	21	AAAB24730	Plant SPD encoded
913	4	36.4	168	21	AAAG29971	Arabidopsis thalia
914	4	36.4	169	21	AAAG08001	Arabidopsis thalia
915	4	36.4	169	21	AAAG19850	Arabidopsis thalia
916	4	36.4	169	21	AAAG19826	Arabidopsis thalia
917	4	36.4	169	21	AAAG55909	Arabidopsis thalia
918	4	36.4	169	21	AAAG60711	Arabidopsis thalia
919	4	36.4	170	21	AAAY74833	Neisseria gonorrhe
920	4	36.4	171	21	AAAB42103	Human ORFX ORF1867
921	4	36.4	171	21	AAAY95649	Neisseria meningit
922	4	36.4	171	21	AAAG06293	Arabidopsis thalia
923	4	36.4	171	21	AAAG39723	Arabidopsis thalia
924	4	36.4	171	21	AAAG60024	Arabidopsis thalia
925	4	36.4	172	21	AAAY99567	Vibrio cholerae ju
926	4	36.4	172	21	AAAG06271	Arabidopsis thalia
927	4	36.4	172	21	AAAG23200	Arabidopsis thalia
928	4	36.4	172	21	AAAG26404	Arabidopsis thalia
929	4	36.4	172	21	AAAG50704	Arabidopsis thalia
930	4	36.4	172	21	AAAG58325	Arabidopsis thalia
931	4	36.4	172	21	AAAG61127	Arabidopsis thalia
932	4	36.4	173	21	AAAG06270	Arabidopsis thalia
933	4	36.4	173	21	AAAG58324	Arabidopsis thalia
934	4	36.4	173	21	AAAG61126	Arabidopsis thalia
935	4	36.4	174	21	AAAG10209	Arabidopsis thalia
936	4	36.4	174	21	AAAG33901	Arabidopsis thalia
937	4	36.4	174	21	AAAG48760	Arabidopsis thalia
938	4	36.4	174	21	AAAG58553	Arabidopsis thalia
939	4	36.4	174	22	AAAB79407	Corynebacterium gl
940	4	36.4	175	21	AAAY81624	Streptococcus pneu
941	4	36.4	175	21	AAAB57224	Human prostate can
942	4	36.4	176	21	AAAB58426	Lung cancer associ
943	4	36.4	176	21	AAAG20227	Arabidopsis thalia
944	4	36.4	176	21	AAAG33900	Arabidopsis thalia
945	4	36.4	176	21	AAAG41596	Arabidopsis thalia
946	4	36.4	177	9	AAAP81164	Sequence of protei
947	4	36.4	177	20	AAAY33001	Human serine prote
948	4	36.4	177	21	AAAG32029	Arabidopsis thalia
949	4	36.4	178	13	AAAR20231	Human endothelin-2
950	4	36.4	178	13	AAAR23784	Precursor ET-2 seq
951	4	36.4	178	20	AAAY59888	Human normal uteru
952	4	36.4	178	20	AAAY04279	Borrelia afzeiell A
953	4	36.4	178	21	AAAG45944	zea mays protein f
954	4	36.4	178	21	AAAG20394	Arabidopsis thalia
955	4	36.4	179	18	AAAM20394	H. pylori outer me
956	4	36.4	179	18	AAAM24651	H. pylori outer me
957	4	36.4	179	20	AAAM89813	Protein encoded by
958	4	36.4	179	20	AAAM89813	Expressed antigen
959	4	36.4	179	21	AAAB43346	Human ORFX ORF3110
960	4	36.4	179	21	AAAG04243	Arabidopsis thalia

669	4	36.4	120	21	AA643216	Arabidopsis thalia	742	4	36.4	133	10	AA694786	Protein G variant.
670	4	36.4	120	21	AA652566	Arabidopsis thalia	743	4	36.4	133	11	AA607005	Protein G variant.
671	4	36.4	120	21	AA603428	Human secreted pro	744	4	36.4	133	12	AA610010	Type 5 GX7809 prot
672	4	36.4	121	21	AA640960	Human ORFX ORF724	745	4	36.4	133	14	AA634012	dtbD-4-keto-6-deox
673	4	36.4	121	21	AA619852	Arabidopsis thalia	746	4	36.4	133	15	AA653286	IgG-binding Strept
674	4	36.4	121	21	AA654575	Zea mays protein f	747	4	36.4	133	20	AA610132	Wilo-type Kexlatin
675	4	36.4	122	16	AA681442	Hepatitis GB virus	748	4	36.4	133	21	AA620228	Arabidopsis thalia
676	4	36.4	122	20	AA625862	Human secreted pro	749	4	36.4	133	21	AA627173	Zea mays protein f
677	4	36.4	122	21	AA623551	Invertase/Thiored	750	4	36.4	133	21	AA641136	Zea mays protein f
678	4	36.4	122	21	AA618866	Zea mays protein f	751	4	36.4	133	21	AA648755	Arabidopsis thalia
679	4	36.4	122	21	AA654608	Zea mays protein f	752	4	36.4	134	11	AA604087	Protein encoded by
680	4	36.4	122	21	AA654636	Zea mays protein f	753	4	36.4	134	11	AA606603	Human Brain Natriu
681	4	36.4	122	21	AA608928	Human secreted pro	754	4	36.4	134	15	AA656036	Mutant human Inter
682	4	36.4	122	15	AA609019	Hepatitis GB virus	755	4	36.4	134	20	AA605325	Human gamma-BNP pr
683	4	36.4	123	15	AA654984	Iron oxide binding	756	4	36.4	134	21	AA616614	Bacteriophage 192
684	4	36.4	123	21	AA612977	Arabidopsis thalia	757	4	36.4	134	21	AA632664	Zea mays protein f
685	4	36.4	123	21	AA633788	Arabidopsis thalia	758	4	36.4	134	21	AA657449	Arabidopsis thalia
686	4	36.4	123	21	AA654874	Arabidopsis thalia	759	4	36.4	134	21	AA657745	Arabidopsis thalia
687	4	36.4	123	21	AA657374	Drosophila Shaker	760	4	36.4	135	20	AA648498	Human BNP preprope
688	4	36.4	123	21	AA650565	Drosophila Shaker	761	4	36.4	135	21	AA643215	Human breast tumou
689	4	36.4	124	20	AA66182	Human bladder tumo	762	4	36.4	136	16	AA64971	Arabidopsis thalia
690	4	36.4	125	20	AA629529	Human lung tumour	763	4	36.4	136	20	AA637091	Gag region p19 pro
691	4	36.4	125	21	AA657166	Human prostate can	764	4	36.4	136	21	AA658506	Amino acid sequenc
692	4	36.4	125	21	AA644425	Human lung tumour	765	4	36.4	136	21	AA658506	Lung cancer associ
693	4	36.4	125	21	AA611722	Arabidopsis thalia	766	4	36.4	136	21	AA622380	Arabidopsis thalia
694	4	36.4	125	21	AA633329	Arabidopsis thalia	767	4	36.4	136	21	AA624478	Arabidopsis thalia
695	4	36.4	125	21	AA644972	Zea mays protein f	768	4	36.4	136	21	AA638985	Arabidopsis thalia
696	4	36.4	125	21	AA667284	Zea mays protein f	769	4	36.4	136	21	AA641099	Arabidopsis thalia
697	4	36.4	126	14	AA643681	Signature pattern	770	4	36.4	136	21	AA601430	Zea mays protein f
698	4	36.4	126	14	AA643681	PBI.3/Humanised 11	771	4	36.4	136	21	AA601430	Human secreted pro
699	4	36.4	126	14	AA643681	PBI.3/Humanised 11	772	4	36.4	137	14	AA642796	Partial B4 Ab vari
700	4	36.4	126	15	AA62677	CY1748RLD VL regio	773	4	36.4	137	21	AA659678	Secreted protein 1
701	4	36.4	126	15	AA62677	CY1748RLD VL regio	774	4	36.4	137	21	AA654558	Zea mays protein f
702	4	36.4	126	15	AA62677	CY1748RLD VL regio	775	4	36.4	137	21	AA645606	A human small prol
703	4	36.4	126	18	AA628201	Staphylococcus aur	776	4	36.4	137	22	AA631675	Amino acid sequenc
704	4	36.4	126	18	AA628201	Staphylococcus aur	777	4	36.4	138	20	AA612378	Human 5' EST secre
705	4	36.4	126	21	AA608937	Arabidopsis thalia	778	4	36.4	138	20	AA684159	Human 5' EST secre
706	4	36.4	126	21	AA642099	Arabidopsis thalia	779	4	36.4	138	21	AA619895	Arabidopsis thalia
707	4	36.4	127	21	AA628907	Arabidopsis thalia	780	4	36.4	138	21	AA643223	Arabidopsis thalia
708	4	36.4	127	21	AA656716	Amino acid sequenc	781	4	36.4	138	21	AA653949	Arabidopsis thalia
709	4	36.4	128	20	AA629530	Human lung tumour	782	4	36.4	138	20	AA692366	MAS-like G protein
710	4	36.4	128	21	AA654340	Human pancreatic c	783	4	36.4	139	20	AA652779	Chlamydia pneumoni
711	4	36.4	128	21	AA644427	Human lung tumour	784	4	36.4	139	21	AA642428	Human ORFX ORF2192
712	4	36.4	128	21	AA619851	Arabidopsis thalia	785	4	36.4	139	21	AA633787	Arabidopsis thalia
713	4	36.4	128	21	AA686527	Human gene 72-enco	786	4	36.4	139	21	AA641154	Zea mays protein f
714	4	36.4	128	21	AA653382	Human 5' EST relat	787	4	36.4	139	21	AA647096	Arabidopsis thalia
715	4	36.4	128	22	AA648027	Light chain sequen	788	4	36.4	139	22	AA654522	Zea mays protein f
716	4	36.4	129	10	AA647922	Protein G variant.	789	4	36.4	139	22	AA679482	Corynebacterium gl
717	4	36.4	129	12	AA610016	Type 11 GX7809 pro	790	4	36.4	140	20	AA659723	Secreted protein 6
718	4	36.4	129	15	AA654716	IgG-binding Strept	791	4	36.4	140	20	AA65347	Human adult testis
719	4	36.4	129	21	AA640968	Zea mays protein f	792	4	36.4	140	21	AA618734	Zea mays protein f
720	4	36.4	130	20	AA697713	Staphylococcus aur	793	4	36.4	140	21	AA659789	MMpPp-WMmp20-(His
721	4	36.4	130	21	AA640588	Human ORFX ORF352	794	4	36.4	141	22	AA668882	Human RECAP polype
722	4	36.4	130	21	AA644026	Arabidopsis thalia	795	4	36.4	141	14	AA642797	Human RECAP polype
723	4	36.4	130	21	AA654638	Arabidopsis thalia	796	4	36.4	141	17	AA644413	Partial B13/B14 Ab
724	4	36.4	130	22	AA656733	Zea mays protein f	797	4	36.4	141	17	AA644413	Met-KGF delta-N23/
725	4	36.4	130	22	AA67978	Amino acid sequenc	798	4	36.4	141	19	AA614895	Keratinocyte growt
726	4	36.4	130	22	AA680017	Corynebacterium gl	799	4	36.4	141	20	AA614895	Keratinocyte growt
727	4	36.4	130	22	AA646816	C. glutamicum folb	800	4	36.4	142	21	AA65726	Amino acid sequenc
728	4	36.4	130	22	AA648028	Light chain sequen	801	4	36.4	142	21	AA625405	Pinus radiata cell
729	4	36.4	131	10	AA694791	Protein G variant.	802	4	36.4	142	21	AA615311	Arabidopsis thalia
730	4	36.4	131	12	AA607008	Protein G variant.	803	4	36.4	142	21	AA656751	Arabidopsis thalia
731	4	36.4	131	12	AA610017	Type 10 GX7809 pro	804	4	36.4	143	18	AA611306	S. pneumoniae enol
732	4	36.4	131	15	AA653300	IgG-binding Strept	805	4	36.4	143	21	AA608108	Arabidopsis thalia
733	4	36.4	131	15	AA648625	Sequence of mouse	806	4	36.4	144	21	AA620404	Arabidopsis thalia
734	4	36.4	131	18	AA619533	HSV 863 antibody 1	807	4	36.4	144	22	AA641050	Zea mays protein f
735	4	36.4	131	18	AA626652	64-863 antibody HS	808	4	36.4	145	20	AA680201	Corynebacterium gl
736	4	36.4	131	20	AA67836	Amino acid sequenc	809	4	36.4	145	20	AA629499	Human lung tumour
737	4	36.4	131	20	AA658555	Arabidopsis thalia	810	4	36.4	145	21	AA644433	Human lung tumour
738	4	36.4	132	20	AA607483	Anti-HIV-1 gp120 a	811	4	36.4	145	21	AA635500	Arabidopsis thalia
739	4	36.4	132	21	AA612012	Arabidopsis thalia	812	4	36.4	146	18	AA616312	Streptomyces venez
740	4	36.4	132	21	AA615312	Arabidopsis thalia	813	4	36.4	146	21	AA657448	Arabidopsis thalia
741	4	36.4	132	21	AA694946	Human secreted pro	814	4	36.4	147	22	AA688537	Haemophilus influe
					AA658203	Canine Interleukin					19	AA672404	Arabidopsis thalia

523	4	36.4	107	21	AAG41155	Zee mays protein f	596	4	36.4	112	21	AAB39522	Anti-IL12 antibody
524	4	36.4	107	21	AAV78860	Streptomycin subti	597	4	36.4	112	21	AAB39524	Anti-IL12 antibody
525	4	36.4	107	21	AAV56680	Anti-erythropoietin	598	4	36.4	112	21	AAB39526	Anti-IL12 antibody
526	4	36.4	108	21	AAB19749	Erythropoietin rec	599	4	36.4	112	21	AAB39528	Anti-IL12 antibody
527	4	36.4	108	21	AAB19750	Erythropoietin rec	600	4	36.4	112	21	AAB39530	Anti-IL12 antibody
528	4	36.4	108	21	AAB19751	Erythropoietin rec	601	4	36.4	112	21	AAB39532	Anti-IL12 antibody
529	4	36.4	108	21	AAB19752	Erythropoietin rec	602	4	36.4	112	21	AAB39534	Anti-IL12 antibody
530	4	36.4	108	21	AAG22382	Arbidopsis thalia	603	4	36.4	112	21	AAB39536	Anti-IL12 antibody
531	4	36.4	108	21	AAG02229	Human secreted pro	604	4	36.4	112	21	AAB39538	Anti-IL12 antibody
532	4	36.4	108	21	AAV58205	Canine mature inte	605	4	36.4	112	21	AAB39540	Anti-IL12 antibody
533	4	36.4	109	11	AAAR07009	Protein G variant.	606	4	36.4	112	21	AAB39542	Anti-IL12 antibody
534	4	36.4	109	12	AAAR15646	Thioredoxin.	607	4	36.4	112	21	AAB39544	Anti-IL12 antibody
535	4	36.4	109	16	AAAR75767	Hls-patch thioredo	608	4	36.4	112	21	AAB39546	Anti-IL12 antibody
536	4	36.4	109	16	AAAR75768	Histidine patch-2	609	4	36.4	112	21	AAB39548	Anti-IL12 antibody
537	4	36.4	109	16	AAAR75769	E. coli thioredoxi	610	4	36.4	112	21	AAB39550	Anti-IL12 antibody
538	4	36.4	109	18	AAAW37348	Immunoglobulin C-1	611	4	36.4	112	21	AAB39552	Anti-IL12 antibody
539	4	36.4	109	18	AAAW27547	Human Ab 11ght cha	612	4	36.4	112	21	AAB39554	Anti-IL12 antibody
540	4	36.4	109	20	AAV25383	Plasmd d pTRX thior	613	4	36.4	112	21	AAB39556	Anti-IL12 antibody
541	4	36.4	109	20	AAV05567	HIV-1 group O isol	614	4	36.4	112	21	AAB39558	Anti-IL12 antibody
542	4	36.4	109	20	AAV02639	Thioredoxin protei	615	4	36.4	112	21	AAB39560	Anti-IL12 antibody
543	4	36.4	109	20	AAAM88817	Polypeptide fragme	616	4	36.4	112	21	AAB33149	Anti-IL12 antibody
544	4	36.4	109	20	AAAS65903	Human prostate can	617	4	36.4	112	21	AAAG08002	Pinus radiata tran
545	4	36.4	109	21	AAAB23553	Thioredoxin protei	618	4	36.4	112	21	AAV94933	Arbidopsis thalia
546	4	36.4	109	21	AAAB24873	Plant SDF encoded	619	4	36.4	112	22	AAAB48019	Human secreted pro
547	4	36.4	109	21	AAAG19832	Arbidopsis thalia	620	4	36.4	113	14	AAAR34276	Glamda-1 light ch
548	4	36.4	109	21	AAAG32030	Arbidopsis thalia	621	4	36.4	113	14	AAAR34277	Human Vlambdal-1-1
549	4	36.4	109	21	AAAG32665	Zee mays protein f	622	4	36.4	113	14	AAAR34278	Human Vlambdal-1-1
550	4	36.4	109	21	AAAG45707	Arbidopsis thalia	623	4	36.4	113	19	AAAW75885	Human Vlambdal-1-1
551	4	36.4	109	21	AAAG00954	Arbidopsis thalia	624	4	36.4	113	19	AAAW75885	Peptide inhibitor
552	4	36.4	109	21	AAV95204	Human secreted pro	625	4	36.4	113	21	AAAG18475	Zee mays protein f
553	4	36.4	109	21	AAV95205	Anti-platelet glyc	626	4	36.4	113	21	AAAG00802	Human secreted pro
554	4	36.4	109	22	AAAB80367	Anti-platelet glyc	627	4	36.4	113	22	AAV78865	Streptomycin subti
555	4	36.4	110	14	AAAR33331	Human prostate can	628	4	36.4	114	20	AAAB63888	Human prostate can
556	4	36.4	110	16	AAAR80621	Variant IGE - muta	629	4	36.4	114	20	AAV34698	Chlamydia pneumoni
557	4	36.4	110	19	AAAW14425	Human tumor-associ	630	4	36.4	114	21	AAAG07906	Arbidopsis thalia
558	4	36.4	110	19	AAV01128	Kex2 protease inhi	631	4	36.4	114	21	AAAG54523	Zee mays protein f
559	4	36.4	110	20	AAAB40424	Wild-type Kexcatin	632	4	36.4	115	20	AAV41019	RKSI protein RGS f
560	4	36.4	110	21	AAAG15654	Human ORFX ORF18	633	4	36.4	115	21	AAAG45003	Zee mays protein f
561	4	36.4	110	21	AAAG20405	Arbidopsis thalia	634	4	36.4	117	14	AAAR33272	T cell receptor al
562	4	36.4	110	21	AAAG40977	Arbidopsis thalia	635	4	36.4	117	14	AAAR33273	T cell receptor al
563	4	36.4	110	21	AAV95182	Zee mays protein f	636	4	36.4	117	14	AAAR33274	T cell receptor al
564	4	36.4	111	12	AAAR12263	Anti-platelet glyc	637	4	36.4	117	14	AAAR33275	T cell receptor al
565	4	36.4	111	17	AAAM03175	Anti-human RND FOG	638	4	36.4	117	21	AAAG14004	Neuron-associated
566	4	36.4	111	17	AAAR85506	SVRT2 DNA binding	639	4	36.4	117	21	AAAG15989	Arbidopsis thalia
567	4	36.4	111	17	AAAR89148	Vilambda for antib	640	4	36.4	117	21	AAAG40973	Arbidopsis thalia
568	4	36.4	111	17	AAAR92795	Human anti-Pseudom	641	4	36.4	117	21	AAAG03408	Zee mays protein f
569	4	36.4	111	18	AAAM13528	Murine p600. Mus	642	4	36.4	117	21	AAAG03857	Human secreted pro
570	4	36.4	111	18	AAAM13515	Anti-melanoma 11gh	643	4	36.4	117	21	AAAG03859	Human secreted pro
571	4	36.4	111	18	AAAM13513	Anti-melanoma 11gh	644	4	36.4	118	20	AAV12136	Human 5' EST secre
572	4	36.4	111	18	AAAM08489	C6 human sfv antib	645	4	36.4	118	21	AAAB18933	Human acid sequenc
573	4	36.4	111	18	AAAM08491	C6 human sfv antib	646	4	36.4	118	21	AAAB18935	Beta megaspermia p
574	4	36.4	111	18	AAAM08492	C6 human sfv antib	647	4	36.4	118	21	AAAG08050	Arbidopsis thalia
575	4	36.4	111	19	AAAM52223	Antibody LD2-1-VL	648	4	36.4	118	21	AAAG22381	Arbidopsis thalia
576	4	36.4	111	20	AAAM90281	Human anti-GP1b/I	649	4	36.4	118	21	AAAG30057	Arbidopsis thalia
577	4	36.4	111	20	AAAM90279	Human anti-GP1b/I	650	4	36.4	119	9	AAAP81366	Arbidopsis thalia
578	4	36.4	111	20	AAV01129	Kexcatin I mutant	651	4	36.4	119	21	AAAG11074	Light chain variab
579	4	36.4	111	20	AAV01130	Kexcatin I mutant	652	4	36.4	119	21	AAAG19518	Arbidopsis thalia
580	4	36.4	111	20	AAV01131	Kexcatin I mutant	653	4	36.4	119	21	AAAG25089	Arbidopsis thalia
581	4	36.4	111	21	AAAB40700	Human ORFX ORF464	654	4	36.4	119	21	AAAG25513	Arbidopsis thalia
582	4	36.4	111	22	AAAB48025	Glamda-1A single	655	4	36.4	119	21	AAAG26139	Arbidopsis thalia
583	4	36.4	112	16	AAAR76937	PHF-tau (143-254)	656	4	36.4	119	21	AAAG34376	Zee mays protein f
584	4	36.4	112	18	AAAM13523	Anti-melanoma 11gh	657	4	36.4	119	21	AAAG35119	Arbidopsis thalia
585	4	36.4	112	18	AAAM08488	C6 human sfv antib	658	4	36.4	119	21	AAAG38181	Arbidopsis thalia
586	4	36.4	112	19	AAAM06475	Human lung cancer	659	4	36.4	119	21	AAAG38472	Arbidopsis thalia
587	4	36.4	112	19	AAAM06475	Antibody HB4C5 119	660	4	36.4	119	21	AAAG38472	Arbidopsis thalia
588	4	36.4	112	20	AAV60037	Human endometrium	661	4	36.4	119	21	AAAG40975	Zee mays protein f
589	4	36.4	112	21	AAAB52208	Human anti-HBs ant	662	4	36.4	119	21	AAAG40987	Zee mays protein f
590	4	36.4	112	21	AAAB39492	Anti-IL12 antibo	663	4	36.4	119	21	AAAB52208	Arbidopsis thalia
591	4	36.4	112	21	AAAB39500	Anti-IL12 antibo	664	4	36.4	119	22	AAAB78992	E. coli proliferat
592	4	36.4	112	21	AAAB39508	Anti-IL12 antibo	665	4	36.4	120	15	AAAR47044	C. glutamicum SRT
593	4	36.4	112	21	AAAB39516	Anti-IL12 antibo	666	4	36.4	120	20	AAV48601	Lipoprotein. Synt
594	4	36.4	112	21	AAAB39518	Anti-IL12 antibody	667	4	36.4	120	21	AAAG24563	Human breast tumo
595	4	36.4	112	21	AAAB39520	Anti-IL12 antibody	668	4	36.4	120	21	AAAG28908	Arbidopsis thalia

377	4	36.4	70	21	AAB52587	Helicobacter pylori	450	4	36.4	96	21	AA626874	Zea mays protein f
378	4	36.4	71	18	AAW20467	H. pylori cytoplas	451	4	36.4	96	21	AA654577	Zea mays protein f
379	4	36.4	71	18	AAW24669	H. pylori cytoplas	452	4	36.4	97	21	AA640435	Arabidopsis thalia
380	4	36.4	71	20	AAV41589	Fragment of human	453	4	36.4	97	21	AA623454	Arabidopsis thalia
381	4	36.4	71	21	AA602695	Human secreted pro	454	4	36.4	97	21	AA645298	Arabidopsis thalia
382	4	36.4	72	21	AAB34764	Human secreted pro	455	4	36.4	98	14	AA634275	Human TNF binding
383	4	36.4	72	21	AA626400	Arabidopsis thalia	456	4	36.4	98	18	AAW14540	Streptococcus pneu
384	4	36.4	72	21	AA638456	Arabidopsis thalia	457	4	36.4	98	21	AAAB18934	Amino acid sequenc
385	4	36.4	73	21	AA607980	Arabidopsis thalia	458	4	36.4	98	21	AAAB40142	Anti-hi112 antibod
386	4	36.4	73	21	AA608477	Arabidopsis thalia	459	4	36.4	98	21	AAAB40143	Anti-hi112 antibod
387	4	36.4	73	22	AAB48747	Mouse liver growth	460	4	36.4	98	21	AAAB40144	Anti-hi112 antibod
388	4	36.4	74	18	AAW20946	H. pylori cytoplas	461	4	36.4	98	21	AAAB40145	Anti-hi112 antibod
389	4	36.4	74	20	AAV33812	ScmE-YOR159C a ye	462	4	36.4	98	21	AAAB40149	Arabidopsis thalia
390	4	36.4	74	21	AAAG19051	Zea mays protein f	463	4	36.4	98	21	AAAG15354	Zea mays protein f
391	4	36.4	74	21	AAAG26399	Arabidopsis thalia	464	4	36.4	98	21	AAAG34149	Zea mays protein f
392	4	36.4	74	21	AAAG3601	Human secreted pro	465	4	36.4	98	21	AAAG01380	Human secreted pro
393	4	36.4	75	19	AAW42018	Clone BL341.4 prot	466	4	36.4	99	21	AAAB40147	Anti-hi112 antibod
394	4	36.4	75	20	AAV08625	Human secreted pro	467	4	36.4	99	21	AAAB40148	Anti-hi112 antibod
395	4	36.4	75	20	AAV11795	Human 5' EST secre	468	4	36.4	99	21	AAAG41137	Zea mays protein f
396	4	36.4	75	20	AAV01332	Modified sp6 RNA p	469	4	36.4	99	21	AAAG01078	Human secreted pro
397	4	36.4	75	21	AAV01363	Human ORFX ORP905	470	4	36.4	99	21	AAV76755	Human protein kina
398	4	36.4	75	21	AAAB4141	Human ORFX ORP905	471	4	36.4	100	21	AAAB40576	Human ORFX ORP340
399	4	36.4	75	21	AAV67316	Human secreted pro	472	4	36.4	100	21	AAV93883	Amino acid sequenc
400	4	36.4	76	21	AAAB41661	Human ORFX ORP1425	473	4	36.4	101	14	AAAB38604	NEWM light chain.
401	4	36.4	76	21	AAAG54780	Arabidopsis thalia	474	4	36.4	101	20	AAV12102	Human 5' EST secre
402	4	36.4	76	21	AAAG58573	Arabidopsis thalia	475	4	36.4	102	21	AAAB41432	Human ORFX ORP196
403	4	36.4	76	21	AAAG3551	Human secreted pro	476	4	36.4	102	21	AAAG08003	Arabidopsis thalia
404	4	36.4	77	11	AAAR7049	Alkaline phosphata	477	4	36.4	102	21	AAAG22573	Zea mays protein f
405	4	36.4	77	20	AAV60212	Human endometrium	478	4	36.4	102	21	AAAG32918	Human secreted pro
406	4	36.4	77	20	AAV11964	Human 5' EST secre	479	4	36.4	102	21	AAV03918	Humanized 369 Ligh
407	4	36.4	77	21	AAAG38455	Arabidopsis thalia	480	4	36.4	102	22	AAV56683	Human gastric canc
408	4	36.4	78	21	AAAG28397	Arabidopsis thalia	481	4	36.4	103	14	AAAB63506	NEWM light chain.
409	4	36.4	79	20	AAAG7979	Ubiquitin-like dom	482	4	36.4	103	15	AAAR38605	NEWM light chain.
410	4	36.4	79	21	AAAG07979	Arabidopsis thalia	483	4	36.4	103	15	AAAR52037	Light chain variab
411	4	36.4	79	21	AAAG58711	Arabidopsis thalia	484	4	36.4	103	18	AAAR21635	NEWM human antibod
412	4	36.4	80	21	AAAB4219	Human pancreatic c	485	4	36.4	103	18	AAAR32442	Mycobacterium tube
413	4	36.4	80	21	AAAG1350	Arabidopsis thalia	486	4	36.4	103	18	AAW32374	Mycobacterium tube
414	4	36.4	81	9	AAAP81320	MMP signal and N-t	487	4	36.4	103	19	AAAB1677	M. tuberculosis im
415	4	36.4	81	20	AAAB7980	Ubiquitin-like dom	488	4	36.4	103	19	AAW64314	Mycobacterium tube
416	4	36.4	81	21	AAAG1420	Arabidopsis thalia	489	4	36.4	103	20	AAW58484	Human NEWM antibod
417	4	36.4	82	15	AAAR58336	Hypotensive polype	490	4	36.4	103	20	AAV60148	Human endometrium
418	4	36.4	83	11	AAAR05708	Pseudomonas aerugi	491	4	36.4	103	20	AAV39116	M. tuberculosis an
419	4	36.4	83	16	AAAR6924	Pseudomonas aerugi	492	4	36.4	103	20	AAV38979	M. tuberculosis re
420	4	36.4	83	16	AAW41427	Kex2 protease inh	493	4	36.4	103	21	AAAB41048	Human ORFX ORF812
421	4	36.4	83	20	AAV73979	Human prostate tum	494	4	36.4	103	21	AAAG18812	Zea mays protein f
422	4	36.4	83	21	AAAG56133	Arabidopsis thalia	495	4	36.4	104	16	AAAG59566	Arabidopsis thalia
423	4	36.4	84	8	AAAP70614	Sequence encoded b	496	4	36.4	104	16	AAAR80087	Human derived 19th
424	4	36.4	84	20	AAV07794	Human secreted pro	497	4	36.4	104	20	AAW95485	Human-derived RT3
425	4	36.4	85	9	AAAP80331	Sequence of polype	498	4	36.4	104	21	AAAG33330	Zea mays protein f
426	4	36.4	85	17	AAAR89425	Mucin-derived prot	499	4	36.4	105	9	AAAP81776	Sequence encoded b
427	4	36.4	85	21	AAAG02578	Human secreted pro	500	4	36.4	105	11	AAAR04028	R gene product of
428	4	36.4	85	21	AAV69790	MMPsp-MMPm20-(His	501	4	36.4	105	13	AAAR20601	ROD HIV-2 R protei
429	4	36.4	87	20	AAV72569	Human secreted pro	502	4	36.4	105	13	AAAR20603	Native Vpr protein
430	4	36.4	88	21	AAAB41338	Human ORFX ORP102	503	4	36.4	105	17	AAAR94545	Mucin-derived prot
431	4	36.4	88	21	AAAB27257	Soybean cyclin-dep	504	4	36.4	105	17	AAAR89427	Human lambda CL do
432	4	36.4	88	21	AAV56651	Partial peptide fr	505	4	36.4	105	19	AAW40579	Human lambda CL do
433	4	36.4	88	21	AAV56668	Partial peptide fr	506	4	36.4	105	19	AAW52231	Antibody LP2-11-VL
434	4	36.4	89	16	AAAR71124	SG-2. Synthetic.	507	4	36.4	105	20	AAW52235	Antibody LP2-17-VL
435	4	36.4	89	20	AAV73958	Human prostate tum	508	4	36.4	105	20	AAV28886	Lactobacillus brev
436	4	36.4	90	20	AAV35733	Chlamydia pneumoni	509	4	36.4	105	20	AAV08746	Human lambda-CL do
437	4	36.4	90	21	AAAB58188	Lung cancer associ	510	4	36.4	105	20	AAW92426	Human lambda prote
438	4	36.4	90	21	AAAG28396	Arabidopsis thalia	511	4	36.4	105	21	AAAB42644	Human ORFX ORF2408
439	4	36.4	90	22	AAAB48026	Light chain sequen	512	4	36.4	105	21	AAAB27001	Human lambda CL do
440	4	36.4	91	21	AAAB42378	Human ORFX ORF2142	513	4	36.4	105	21	AAV51981	HIV-2 ROD isolate
441	4	36.4	91	21	AAAG57450	Arabidopsis thalia	514	4	36.4	105	9	AAV53248	HIV-2 ROD strain V
442	4	36.4	92	12	AAAR15179	hCG/DCG alpha subu	515	4	36.4	106	17	AAAP80814	Sequence of R prot
443	4	36.4	92	21	AAAG02256	Human secreted pro	516	4	36.4	106	17	AAAR92516	Microtubule-associ
444	4	36.4	93	21	AAV91011	Fowlpox virus 7.3	517	4	36.4	106	18	AAV31727	Alpha light chain
445	4	36.4	94	20	AAV28572	Secreted peptide c	518	4	36.4	106	18	AAW60941	Streptococcus pneu
446	4	36.4	95	20	AAW87985	Ubiquitin-like dom	519	4	36.4	106	20	AAW70803	Amino acid sequenc
447	4	36.4	95	20	AAW87986	Ubiquitin-like dom	520	4	36.4	106	21	AAAG18736	Zea mays protein f
448	4	36.4	95	21	AAAG41103	Zea mays protein f	521	4	36.4	107	19	AAV92193	Human IgG1 lambda
449	4	36.4	96	12	AAAR15188	hCG/DCG alpha subu	522	4	36.4	107	19	AAW75895	Peptide inhibitor
												AAW54013	Anti-Cda antibody

231	4	36.4	9	21	AAB37084	B. brevis HMPp9 P	304	4	36.4	34	20	AAV27769	Human secreted pro
232	4	36.4	10	18	AAW41835	Modified B. burgdo	305	4	36.4	35	19	AAW79008	Rieske motif in KP
233	4	36.4	10	20	AAV46330	Immunogenic peptid	306	4	36.4	35	19	AAW79009	Rieske motif in KP
234	4	36.4	10	21	AAB22031	p67SRF protein fra	307	4	36.4	35	19	AAW79010	Rieske motif in B-
235	4	36.4	10	21	AAB22074	p67SRF protein fra	308	4	36.4	35	19	AAW79011	Rieske motif in B-
236	4	36.4	10	21	AAV95865	O-glycosylation si	309	4	36.4	35	19	AAW79012	Rieske motif in p5
237	4	36.4	10	21	AAV69786	Bacillus brevis MW	310	4	36.4	35	19	AAW59701	Amino acid sequenc
238	4	36.4	11	14	AAV54627	Listeria innocua p	311	4	36.4	35	21	AAW56466	Arbidops is thalia
239	4	36.4	11	19	AAW41761	Colony stimulating	312	4	36.4	36	20	AAW94500	Bnl brain-specific
240	4	36.4	11	21	AAB26618	Partial sequence #	313	4	36.4	37	21	AAB32038	Human secreted pro
241	4	36.4	11	21	AAV87645	SV40 large T antige	314	4	36.4	37	14	AAR39893	Lipopeptide TPRV-C
242	4	36.4	12	15	AAR49286	Lipoprotein derive	315	4	36.4	37	21	AAV94558	Human big endothel
243	4	36.4	12	15	AAR57484	Lipoprotein (a)-pe	316	4	36.4	37	21	AAB09564	Human Op-1 mutant
244	4	36.4	12	18	AAW25458	SH3 domain binding	317	4	36.4	37	21	AAV09572	Human Op-1 mutant
245	4	36.4	12	21	AAV44719	SV40 large T antige	318	4	36.4	38	21	AAB09575	Human Op-1 mutant
246	4	36.4	13	15	AAR67111	Anti-contraction p	319	4	36.4	38	21	AAB45413	Human secreted pro
247	4	36.4	13	21	AAV99293	HLA class II bindi	320	4	36.4	39	21	AAW56465	Arbidops is thalia
248	4	36.4	14	21	AAV99294	HLA class II bindi	321	4	36.4	40	19	AAW73052	Mycobacterium tube
249	4	36.4	14	22	AAB65584	Immunogenic peptid	322	4	36.4	40	20	AAV08801	Yeast Nup2 protein
250	4	36.4	15	17	AAR94518	GVAP fragment p85	323	4	36.4	40	20	AAV08829	Yeast YNp2 protei
251	4	36.4	15	20	AAV43588	Internal peptide o	324	4	36.4	42	20	AAV60384	Human normal blad
252	4	36.4	15	20	AAV05912	Thermophilus them	325	4	36.4	42	22	AAB72672	polyglutamine trac
253	4	36.4	16	14	AAR39522	Human big endothel	326	4	36.4	44	17	AAR93587	(1-3)-beta-D-gluc
254	4	36.4	16	15	AAR52128	Mouse light chain	327	4	36.4	45	21	AAW38419	Arbidops is thalia
255	4	36.4	16	15	AAR52129	Mouse light chain	328	4	36.4	48	20	AAV12839	Human 5' EST seque
256	4	36.4	16	15	AAR52130	Mouse light chain	329	4	36.4	48	21	AAB45048	Human secreted pro
257	4	36.4	16	15	AAR52131	Mouse light chain	330	4	36.4	48	21	AAW54856	Arbidops is thalia
258	4	36.4	16	15	AAR52132	Mouse light chain	331	4	36.4	48	21	AAW57356	Arbidops is thalia
259	4	36.4	16	15	AAR52133	Mouse light chain	332	4	36.4	48	21	AAW60514	Arbidops is thalia
260	4	36.4	16	15	AAR52135	Mouse light chain	333	4	36.4	49	19	AAW74806	Human secreted pro
261	4	36.4	16	15	AAR52139	Mouse light chain	334	4	36.4	50	20	AAV36060	Extended human sec
262	4	36.4	16	15	AAR52124	Mouse light chain	335	4	36.4	50	20	AAV01152	Secreted protein e
263	4	36.4	16	17	AAR98414	Interferon-gamma r	336	4	36.4	51	21	AAW07981	Arbidops is thalia
264	4	36.4	16	18	AAW38968	Peptide resembling	337	4	36.4	52	20	AAV02982	Fragment of human
265	4	36.4	17	11	AAR06876	HTLV-II gag 4-20 d	338	4	36.4	52	21	AAB43415	Human cancer assoc
266	4	36.4	17	13	AAR28142	Leucine aminopepti	339	4	36.4	52	21	AAB16818	Bacteriophage Dp-1
267	4	36.4	17	21	AAV90743	Epsilon-sarcoglyca	340	4	36.4	52	21	AAW57355	Arbidops is thalia
268	4	36.4	18	19	AAW41423	Kex2 protease inh	341	4	36.4	52	21	AAW60513	Arbidops is thalia
269	4	36.4	19	19	AAW4525	GVAP tyryptic pept	342	4	36.4	52	21	AAW02040	Human secreted pro
270	4	36.4	19	17	AAR94510	GVAP fragment p85	343	4	36.4	52	21	AAW02041	Human secreted pro
271	4	36.4	19	19	AAW81232	Human ENOS peptide	344	4	36.4	52	21	AAW03409	Human secreted pro
272	4	36.4	19	19	AAW81232	Human INOS peptide	345	4	36.4	53	13	AAR25038	Sequence encoded b
273	4	36.4	19	19	AAW41428	Kex2 protease inh	346	4	36.4	53	21	AAW03429	Human secreted pro
274	4	36.4	19	20	AAV43587	Internal peptide o	347	4	36.4	53	22	AAB37486	AGP-1 protein.. S
275	4	36.4	19	20	AAV43595	Internal peptide o	348	4	36.4	54	15	AAR58335	Hypotensive polype
276	4	36.4	19	21	AAB51600	Yada homologous pe	349	4	36.4	54	21	AAV13143	Human secreted pro
277	4	36.4	20	17	AAR89385	Kentucky Blue Gras	350	4	36.4	54	21	AAW01724	Human secreted pro
278	4	36.4	20	20	AAV01694	Peptide derived fr	351	4	36.4	55	21	AAW40992	zea mays protein f
279	4	36.4	20	21	AAB09169	Hepatitis GB virus	352	4	36.4	55	17	AAR89417	WC1 N-terminal pe
280	4	36.4	20	21	AAV52511	House dust mite al	353	4	36.4	56	19	AAW38491	S. pneumoniae pne
281	4	36.4	20	22	AAB55820	PL peptide #31. S	354	4	36.4	56	20	AAV60462	Human normal blad
282	4	36.4	20	22	AAB57682	Syndecan-2 PL pept	355	4	36.4	58	19	AAW71565	Hepatocyte nuclear
283	4	36.4	20	22	AAB56092	Syndecan-2 PL pept	356	4	36.4	59	20	AAV41511	Fragment of human
284	4	36.4	21	21	AAB51528	Proteobacterial ex	357	4	36.4	59	19	AAV20977	Human glial fibril
285	4	36.4	23	19	AAR45167	Listeria p60 pepti	358	4	36.4	60	21	AAB38161	Human secreted pro
286	4	36.4	23	19	AAV20505	Human neurofilamen	359	4	36.4	60	21	AAW02638	Human secreted pro
287	4	36.4	23	22	AAB73023	Rhinovirus genome-	360	4	36.4	60	21	AAW02833	Human secreted pro
288	4	36.4	26	15	AAR52411	Mouse heavy chain	361	4	36.4	62	17	AAR89416	WC1 N-terminal. pe
289	4	36.4	26	15	AAR52407	Mouse heavy chain	362	4	36.4	62	17	AAW26875	zea mays protein f
290	4	36.4	26	15	AAR52381	Mouse heavy chain	363	4	36.4	63	21	AAW28398	Arbidops is thalia
291	4	36.4	26	15	AAR52360	Mouse heavy chain	364	4	36.4	63	17	AAR99624	P. aeruginosa opri
292	4	36.4	26	15	AAR51725	Neurotrophic facto	365	4	36.4	64	14	AAR37963	KGFR Ig-1-like domai
293	4	36.4	27	18	AAW01786	Residual protease	366	4	36.4	64	20	AAV73836	Human prostate tum
294	4	36.4	27	20	AAW78130	Human secreted pro	367	4	36.4	64	20	AAV60177	Human endometrium
295	4	36.4	28	21	AAV93257	Amino acid sequenc	368	4	36.4	65	20	AAV27640	Human secreted pro
296	4	36.4	29	20	AAV41512	Fragment of human	369	4	36.4	65	21	AAW16868	Human secreted pro
297	4	36.4	30	15	AAR47193	N-terminal fragmen	370	4	36.4	66	21	AAW40982	Arbidops is thalia
298	4	36.4	30	22	AAB75250	Human secreted pro	371	4	36.4	69	14	AAR44553	zea mays protein f
299	4	36.4	31	14	AAR34860	Candida acidic pro	372	4	36.4	69	20	AAV19503	vbl protein of fel
300	4	36.4	31	14	AAR34861	Candida acidic pro	373	4	36.4	69	21	AAW21730	Arbidops is thalia
301	4	36.4	32	21	AAB07999	Peptide derived fr	374	4	36.4	69	21	AAW58574	Arbidops is thalia
302	4	36.4	33	21	AAB39405	Human secreted pro	375	4	36.4	70	19	AAV22897	SEQ ID NO. 93 from
303	4	36.4	34	14	AAR39873	C peptide RV-C6, r	376	4	36.4	70	20	AAW67845	Human secreted pro

85	5	45.5	279	17	AAW0803	Thermilase L221Q.	158	5	45.5	635	21	AAV70781	EGFP-VASP fusion p
86	5	45.5	279	17	AAW0769	Thermilase T111N.	159	5	45.5	638	11	AAAR03924	E. coli HSP (dnak)
87	5	45.5	279	17	AAW00770	Thermilase T217G +	160	5	45.5	668	21	AAAB57099	Human prostrate can
88	5	45.5	279	17	AAW00771	Thermilase G139N.	161	5	45.5	668	21	AAAB28595	Maize Scarecrow pr
89	5	45.5	279	19	AAW62226	Subtilase THTHER.F	162	5	45.5	714	19	AAW98361	H. pylori GHPO 137
90	5	45.5	279	20	AAI24912	Thermilase subtlil	163	5	45.5	723	21	AAV75477	Neisseria meningit
91	5	45.5	279	20	AAV21650	Subtilase THTHER.	164	5	45.5	730	17	AAV43385	S. pneumoniae pspc
92	5	45.5	279	20	AAW92816	T. thalophilus TH	165	5	45.5	746	17	AAAR3270	GST-INL fusion int
93	5	45.5	280	21	AAAB3251	Streptomyces coll.	166	5	45.5	756	21	AAAB2605	Human ORF ORF2369
94	5	45.5	292	13	AAAR29312	Cyclin D3 protein.	167	5	45.5	757	21	AAV44364	Human cell cycle r
95	5	45.5	292	14	AAAR4804	Human cyclin D3.	168	5	45.5	758	21	AAAB3319	Human colon cancer
96	5	45.5	296	17	AAW04577	Sensory and motor	169	5	45.5	766	20	AAV13457	Amino acid sequenc
97	5	45.5	296	17	AAAR97224	Sensory and motor	170	5	45.5	770	20	AAV13456	Amino acid sequenc
98	5	45.5	296	19	AAW41263	Sensory and motor	171	5	45.5	783	20	AAV60344	Human normal blad
99	5	45.5	296	19	AAW46465	Sensory and motor	172	5	45.5	818	19	AAW72035	HSV-2 strain SB5 C
100	5	45.5	296	20	AAV06640	Sensory and motor	173	5	45.5	859	20	AAV00991	Human ATP-depend
101	5	45.5	296	21	AAV71177	Human Sensory and	174	5	45.5	859	22	AAAB7463	Human ATP-depend
102	5	45.5	296	21	AAV57385	Sensory and motor	175	5	45.5	888	18	AAAB7463	Human ATP-depend
103	5	45.5	302	19	AAW72214	HSV-2 strain SB5 C	176	5	45.5	950	20	AAV33298	DNA polymerase whl
104	5	45.5	320	18	AAW19990	Type I, p80 IL-1-r	177	5	45.5	1004	21	AAAB01841	Human membrane spa
105	5	45.5	322	15	AAAR52025	Human Interleukin-	178	5	45.5	1010	21	AAAB01840	Haemophilus influe
106	5	45.5	322	15	AAAR52025	Bacillus sp. NKS-2	179	5	45.5	1050	21	AAAB9774	Haemophilus influe
107	5	45.5	323	20	AAV37286	Amino acid sequenc	180	5	45.5	1051	20	AAAB9774	Molecular pathogen
108	5	45.5	323	22	AAAB9174	Human G-protein co	181	5	45.5	1061	21	AAAB7641	A serline/threonine
109	5	45.5	327	21	AAAB33321	Eucalyptus grandis	182	5	45.5	1070	13	AAAR21521	Wild type Escheric
110	5	45.5	339	16	AAAR77317	Protein activated	183	5	45.5	1070	22	AAAB48099	Alpha galactosidas
111	5	45.5	342	22	AAAB48740	Mouse liver growth	184	5	45.5	1116	21	AAAB42449	Amino acid sequenc
112	5	45.5	343	14	AAAR41670	Porcine stalytran	185	5	45.5	1161	21	AAAB42449	Human ORF ORF2213
113	5	45.5	343	16	AAAR65240	L. lactis branched	186	5	45.5	1237	19	AAAB44729	Chicken protein ty
114	5	45.5	344	15	AAAR54222	Human prostate can	187	5	45.5	1257	20	AAAB9347	Chicken transmembr
115	5	45.5	344	21	AAAB56576	Human breast cance	188	5	45.5	1257	17	AAAR87628	Alpha-Ketoglutaric
116	5	45.5	347	22	AAAB63245	Human death associ	189	5	45.5	1339	21	AAAB41781	B. lactofermentum
117	5	45.5	373	21	AAAG04115	Human ORF ORF2089	190	5	45.5	1522	20	AAV03183	Human ORF ORF2651
118	5	45.5	373	21	AAAG1856	Arabidopsis thalia	191	5	45.5	1634	14	AAAR42452	Topoisomerase II b
119	5	45.5	373	21	AAAG54002	Arabidopsis thalia	192	5	45.5	1642	20	AAAB9400	Enzyme involved in
120	5	45.5	398	16	AAAR74206	Arabidopsis thalia	193	5	45.5	1876	18	AAAB9400	S. putrefaciens PK
121	5	45.5	398	19	AAAR71368	Human death associ	194	5	45.5	1896	19	AAAB9400	Phosphatidyl inosl
122	5	45.5	398	21	AAAB42325	Human ORF ORF2089	195	5	45.5	1920	22	AAAB2095	HSV-2 strain SB5 C
123	5	45.5	415	21	AAV77273	Streptomyces viola	196	5	45.5	2023	21	AAAB5656	Novel protein kina
124	5	45.5	415	21	AAV78825	Amino acid sequenc	197	5	45.5	2074	21	AAV54319	Amino acid sequenc
125	5	45.5	429	21	AAV74547	Neisseria meningit	198	5	45.5	2135	22	AAU00019	Amino acid sequenc
126	5	45.5	429	21	AAV74548	Neisseria meningit	199	5	45.5	2735	17	AAAB9462	Human Plexin prote
127	5	45.5	435	21	AAAG36200	Arabidopsis thalia	200	5	45.5	2756	19	AAAB37050	Biosynthetic enzym
128	5	45.5	438	15	AAAR47259	Pre-pro-VGR1. Mus	201	5	45.5	2756	21	AAAB10467	S. putrefaciens BP
129	5	45.5	449	22	AAAB48100	Neisseria acid sequenc	202	5	45.5	3084	10	AAAP94758	Shewanella putrefe
130	5	45.5	451	20	AAV38573	Neisseria meningit	203	5	45.5	3119	19	AAAR72204	Sequence of mouse
131	5	45.5	451	20	AAV38574	DAX-1 protein. Ho	204	5	45.5	3266	21	AAAB42451	HSV-2 strain SB5 C
132	5	45.5	470	18	AAAB12678	CRD domain of huma	205	5	45.5	36.4	6	AAV49176	Human ORF ORF2255
133	5	45.5	478	22	AAAB48101	Mouse CRD amino ac	206	5	45.5	36.4	7	AAAR81831	TATA box recogniz
134	5	45.5	486	22	AAAB48104	Recombinant PDI (A	207	5	45.5	36.4	17	AAAR81832	C-terminal domain
135	5	45.5	491	13	AAAR25296	Polypeptide with p	208	5	45.5	36.4	7	AAW07158	Synthetic peptide
136	5	45.5	508	9	AAAR80664	PDI. Homo sapiens	209	5	45.5	36.4	7	AAV50559	Insulin production
137	5	45.5	508	13	AAAR25287	Human PDI. Homo s	210	5	45.5	36.4	8	AAAB21394	Plasminogen activa
138	5	45.5	508	15	AAAR51696	Bovine protein dis	211	5	45.5	36.4	8	AAAB29834	Human secreted pro
139	5	45.5	510	9	AAAR80615	Amino acid sequenc	212	5	45.5	36.4	8	AAAR84506	Somatic immunoglob
140	5	45.5	513	22	AAAB1008	HSA-PDI fusion pro	213	5	45.5	36.4	9	AAAR05945	Listeria p60 pepti
141	5	45.5	513	22	AAAB48181	B. napus FSH poly	214	5	45.5	36.4	9	AAAR45623	P. faicicparum lact
142	5	45.5	515	13	AAAR25298	Human HSA-PDI fusi	215	5	45.5	36.4	9	AAAR62606	Peptide (38) inh
143	5	45.5	515	15	AAAR51697	Arabidopsis thalia	216	5	45.5	36.4	9	AAAR57358	Peptide (38) inh
144	5	45.5	519	21	AAAG36199	Arabidopsis thalia	217	5	45.5	36.4	9	AAAR57568	Peptide (68) inh
145	5	45.5	520	18	AAAG26640	Arabidopsis thalia	218	5	45.5	36.4	9	AAAR57574	Peptide (74) inh
146	5	45.5	520	19	AAAM40099	Arabidopsis ferula	219	5	45.5	36.4	9	AAAR57532	Peptide (32) inh
147	5	45.5	520	21	AAAB15188	Arabidopsis ferula	220	5	45.5	36.4	9	AAAR57711	Peptide (21) inh
148	5	45.5	520	22	AAAB31007	Amino acid sequenc	221	5	45.5	36.4	9	AAAR57717	Peptide (217) inh
149	5	45.5	520	22	AAAB48179	B. napus FSH poly	222	5	45.5	36.4	9	AAAR57681	Peptide (181) inh
150	5	45.5	520	22	AAAB48180	B. napus FSH poly	223	5	45.5	36.4	9	AAAR57646	Peptide (146) inh
151	5	45.5	521	21	AAAG31483	Arabidopsis thalia	224	5	45.5	36.4	9	AAAR57676	Peptide (176) inh
152	5	45.5	522	21	AAAG36198	Arabidopsis thalia	225	5	45.5	36.4	9	AAAR57640	Peptide (140) inh
153	5	45.5	528	19	AAAM46750	Tomato phosphate t	226	5	45.5	36.4	9	AAAR57604	Peptide (104) inh
154	5	45.5	537	21	AAAG31482	Arabidopsis thalia	227	5	45.5	36.4	9	AAAR57610	Peptide (110) inh
155	5	45.5	540	21	AAAG31481	Arabidopsis thalia	228	5	45.5	36.4	9	AAAR70091	Peptide (237) inh
156	5	45.5	582	20	AAAG7659	A serline/threonine	229	5	45.5	36.4	9	AAW07170	Synthetic peptide
157	5	45.5	635	19	AAW85034	Green fluorescent	230	5	45.5	36.4	9	AAV01696	Peptide derived fr

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:35:31, Search time 56.84 Seconds
(without alignments)
11,732 Million cell updates/sec

Title: US-09-372-036-29

Perfect score: 11

Sequence: 1 QOOTAPKAPRE 11

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Searched: 412676 seqs, 60623988 residues

Word size: 0

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	AA45171	Listeria p60 pepti
2	11	100.0	21	AA473894	Listeria monocytog
3	11	100.0	478	AA45178	Listeria p60 prote
4	11	100.0	484	AA473913	Listeria monocytog
5	9	81.8	9	AA454618	Listeria p60 pepti
6	9	81.8	23	AA45162	Listeria p60 pepti
7	6	63.6	7	AA473906	Listeria monocytog
8	6	54.5	150	AA426181	Rice acetonydroxya
9	6	54.5	890	AA460252	NF-ATP. Mus sp.
10	5	45.5	11	AA454621	Listeria p60 pepti
11	5	45.5	13	AA454625	Listeria innocua p

12	5	45.5	25	14	AA45165	Listeria p60 pepti
13	5	45.5	54	21	AA494958	Human secreted pro
14	5	45.5	95	20	AA460235	Human endometrium
15	5	45.5	96	20	AA429500	Human lung tumour
16	5	45.5	96	21	AA444435	Human lung tumour
17	5	45.5	107	19	AA457218	Desulfovibrio vulg
18	5	45.5	107	19	AA457219	Cytochrome c3 prot
19	5	45.5	107	19	AA457220	Cytochrome c3 prot
20	5	45.5	107	19	AA457221	Cytochrome c3 prot
21	5	45.5	107	21	AA410915	D. vulgaris cytoch
22	5	45.5	107	21	AA410916	D. vulgaris cytoch
23	5	45.5	107	21	AA455095	Mutant cytochrome
24	5	45.5	107	21	AA455096	Mutant cytochrome
25	5	45.5	107	21	AA455097	Mutant cytochrome
26	5	45.5	107	21	AA455098	Mutant cytochrome
27	5	45.5	107	21	AA455099	Wild type cytochro
28	5	45.5	107	21	AA455100	Mutant cytochrome
29	5	45.5	113	20	AA439181	M. tuberculosis an
30	5	45.5	113	20	AA439038	M. tuberculosis re
31	5	45.5	119	19	AA446291	Pneumococcal sur
32	5	45.5	132	20	AA435711	Chlamydia pneumoni
33	5	45.5	135	20	AA413180	Human secreted pro
34	5	45.5	157	21	AA402253	Human secreted pro
35	5	45.5	169	21	AA419128	Polypeptide isolat
36	5	45.5	177	16	AA481429	Hepatitis GB virus
37	5	45.5	177	20	AA450043	Pseudomonas syring
38	5	45.5	177	21	AA409006	Hepatitis GB virus
39	5	45.5	188	22	AA465253	Human breast cance
40	5	45.5	189	22	AA476629	Corynebacterium gl
41	5	45.5	190	22	AA482664	E. coli RNase E.
42	5	45.5	190	20	AA494681	Group B Streptococ
43	5	45.5	206	21	AA491339	Human ORF1 ORF2661
44	5	45.5	209	21	AA4842897	Streptococcus pneu
45	5	45.5	215	18	AA414363	S. pneumoniae prot
46	5	45.5	243	19	AA480691	Sequence of subtl
47	5	45.5	278	9	AA480850	pG4-5-GDK-BP clon
48	5	45.5	278	17	AA490544	Amno acid sequenc
49	5	45.5	279	15	AA480274	Thermilase (P229X)
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51	5	45.5	279	17	AA480766	Thermilase P205Q
52	5	45.5	279	17	AA480788	Thermilase L104D
53	5	45.5	279	17	AA480781	Thermilase Q66N
54	5	45.5	279	17	AA480782	Thermilase P205G
55	5	45.5	279	17	AA480783	Thermilase G206N
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57	5	45.5	279	17	AA480785	Thermilase N66S, S
58	5	45.5	279	17	AA480786	Thermilase S109E
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62	5	45.5	279	17	AA480790	Thermilase A168N
63	5	45.5	279	17	AA480791	Thermilase G135Q
64	5	45.5	279	17	AA480792	Thermilase Y210G
65	5	45.5	279	17	AA480793	Thermilase T195P
66	5	45.5	279	17	AA480794	Thermilase N165D
67	5	45.5	279	17	AA480795	Thermilase W208F
68	5	45.5	279	17	AA480796	Thermilase G67E, S
69	5	45.5	279	17	AA480797	Thermilase S191E
70	5	45.5	279	17	AA480798	Thermilase Y171T
71	5	45.5	279	17	AA480799	Thermilase S192D
72	5	45.5	279	17	AA480800	Thermilase I209A
73	5	45.5	279	17	AA480801	Thermilase Y213S
74	5	45.5	279	17	AA480802	Thermilase L216N
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76	5	45.5	279	17	AA480804	Thermilase V103A
77	5	45.5	279	17	AA480805	Thermilase A164H
78	5	45.5	279	17	AA480806	Thermilase L221V
79	5	45.5	279	17	AA480807	Thermilase S191D
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 13:15:54 ; Search time 317.22 Seconds
(without alignments)
7.693 Million cell updates/sec

Title: US-09-372-036-29

Perfect score: 57

Sequence: 1 000TAKKAPTE 11

Scoring table:

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Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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7	57	100.0	12	8	US-08-412-227C-42
8	57	100.0	12	17	US-09-372-036-42
9	57	100.0	21	8	US-08-479-520-33
10	57	100.0	21	8	US-08-486-050-33

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12	57	100.0	21	13	US-08-988-444-33	Sequence 33, Appl
13	57	100.0	21	16	US-09-217-849-33	Sequence 39, Appl
14	57	100.0	232	8	US-08-412-227-39	Sequence 39, Appl
15	57	100.0	232	8	US-08-412-227A-39	Sequence 39, Appl
16	57	100.0	232	8	US-08-412-227C-39	Sequence 39, Appl
17	57	100.0	232	17	US-09-372-036-39	Sequence 39, Appl
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19	57	100.0	478	8	US-08-412-227A-40	Sequence 40, Appl
20	57	100.0	478	8	US-08-412-227C-40	Sequence 40, Appl
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22	57	100.0	484	8	US-08-479-520-26	Sequence 26, Appl
23	57	100.0	484	8	US-08-486-050-26	Sequence 26, Appl
24	57	100.0	484	8	US-08-486-050A-26	Sequence 26, Appl
25	57	100.0	484	13	US-08-988-444-26	Sequence 26, Appl
26	57	100.0	484	16	US-09-217-849-26	Sequence 26, Appl
27	47	82.5	9	8	US-08-412-227-20	Sequence 20, Appl
28	47	82.5	9	8	US-08-412-227A-20	Sequence 20, Appl
29	47	82.5	23	8	US-08-412-227C-20	Sequence 20, Appl
30	47	82.5	23	17	US-09-372-036-20	Sequence 20, Appl
31	41	71.9	752	16	US-09-252-991A-23017	Sequence 23017, A
32	39	68.4	11	8	US-08-412-227-38	Sequence 38, Appl
33	39	68.4	11	8	US-08-412-227A-38	Sequence 38, Appl
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35	39	68.4	11	17	US-09-372-036-38	Sequence 38, Appl
36	39	68.4	78	23	US-60-147-499-4546	Sequence 4546, Ap
37	39	68.4	149	1	PCT-US01-00663-32909	Sequence 32909, A
38	39	68.4	766	14	US-09-062-085-10	Sequence 10, Appl
39	39	68.4	770	14	US-09-062-085-9	Sequence 9, Appl
40	37	64.9	88	21	US-09-733-089-14011	Sequence 14011, A
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42	37	64.9	127	18	US-09-489-039A-7875	Sequence 7875, Ap
43	37	64.9	492	16	US-09-248-796-14913	Sequence 14913, A
44	37	64.9	693	23	US-60-155-811-763	Sequence 763, App
45	37	64.9	693	23	US-60-155-811-1015	Sequence 1015, App

ALIGNMENTS

RESULT 1
US-08-412-227-29
Sequence 29, Application US/08412227
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKELEIER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: ROBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,227
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1502
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-412-227-29

Query Match 100.0%; Score 57; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
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Db 1 000TAPKAPTE 11

RESULT 2
US-08-412-227A-29
Sequence 29, Application US/08412227A
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,227A
FILING DATE: 27-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA: DE 4239567.4
APPLICATION NUMBER: DE 4239567.4

FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-412-227A-29

Query Match 100.0%; Score 57; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 000TAPKAPTE 11

RESULT 3
US-08-412-227C-29
Sequence 29, Application US/08412227C
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,227C
FILING DATE: 27-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA: DE 4239567.4
APPLICATION NUMBER: DE 4239567.4
APPLICATION NUMBER: DE 4219111.4

FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-412-227C-29

Query Match 100.0%; Score 57; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| 1111111111
DB 1 000TAPKAPTE 11

RESULT 4

US-09-372-036-29

Sequence 29, Application US/09372036

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED

APPLICANT: PAMELZIK, MARTINA

APPLICANT: LINKEWELER, WINFRIED

APPLICANT: BURGER, CHRISTA

APPLICANT: HOFMANN, GOTTFRIED

APPLICANT: BUBERT, ANDREAS

APPLICANT: GOEBEL, WERNER

APPLICANT: KOHLER, STEFAN

TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

TITLE OF INVENTION: LISTERIAS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD., SUITE 1400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: US

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/372,036

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/456,670

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/075,248

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4239567.4

FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4219111.4

FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-09-372-036-29

Query Match 100.0%; Score 57; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
| 1111111111
DB 1 000TAPKAPTE 11

RESULT 5

US-08-412-227-42

Sequence 42, Application US/08412227

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED

APPLICANT: PAMELZIK, MARTINA

APPLICANT: LINKEWELER, WINFRIED

APPLICANT: BURGER, CHRISTA

APPLICANT: HOFMANN, GOTTFRIED

APPLICANT: BUBERT, ANDREAS

APPLICANT: GOEBEL, WERNER

APPLICANT: KOHLER, STEFAN

TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

TITLE OF INVENTION: LISTERIAS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD., SUITE 1400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: US

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/412,227

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/075,248

FILING DATE: 11-JUN-1993

APPLICATION NUMBER: DE 4239567.4

FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4219111.4

FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

```

; REFERENCE/DOCKET NUMBER: MERCK 1502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-412-227-42

Query Match          100.0%; Score 57; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
   |||||
Db 2 QOOTAPKAPTE 12

RESULT 6
US-08-412-227A-42
; Sequence 42, Application US/08412227A
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINXWEILER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: HUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STERN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,227A
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-412-227C-42
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-412-227A-42

Query Match          100.0%; Score 57; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
   |||||
Db 2 QOOTAPKAPTE 12

RESULT 7
US-08-412-227C-42
; Sequence 42, Application US/08412227C
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINXWEILER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: HUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STERN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,227C
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-412-227C-42
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Query Match 100.0%; Score 57; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
111111111111
DB 2 000TAPKAPTE 12

RESULT 8
US-09-372-036-42
Sequence 42, Application US/09372036

GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, COTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P. C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372.036
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/456,670
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-372-036-42

Query Match 100.0%; Score 57; DB 17; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
111111111111
DB 2 000TAPKAPTE 12

RESULT 9
US-08-479-520-33
Sequence 33, Application US/08479520

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,520
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/105/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-479-520-33

Query Match 100.0%; Score 57; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
111111111111
DB 7 000TAPKAPTE 17

RESULT 10
US-08-486-050-33
Sequence 33, Application US/08486050

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,050
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/127,499
;; FILING DATE: 28-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 51916/103/INBI
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; US-08-486-050-33

Query Match 100.0%; Score 57; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
DB 7 000TAPKAPTE 17

RESULT 11
US-08-486-050A-33
;; Sequence 33, Application US/08486050A
;; GENERAL INFORMATION:
;; APPLICANT: VAN ALSTYNE, Diane
;; APPLICANT: SHARMA, Lawrence Rajendra
;; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
;; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
;; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
;; NUMBER OF SEQUENCES: 75
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,050A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/127,499

;; FILING DATE: 28-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 51916/103/INBI
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; US-08-486-050A-33

Query Match 100.0%; Score 57; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 000TAPKAPTE 11
DB 7 000TAPKAPTE 17

RESULT 12
US-08-988-444-33
;; Sequence 33, Application US/08988444
;; GENERAL INFORMATION:
;; APPLICANT: VAN ALSTYNE, Diane
;; APPLICANT: SHARMA, Lawrence Rajendra
;; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
;; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
;; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
;; NUMBER OF SEQUENCES: 75
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/988,444
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/486,050
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US 08/127,499
;; FILING DATE: 28-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 51916/103/INBI
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; US-08-988-444-33

Query Match 100.0%; Score 57; DB 13; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OOOTAPKAPTE 11
 |||||
 Db 7 OOOTAPKAPTE 17

RESULT 13

US-09-217-849-33
 : Sequence 33, Application US/09217849
 : GENERAL INFORMATION:
 : APPLICANT: VAN ALSTYNE, Diane
 : TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 : TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 : TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
 : NUMBER OF SEQUENCES: 75
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Foley & Lardner
 : STREET: 3000 K Street, N.W., Suite 500
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20007-5109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/217,849
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/486,050
 : FILING DATE: 07-JUN-1995
 : APPLICATION NUMBER: US 08/127,499
 : FILING DATE: 28-SEP-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BENT, Stephen A.
 : REGISTRATION NUMBER: 29,768
 : REFERENCE/DOCKET NUMBER: 51916/103/INBI
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202)672-5300
 : TELEFAX: (202)672-5399
 : TELEX: 904136
 : INFORMATION FOR SEQ ID NO: 33:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 21 amino acids
 : TYPE: amino acid
 : STRANDEDNESS:
 : TOPOLOGY: unknown
 : US-09-217-849-33

Query Match 100.0%; Score 57; DB 16; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OOOTAPKAPTE 11
 |||||
 Db 7 OOOTAPKAPTE 17

RESULT 14

US-08-412-227-39
 : Sequence 39, Application US/08412227
 : GENERAL INFORMATION:
 : APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED
 APPLICANT: PAMELZIK, MARTINA
 APPLICANT: LINKWEILER, WINFRIED
 APPLICANT: BURGER, CHRISTA
 APPLICANT: HOFMANN, GOTTFRIED
 APPLICANT: BUBERT, ANDREAS
 APPLICANT: GOEBEL, WERNER
 APPLICANT: KOHLER, STEFAN
 TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
 TITLE OF INVENTION: LISTERIAS
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
 STREET: 2200 CLARENDON BLVD., SUITE 1400
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: US
 ZIP: 22201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/412,227
 FILING DATE:
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/075,248
 FILING DATE: 11-JUN-1993
 APPLICATION NUMBER: DE 4239567.4
 FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 4219111.4
 FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:
 NAME: HAMLET-KING, DIANA
 REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1502
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410

TELEX: 64191

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptid

ORGANISM: Listeria monocytogenes

STRAIN: EGD

US-08-412-227-39

Query Match 100.0%; Score 57; DB 8; Length 232;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OOOTAPKAPTE 11
 |||||
 Db 222 OOOTAPKAPTE 232

RESULT 15

US-08-412-227A-39
 : Sequence 39, Application US/08412227A
 : GENERAL INFORMATION:
 : APPLICANT: SCHUBERT, PETER
 : APPLICANT: NEUMANN, SIEGFRIED
 : APPLICANT: PAMELZIK, MARTINA
 : APPLICANT: LINKWEILER, WINFRIED
 : APPLICANT: BURGER, CHRISTA

APPLICANT: HOEWANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,227A
FILING DATE: 27-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-412-227A-39

Query Match 100.0%; Score 57; DB 8; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
|||||
DB 222 QOOTAPKAPTE 232

Search completed: August 15, 2001, 13:15:54
Job time: 391 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 13:10:30 ; Search time 21.63 Seconds
(without alignments)
7.948 Million cell updates/sec

Title: US-09-372-036-29

Perfect score: 57

Sequence: 1 OQOTAPKAPTE 11

Scoring table: BLOSUM62

Searched: 109802 seqs, 15628634 residues

Total number of hits satisfying chosen parameters: 109802

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	21	5	US-09-489-850-33
2	57	100.0	484	5	US-09-489-850-26
3	36	63.2	100	5	US-09-803-110-9462
4	36	63.2	410	5	US-09-760-443-1455
5	35	61.4	7	5	US-09-489-850-34
6	35	61.4	198	5	US-09-758-453-219
7	35	61.4	310	1	PCR-US01-16450-2703
8	35	61.4	310	1	PCR-US01-18569-3045
9	35	61.4	446	5	US-09-909-446-2
10	35	61.4	2626	5	US-09-477-962-106
11	34	59.6	120	5	US-09-758-468-419
12	34	59.6	239	1	PCR-US01-14827-14067
13	34	59.6	240	5	US-09-758-470-339
14	34	59.6	441	5	US-09-760-462-27
15	33	57.9	143	1	PCR-US01-08656-7761
16	33	57.9	147	5	US-09-758-471-3699
17	33	57.9	211	5	US-09-764-870-414
18	33	57.9	303	1	PCR-US01-04926A-326
19	33	57.9	358	5	US-09-803-110-12650
20	33	57.9	372	1	PCR-US01-04926A-325
21	33	57.9	414	5	US-09-758-471-3744
22	33	57.9	719	1	PCR-US01-14827-14710
23	33	57.9	964	5	US-09-760-468-1491
24	32	56.1	95	5	US-09-760-444-285
25	32	56.1	125	5	US-09-764-847-883
26	32	56.1	180	1	PCR-US01-14827-9696
27	32	56.1	298	5	US-09-765-272-24

28	32	56.1	328	5	US-09-891-126-5	Sequence 5, Appl1
29	32	56.1	483	5	US-09-760-466-1241	Sequence 1241, Ap
30	32	56.1	1074	1	PCR-US01-08656-10235	Sequence 10235, A
31	32	56.1	1162	5	US-09-894-273-2	Sequence 2, Appl1
32	32	56.1	1418	1	PCR-US01-08656-10236	Sequence 10236, A
33	31.5	55.3	780	5	US-09-803-110-13189	Sequence 13189, A
34	31	54.4	48	5	US-09-757-028-2364	Sequence 2364, Ap
35	31	54.4	79	1	PCR-US01-08656-7604	Sequence 7604, Ap
36	31	54.4	96	5	US-09-760-488-704	Sequence 704, Ap
37	31	54.4	115	5	US-09-758-469-681	Sequence 681, Ap
38	31	54.4	117	5	US-09-758-472-8918	Sequence 8918, Ap
39	31	54.4	135	5	US-09-758-472-7896	Sequence 7896, Ap
40	31	54.4	138	5	US-09-758-459-246	Sequence 246, App
41	31	54.4	141	1	PCR-US01-16450-1928	Sequence 1928, Ap
42	31	54.4	144	5	US-09-764-877-1818	Sequence 1818, Ap
43	31	54.4	166	1	PCR-US01-14827-13722	Sequence 13722, A
44	31	54.4	172	1	PCR-US01-08656-8740	Sequence 8740, Ap
45	31	54.4	180	5	US-09-758-466-670	Sequence 670, App

ALIGNMENTS

RESULT 1
US-09-489-850-33
Sequence 33, Application US/09489850
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489, 850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,444
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-489-850-33
Query Match 100.0%; Score 57; DB 5; Length 21;

TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/489,850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/988,444
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 51916/103/INBI

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown

US-09-489-850-34
SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Query Match 61.4%; Score 35; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OCTAPKA 8
DB 1 OCTAPKA 7

RESULT 6

US-09-758-459-219
Sequence 219, Application US/09758459

GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PM029

CURRENT APPLICATION NUMBER: US/09/758,459

CURRENT FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR FILING DATE: 2000-01-31

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 406

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 219
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-09-758-459-219

Query Match 61.4%; Score 35; DB 5; Length 198;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKAPTE 11
DB 161 TAPESPTE 168

RESULT 7

PCT-US01-16450-2703

Sequence 2703, Application PC/TUS0116450

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA131PCT

CURRENT APPLICATION NUMBER: PCT/US01/16450

CURRENT FILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: 60/205,515

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2820

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2703

LENGTH: 310

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US01-16450-2703

Query Match 61.4%; Score 35; DB 1; Length 310;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 TAPKAPTE 11
DB 191 TAPESPTE 198

RESULT 8

PCT-US01-18569-3045

Sequence 3045, Application PC/TUS0118569

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA133PCT

CURRENT APPLICATION NUMBER: PCT/US01/18569

CURRENT FILING DATE: 2001-06-07

PRIOR APPLICATION NUMBER: 60/209,467

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3045

LENGTH: 353

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US01-18569-3045

Query Match 61.4%; Score 35; DB 1; Length 353;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 OTAPKAPTE 11
DB 53 ETAPRAPRE 61

RESULT 9

US-09-909-446-2

Sequence 2, Application US/09909446

GENERAL INFORMATION:
APPLICANT: ENMARK, EVA

```

; GUSTAFSSON, JAN
; TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
; TO THE NUCLEAR RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Wilcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,446
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/776,844
; FILING DATE: <Unknown>
; APPLICATION NUMBER: UK 9413536.2
; FILING DATE: 16-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 332141
; REFERENCE/DOCKET NUMBER: 00487.04029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-909-446-2

Query Match          61.4%; Score 35; DB 5; Length 446;
Best Local Similarity 63.6%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 QOQTAPKAPTE 11
    111 1 111
Db 164 QQQQQPPPTPE 174

RESULT 10
US-09-477-962-106
; Sequence 106, Application US/09477962
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; APPLICANT: DU, LIANGCHENG
; APPLICANT: SANCHEZ, CESAR
; APPLICANT: CHEN, MEI
; APPLICANT: EDWARDS, DANIEL J.
; TITLE OF INVENTION: BLEOMYCIN GENE CLUSTER COMPONENTS AND THEIR USES
; FILE REFERENCE: 407T-895820US
; CURRENT APPLICATION NUMBER: US/09/477,962
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/115,435
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/118,848
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 106
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; LENGTH: 2626
; TYPE: PRT
; ORGANISM: Streptomyces verticillius
; FEATURE:
; OTHER INFORMATION: ORF17
US-09-477-962-106
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Query Match          61.4%; Score 35; DB 5; Length 2626;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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OY 4 TAPKAPTE 11
    111 111
Db 960 TAPPTPE 967
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RESULT 11
US-09-758-469-419
; Sequence 419, Application US/09758469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM008
; CURRENT APPLICATION NUMBER: US/09/758,469
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 419
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-469-419
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Query Match          59.6%; Score 34; DB 5; Length 120;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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OY 2 QOQTAPKAPTE 11
    1 1111111
Db 55 QLSAPRAPSE 64
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RESULT 12
PCT-US01-14827-14067
; Sequence 14067, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 14067
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(239)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-14827-14067
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Query Match          59.6%; Score 34; DB 1; Length 239;
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Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QOQTAPKAPT 9
|||
Db 187 QDQTTPKGP 195

RESULT 13

US-09-758-470-399
; Sequence 399, Application US/09758470
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM030
; CURRENT APPLICATION NUMBER: US/09/758,470
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 722
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 399
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-470-399

Query Match 59.6%; Score 34; DB 5; Length 240;
Best Local Similarity 70.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QOQTAPKAPT 10
|||
Db 168 QOQCAPNAPT 177

RESULT 14

US-09-760-462-27
; Sequence 27, Application US/09760462
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT256
; CURRENT APPLICATION NUMBER: US/09/760,462
; CURRENT FILING DATE: 2001-01-16
; Prior Application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (139)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (309)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (310)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-462-27

Query Match 59.6%; Score 34; DB 5; Length 441;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QOQTAPKAPT 10

Db 20 QRRVAPSAFT 29
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PCT-US01-08656-7761

RESULT 15

PCT-US01-08656-7761
; Sequence 7761, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 7761
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(143)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08656-7761

Query Match 57.9%; Score 33; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PKAPTE 11
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Db 111 PKAPTE 116

Search completed: August 15, 2001, 13:10:30
Job time: 67 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2001, 13:10:02 ; Search time 30.68 seconds
(without alignments)
8.054 Million cell updates/sec

Title: US-09-372-036-30
Perfect score: 60
Sequence: 1 STRVAPTEGVKK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/p/ptodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/p/ptodata/2/1aa/6A.COMB.pep.*
- 4: /cgn2_6/p/ptodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/p/ptodata/2/1aa/PCITUS.COMB.pep.*
- 6: /cgn2_6/p/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	12	US-08-456-670B-30	Sequence 30, Appl
2	60	100.0	21	US-08-127-499A-27	Sequence 27, Appl
3	60	100.0	21	US-08-482-847-27	Sequence 27, Appl
4	60	100.0	232	US-08-456-670B-39	Sequence 39, Appl
5	60	100.0	478	US-08-456-670B-40	Sequence 40, Appl
6	60	100.0	484	US-08-127-499A-26	Sequence 26, Appl
7	60	100.0	484	US-08-482-847-26	Sequence 26, Appl
8	51	85.0	10	US-08-456-670B-31	Sequence 31, Appl
9	41	68.3	9	US-08-456-670B-26	Sequence 26, Appl
10	38	63.3	770	US-08-525-654A-1	Sequence 1, Appl
11	38	63.3	771	US-08-525-654A-3	Sequence 3, Appl
12	37	61.7	803	US-09-063-035-2	Sequence 2, Appl
13	36	60.0	7	US-08-127-499A-28	Sequence 28, Appl
14	36	60.0	7	US-08-482-847-28	Sequence 28, Appl
15	36	60.0	1566	US-08-687-956A-23	Sequence 23, Appl
16	35	58.3	12	US-08-389-011-16	Sequence 16, Appl
17	35	58.3	12	US-08-403-917A-16	Sequence 16, Appl
18	35	58.3	12	US-08-403-917A-16	Sequence 16, Appl
19	35	58.3	26	US-08-389-011-7	Sequence 7, Appl
20	35	58.3	26	US-08-403-917A-7	Sequence 7, Appl
21	35	58.3	26	US-08-348-952A-7	Sequence 7, Appl
22	35	58.3	33	US-08-244-951A-2	Sequence 2, Appl
23	35	58.3	33	US-08-389-011-2	Sequence 2, Appl
24	35	58.3	33	US-08-403-917A-2	Sequence 2, Appl
25	35	58.3	33	US-08-348-952A-2	Sequence 2, Appl
26	35	58.3	35	US-08-244-951A-6	Sequence 6, Appl
27	35	58.3	106	US-08-776-404B-1	Sequence 1, Appl

28	35	58.3	112	US-08-666-360-1	Sequence 1, Appl
29	35	58.3	126	5514582-35	Patent No. 5514582
30	35	58.3	250	US-09-216-295-14	Sequence 14, Appl
31	35	58.3	351	US-08-159-969-2	Sequence 2, Appl
32	35	58.3	352	US-08-726-306A-17	Sequence 17, Appl
33	35	58.3	391	US-08-244-951A-10	Sequence 10, Appl
34	35	58.3	391	US-08-389-011-23	Sequence 23, Appl
35	35	58.3	391	US-08-403-917A-23	Sequence 23, Appl
36	35	58.3	391	US-08-348-952A-23	Sequence 23, Appl
37	35	58.3	441	US-08-244-603A-1	Sequence 1, Appl
38	35	58.3	605	US-08-687-956A-1	Sequence 1, Appl
39	35	58.3	1466	5256642-6	Patent No. 5256642
40	35	58.3	1466	5472939-6	Patent No. 5472939
41	35	58.3	1537	5256642-5	Patent No. 5256642
42	35	58.3	1537	5472939-5	Patent No. 5472939
43	35	58.3	1847	5256642-10	Patent No. 5256642
44	35	58.3	1847	5472939-10	Patent No. 5472939
45	35	58.3	2039	5256642-2	Patent No. 5256642

ALIGNMENTS

RESULT 1
US-08-456-670B-30
Sequence 30 Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELTER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: *Listeria monocytogenes*
STRAIN: EGD
US-08-436-670B-30

Query Match 100.0%; Score 60; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAPTOEVKK 12
DB 1 STVPAPTOEVKK 12

RESULT 2
US-08-127-499A-27
Sequence 27, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-27

Query Match 100.0%; Score 60; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAPTOEVKK 12
DB 3 STVPAPTOEVKK 14

RESULT 3
US-08-482-847-27
Sequence 27, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-27

Query Match 100.0%; Score 60; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAPTOEVKK 12
DB 3 STVPAPTOEVKK 14

RESULT 4
US-08-456-670B-39
Sequence 39, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWETTER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

```

; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
; US-08-456-670B-39

Query Match 100.0%; Score 60; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. NO. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
DB 77 STPVAPTOEVKK 88

RESULT 5
US-08-456-670B-40
; Sequence 40, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINKEWELER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
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; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
; US-08-456-670B-40

Query Match 100.0%; Score 60; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. NO. 0.0047;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
DB 146 STPVAPTOEVKK 157

RESULT 6
US-08-127-499A-26
; Sequence 26, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
```

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-26

Query Match 100.0%; Score 60; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
Db 146 STPVAPTOEVKK 157

RESULT 7
US-08-482-847-26
Sequence 26, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-26

Query Match 100.0%; Score 60; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
Db 146 STPVAPTOEVKK 157

RESULT 8
US-08-456-670B-31
Sequence 31, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, Siegfried
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINKEWILLER, WILFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANNIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

TELEX: 64191
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

Query Match 85.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PVAPTOEVKK 12
|||||
Db 1 PVAPTOEVKK 10

RESULT 9
US-08-456-670B-26
Sequence 26, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWIELER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456, 670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-26

Query Match 68.3%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STPVAPTO 8
|||||
Db 2 STPVAPTO 9

RESULT 10
US-08-525-654A-1
Sequence 1, Application US/08525654A
Patent No. 5736356
GENERAL INFORMATION:

APPLICANT: SANO, KOHICHIRO
APPLICANT: KUMAZAWA, YOSHIYUKI
APPLICANT: YASEUDA, HISASHI
APPLICANT: SEGURO, KATSUYA
APPLICANT: MOTOKI, MASANO
TITLE OF INVENTION: TRANSGLUTAMINASE ORIGINATED FROM
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525, 654A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6/8283
FILING DATE: 28-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7/3876
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-760-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

ORIGINAL SOURCE:
ORGANISM: Crassostrea gigas
US-08-525-654A-1

Query Match 63.3%; Score 38; DB 1; Length 770;
Best Local Similarity 58.3%; Pred. No. 58;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 STPVAPTOEVKK 12
|:|:| |
Db 711 SSPKPGDEVKK 722

RESULT 11
US-08-525-654A-3
Sequence 3, Application US/08525654A
Patent No. 5736356
GENERAL INFORMATION:
APPLICANT: SANO, KOICHIRO
APPLICANT: KUMAZAWA, YOSHIYUKI
APPLICANT: YASEUDA, HISASHI
APPLICANT: SEGURO, KATSUYA
APPLICANT: MOTOKI, MASAO
TITLE OF INVENTION: TRANSGUTAMINASE ORIGINATED FROM
TITLE OF INVENTION: CRASSOSTREA GIGAS
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,654A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6/8283
FILING DATE: 28-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7/3876
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-760-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Crassostrea gigas
US-08-525-654A-3

Query Match 63.3%; Score 38; DB 1; Length 771;
Best Local Similarity 58.3%; Pred. No. 58;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
|:|:| |
Db 712 SSPKPGDEVKK 723

RESULT 12
US-09-063-035-2
Sequence 2, Application US/09063035
Patent No. 6160091
GENERAL INFORMATION:
APPLICANT: PEUKERT, Karen; HAENEL, Frank; and ELLERS,
APPLICANT: Martin
TITLE OF INVENTION: Myc-binding zinc finger proteins,
TITLE OF INVENTION: their preparation and their use
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinlauf
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.2 mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.1
SOFTWARE: Wordperfect version 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/063,035
FILING DATE: 21-APR-1998
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-063-035-2

Query Match 61.7%; Score 37; DB 4; Length 803;
Best Local Similarity 41.7%; Pred. No. 91;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
|:|:| |
Db 156 STPGPSRDLKE 167

RESULT 13
US-08-127-499A-28
Sequence 28, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-28

Query Match 60.0%; Score 36; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTOEVKK 12
|||||
DB 1 PTOEVKK 7

RESULT 14
US-08-482-847-28
Sequence 28, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHAWA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-28

Query Match 60.0%; Score 36; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTOEVKK 12
|||||
DB 1 PTOEVKK 7

RESULT 15
US-08-687-956A-23
Sequence 23, Application US/08687956A
Patent No. 5861157
GENERAL INFORMATION:
APPLICANT: BURNIE, JAMES P
APPLICANT: MATTHEWS, RUTH C
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
FLOOR
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,956A
FILING DATE: 29-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401689.6
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 50885/222892
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1566 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Streptococcus sobrinus
US-08-687-956A-23

Query Match 60.0%; Score 36; DB 2; Length 1566;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 PVAPTQEVKK 12
|||
DB 867 PVEPTVEVK 896

Search completed: August 15, 2001, 13:10:02
Job time: 39 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 13:09:23 ; Search time 30.68 Seconds
(without alignments)
6.040 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 45

Sequence: 1 VSTRPVAPQTQ 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	45	100.0	21	1	US-08-127-499A-27
3	45	100.0	21	1	US-08-482-847-27
4	45	100.0	232	2	US-08-456-670B-39
5	45	100.0	478	2	US-08-456-670B-40
6	45	100.0	484	1	US-08-127-499A-26
7	45	100.0	12	2	US-08-482-847-26
8	41	91.1	12	2	US-08-456-670B-30
9	32	71.1	10	2	US-08-456-670B-31
10	32	71.1	20	2	US-08-456-670B-17
11	32	71.1	493	3	US-09-090-808-4
12	31	68.9	45	3	US-08-856-074A-29
13	31	68.9	250	4	US-09-216-295-14
14	31	68.9	469	2	US-08-484-126-1
15	31	68.9	763	2	US-08-473-122-2
16	31	68.9	763	2	US-08-472-478-2
17	31	68.9	763	2	US-08-463-081B-8
18	31	68.9	763	2	US-08-461-379A-8
19	31	68.9	763	2	US-08-462-390B-8
20	31	68.9	763	3	US-08-463-074B-8
21	31	68.9	763	3	US-08-465-585C-8
22	31	68.9	763	3	US-08-652-446-8
23	31	68.9	2476	2	US-08-276-967-2
24	30	66.7	282	1	US-07-712-476A-5
25	30	66.7	296	1	US-07-712-476A-1
26	30	66.7	341	1	US-08-356-180-4
27	30	66.7	404	1	US-08-696-770-2

28	30	66.7	404	2	US-09-015-557-2	Sequence 2, Appl1
29	30	66.7	433	1	US-07-672-483-4	Sequence 4, Appl1
30	30	66.7	604	2	US-08-468-576B-12	Sequence 12, Appl1
31	30	66.7	604	2	US-08-468-576B-12	Sequence 12, Appl1
32	30	66.7	604	3	US-08-468-577B-12	Sequence 12, Appl1
33	30	66.7	1308	3	US-08-996-644-2	Sequence 2, Appl1
34	30	66.7	1308	3	US-09-352-552-2	Sequence 2, Appl1
35	30	66.7	1436	2	US-08-652-971-2	Sequence 2, Appl1
36	30	66.7	1436	2	US-08-991-258A-2	Sequence 2, Appl1
37	30	66.7	1436	2	US-08-769-399-2	Sequence 2, Appl1
38	30	66.7	1436	2	US-08-991-953A-2	Sequence 2, Appl1
39	30	66.7	1618	1	US-07-853-913-4	Sequence 4, Appl1
40	30	66.7	15281	2	US-08-471-119A-2	Sequence 2, Appl1
41	29	64.4	15	1	US-08-116-733-15	Sequence 15, Appl1
42	29	64.4	310	1	US-08-078-683A-3	Sequence 3, Appl1
43	29	64.4	310	2	US-08-488-199-4	Sequence 3, Appl1
44	29	64.4	327	2	US-08-651-818A-3	Sequence 3, Appl1
45	29	64.4	327	4	US-09-184-826-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-456-670B-26
; Sequence 26, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINXMEIER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; NUMBER OF SEQUENCES: 43
; TITLE OF INVENTION: LISTERIAS
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 421911.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: *Listeria monocytogenes*
STRAIN: EGD
US-08-456-6708-26

Query Match 100.0%; Score 45; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPQ 9
DB 1 VSTPVAPQ 9

RESULT 2
US-08-127-499A-27
Sequence 27, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-27

Query Match 100.0%; Score 45; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPQ 9
DB 2 VSTPVAPQ 10

RESULT 3
US-08-482-847-27
Sequence 27, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-27

Query Match 100.0%; Score 45; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPQ 9
DB 2 VSTPVAPQ 10

RESULT 4
US-08-456-6708-39
Sequence 39, Application US/084566708
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

```

: TITLE OF INVENTION: LISTERIAS
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
: STREET: 2200 CLARENDON BLVD., SUITE 1400
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: US
: ZIP: 22201
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/456,670B
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/412,227
: FILING DATE: 27-MAR-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/075,248
: FILING DATE: 11-JUN-1993
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: DE 4239567.4
: FILING DATE: 25-NOV-1992
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: DE 4219111.4
: FILING DATE: 11-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: HAMLET-KING, DIANA
: REGISTRATION NUMBER: 33,302
: REFERENCE/DOCKET NUMBER: MERCK 1694D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-243-6333
: TELEFAX: 703-243-6410
: TELEX: 64191
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 232 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Listeria monocytogenes
: STRAIN: EGD
: US-08-456-670B-39

Query Match 100.0%; Score 45; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPTQ 9
Db 76 VSTPVAPTQ 84

RESULT 5
US-08-456-670B-40
: Sequence 40, Application US/08456670B
: Patent No. 5932415
: GENERAL INFORMATION:
: APPLICANT: SCHUBERT, PETER
: APPLICANT: NEUMANN, SIEGFRIED
: APPLICANT: PAMELTIK, MARTINA
: APPLICANT: LINXWEILER, WINFRIED
: APPLICANT: BURGER, CHRISTA
: APPLICANT: HOFMANN, GOTTFRED
: APPLICANT: BOBERT, ANDREAS
: APPLICANT: GOEBEL, WERNER
: APPLICANT: KOHLER, STEFAN
```

```

: TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
: STREET: 2200 CLARENDON BLVD., SUITE 1400
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: US
: ZIP: 22201
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/456,670B
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/412,227
: FILING DATE: 27-MAR-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/075,248
: FILING DATE: 11-JUN-1993
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: DE 4239567.4
: FILING DATE: 25-NOV-1992
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: DE 4219111.4
: FILING DATE: 11-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: HAMLET-KING, DIANA
: REGISTRATION NUMBER: 33,302
: REFERENCE/DOCKET NUMBER: MERCK 1694D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-243-6333
: TELEFAX: 703-243-6410
: TELEX: 64191
: INFORMATION FOR SEQ ID NO: 40:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 478 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Listeria monocytogenes
: STRAIN: EGD
: US-08-456-670B-40

Query Match 100.0%; Score 45; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPTQ 9
Db 145 VSTPVAPTQ 153

RESULT 6
US-08-127-499A-26
: Sequence 26, Application US/08127499A
: Patent No. 5510264
: GENERAL INFORMATION:
: APPLICANT: VAN ALSTYNE, Diane
: APPLICANT: SHARMA, Lawrence Rajendra
: TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
: TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
```

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-26

Query Match 100.0%; Score 45; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTO 9
|||||||
Db 145 VSTPVAPTO 153

RESULT 7
US-08-482-847-26
Sequence 26, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-26

Query Match 100.0%; Score 45; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTO 9
|||||||
Db 145 VSTPVAPTO 153

RESULT 8
US-08-456-670B-30
Sequence 30, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEGFRIED
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINKWELTER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

TELEX: 64191
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-30

Query Match 91.1%; Score 41; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVAPQ 9
DB 1 STPVAPQ 8

RESULT 9
US-08-456-670B-31
Sequence 31, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567,4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111,4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

Query Match 71.1%; Score 32; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPQ 9
DB 1 PVAPQ 6

RESULT 10
US-08-456-670B-17
Sequence 17, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567,4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111,4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: *Listeria monocytogenes*
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14-20
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-17

Query Match 71.1%; Score 32; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPTO 9
|||||
DB 8 PVAPTO 13

RESULT 11
US-09-90-808-4
Sequence 4, Application US/09090808
Patent No. 6127159
GENERAL INFORMATION:
APPLICANT: Fuller, Margaret
TITLE OF INVENTION: Mitofusin Genes and their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,808
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,961
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SUN-63P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-090-808-4

Query Match 71.1%; Score 32; DB 3; Length 493;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 STPVAPT 8
|||||
DB 313 STPVAPT 319

RESULT 12
US-08-856-074A-29

Sequence 29, Application US/08856074A
Patent No. 6004798

GENERAL INFORMATION:

APPLICANT: Anderson, W. French

APPLICANT: Wu, Bonnie W.

TITLE OF INVENTION: Retroviral Envelopes Having

TITLE OF INVENTION: Modified Hypervariable polypoline Regions

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carrella, Byrne, Bain, Gillfillan, Cecchi, Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: WINDOWS 95

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856,074A

FILING DATE: 14-May-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliot M.

REGISTRATION NUMBER: 24,025

REFERENCE/DOCKET NUMBER: 271010-378

TELECOMMUNICATION INFORMATION:

TELEPHONE: 973-994-1700

TELEFAX: 973-994-1744

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

FEATURE:

NAME/KEY: Ecotropic hypervariable polypoline region of a retroviral envelope

US-08-856-074A-29

Query Match 68.9%; Score 31; DB 3; Length 45;
Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAPTQ 9
|||||
DB 36 TPVAPTQ 42

RESULT 13
US-09-216-295-14
; Sequence 14, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colln
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Fusarium javanicum (2)
US-09-216-295-14

Query Match 68.9%; Score 31; DB 4; Length 250;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VSTPVPQTQ 9
|:|:|:|:
DB 16 VAIPTPTTE 24

RESULT 14
US-08-484-126-1
; Sequence 1, Application US/08484126
; Patent No. 5985655
; GENERAL INFORMATION:
; APPLICANT: Anderson, W. French
; APPLICANT: Baltucki, Leon F.
; APPLICANT: Mason, James M.
; TITLE OF INVENTION: Targetable Vector Particles
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,126
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,347
; FILING DATE: 20-OCT-1994
; APPLICATION NUMBER: 08/973,307
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lillie, Raymond J.
; REGISTRATION NUMBER: 31,778
; REFERENCE/DOCKET NUMBER: 271010-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid

STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Ecotropic gp70 Protein
US-08-484-126-1

Query Match 68.9%; Score 31; DB 2; Length 469;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVPQTQ 9
|:|:|:|:
DB 298 TPSPQTQ 304

RESULT 15
US-08-473-122-2
; Sequence 2, Application US/08473122
; Patent No. 5652340
; GENERAL INFORMATION:
; APPLICANT: KOHMI-SHIGEMATSU, TERUMI
; APPLICANT: KOHMI, YOSHINORI
; APPLICANT: DICKINSON, LILIANE A
; TITLE OF INVENTION: MATRIX-ASSOCIATING DNA-BINDING PROTEIN,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME AND METHODS FOR DETECTING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,122
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,034
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619 535-9001
; TELEFAX: 619 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-473-122-2

Query Match 68.9%; Score 31; DB 1; Length 763;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVP 7
|:|:|:|:
DB 308 VSTPISP 314

Search completed: August 15, 2001, 13:10:02
Job time: 39 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:32:55 ; Search time 56.84 Seconds
(without alignments)
9.599 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 9

Sequence: 1 VSTRPVAPQTQ 9

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	9	14	AA845168	Listeria p60 pepti
2	100.0	21	16	AA873891	Listeria monocytog
3	100.0	478	14	AA845178	Listeria p60 prote
4	100.0	484	16	AA873913	Listeria monocytog
5	88.9	12	14	AA845172	Listeria p60 pepti
6	66.7	6	14	AA854615	Listeria p60 pepti
7	66.7	10	14	AA845173	Listeria p60 pepti
8	66.7	20	14	AA845159	Listeria p60 pepti
9	66.7	157	20	AA873718	Amino acid sequenc
10	66.7	343	21	AA841666	Human ORFX ORF1430
11	66.7	750	20	AA805477	C. albicans Rbt1 p

12	66.7	999	22	AA859817	Tu1D protein #8.
13	66.7	1592	22	AA859827	Protein #4 encoded
14	55.6	7	19	AA821365	Human HUPF-I mutan
15	55.6	9	19	AA870120	Peptide produced b
16	55.6	11	22	AA870126	Peptide produced b
17	55.6	11	22	AA872848	Human p53 A76T mut
18	55.6	20	20	AA882295	Dynamn 41.20 Zela
19	55.6	23	20	AA882310	Transport peptide
20	55.6	25	16	AA879982	Signal transductio
21	55.6	27	20	AA878130	Human secreted pro
22	55.6	43	20	AA882294	Dynamn 41.2 Zelan
23	55.6	45	20	AA801143	Secreted protein e
24	55.6	48	21	AA833087	Plus radiata tran
25	55.6	57	21	AA844975	Human secreted pro
26	55.6	59	21	AA844976	Human secreted pro
27	55.6	72	21	AA839069	Human secreted pro
28	55.6	87	20	AA827568	Human secreted pro
29	55.6	89	21	AA841518	Human ORFX ORF1282
30	55.6	94	15	AA847117	Complete sequence
31	55.6	98	21	AA854394	Arabidopsis thalia
32	55.6	101	21	AA82898	CUB domain from BM
33	55.6	102	22	AA872875	Human p53 A76T/V12
34	55.6	104	19	AA856088	Murine monocyte ch
35	55.6	104	19	AA857322	Mouse monocyte che
36	55.6	112	21	AA854393	Arabidopsis thalia
37	55.6	114	19	AA811113	H. pylori ORF hp6e
38	55.6	114	21	AA803726	Human secreted pro
39	55.6	121	21	AA854455	Zea mays protein f
40	55.6	125	21	AA840264	Human ORFX ORF28 p
41	55.6	125	21	AA854454	Zea mays protein f
42	55.6	130	19	AA877657	Staphylococcus aur
43	55.6	130	21	AA853631	Human colon cancer
44	55.6	132	21	AA855449	Human prostate can
45	55.6	151	21	AA845699	Human cancer assoc
46	55.6	152	21	AA854453	Zea mays protein f
47	55.6	152	22	AA879973	Corynebacterium g1
48	55.6	152	22	AA879981	Corynebacterium g1
49	55.6	152	22	AA879987	Corynebacterium g1
50	55.6	152	22	AA824690	Plant SDF encoded
51	55.6	158	21	AA825075	Plant SDF encoded
52	55.6	160	21	AA812578	Zea mays protein f
53	55.6	160	21	AA810791	M. avium Innazaine
54	55.6	168	22	AA879120	Corynebacterium g1
55	55.6	168	22	AA879813	Corynebacterium g1
56	55.6	179	21	AA855986	Arabidopsis thalia
57	55.6	179	21	AA855986	Arabidopsis thalia
58	55.6	180	21	AA855942	Arabidopsis thalia
59	55.6	180	21	AA855941	Arabidopsis thalia
60	55.6	181	21	AA855985	Arabidopsis thalia
61	55.6	181	21	AA855985	Arabidopsis thalia
62	55.6	184	22	AA810820	Arabidopsis thalia
63	55.6	184	22	AA880053	Arabidopsis thalia
64	55.6	185	21	AA854822	Corynebacterium g1
65	55.6	191	20	AA894495	Arabidopsis thalia
66	55.6	191	16	AA869639	Human delta-2 prot
67	55.6	192	17	AA889510	Hepatitis C virus
68	55.6	193	14	AA833986	Hepatitis C virus
69	55.6	193	21	AA806865	HCT27 El protein.
70	55.6	196	21	AA810819	Arabidopsis thalia
71	55.6	196	21	AA855984	Arabidopsis thalia
72	55.6	202	18	AA859940	Arabidopsis thalia
73	55.6	202	18	AA825065	BRC42 cancer suscep
74	55.6	202	21	AA809042	Arabidopsis thalia
75	55.6	202	21	AA838651	Arabidopsis thalia
76	55.6	205	21	AA806864	Arabidopsis thalia
77	55.6	205	21	AA810818	Arabidopsis thalia
78	55.6	214	21	AA850386	Human uncoupling p
79	55.6	216	22	AA875329	Human secreted pro
80	55.6	217	21	AA804638	Arabidopsis thalia
81	55.6	219	20	AA830653	Human secreted pro
82	55.6	228	21	AA832101	Human secreted pro
83	55.6	236	21	AA813699	Chlamydia sp. prot
84	55.6	243	19	AA880702	S. pneumoniae cati
		247	20	AA827338	Group B Streptococ

85	5	55.6	253	21	AA05005	Arabidopsis thalia	158	5	55.6	500	20	AA094496	Human delta-2 prot
86	5	55.6	255	20	AA037385	Amino acid sequenc	159	5	55.6	501	21	AA032978	Pinus radiata tran
87	5	55.6	256	20	AA04637	Arabidopsis thalia	160	5	55.6	503	21	AA08936	Amino acids 29-531
88	5	55.6	264	13	AA029638	PCPD ORF 3. Chlam	161	5	55.6	504	21	AA068935	Amino acids 28-531
89	5	55.6	276	10	AA081577	EDG-1-like G-prote	162	5	55.6	505	21	AA068918	Amino acids 28-532
90	5	55.6	280	21	AA04636	Arabidopsis thalia	163	5	55.6	505	21	AA068934	Amino acids 27-531
91	5	55.6	281	21	AA05004	Arabidopsis thalia	164	5	55.6	506	21	AA068917	Amino acids 27-532
92	5	55.6	283	21	AA051248	Hydrophobic domain	165	5	55.6	506	21	AA068933	Amino acids 26-531
93	5	55.6	283	21	AA04952	Human secreted pro	166	5	55.6	507	21	AA068916	Amino acids 26-532
94	5	55.6	286	17	AA03566	Mycobacterium tube	167	5	55.6	507	21	AA068932	Amino acids 25-531
95	5	55.6	302	21	AA05003	Arabidopsis thalia	168	5	55.6	508	21	AA068915	Amino acids 25-532
96	5	55.6	305	17	AA060650	Protein phosphatas	169	5	55.6	508	21	AA068931	Amino acids 24-531
97	5	55.6	323	21	AA075550	Neisseria gonorrhe	170	5	55.6	509	19	AA080935	Amino acid sequenc
98	5	55.6	323	22	AA051240	TPAI protein sequ	171	5	55.6	510	21	AA068914	Amino acids 24-532
99	5	55.6	325	17	AA03565	Mycobacterium tube	172	5	55.6	510	21	AA068913	Amino acids 23-532
100	5	55.6	327	21	AA07281	Fibronectin attach	173	5	55.6	524	21	AA068942	Amino acids 29-552
101	5	55.6	327	21	AA09947	Arabidopsis thalia	174	5	55.6	525	21	AA068941	Amino acids 28-552
102	5	55.6	328	21	AA09946	Arabidopsis thalia	175	5	55.6	526	21	AA068924	Amino acids 28-553
103	5	55.6	332	18	AA032418	Mycobacterium tube	176	5	55.6	526	21	AA068940	Amino acids 27-552
104	5	55.6	332	18	AA032350	M. tuberculosis Im	177	5	55.6	527	21	AA068923	Amino acids 27-553
105	5	55.6	332	19	AA061683	Mycobacterium tube	178	5	55.6	527	21	AA068939	Amino acids 26-552
106	5	55.6	332	19	AA064322	M. tuberculosis an	179	5	55.6	528	21	AA068922	Amino acids 26-553
107	5	55.6	332	20	AA039083	M. tuberculosis re	180	5	55.6	528	21	AA068938	Amino acids 25-552
108	5	55.6	332	20	AA038945	Arabidopsis thalia	181	5	55.6	529	21	AA068921	Amino acids 25-553
109	5	55.6	336	21	AA046021	Arabidopsis thalia	182	5	55.6	529	21	AA068937	Amino acids 24-552
110	5	55.6	343	21	AA046020	Arabidopsis thalia	183	5	55.6	530	21	AA068920	Amino acids 24-553
111	5	55.6	351	21	AA046019	Arabidopsis thalia	184	5	55.6	531	21	AA068919	Amino acids 23-553
112	5	55.6	357	21	AA075397	Neisseria gonorrhe	185	5	55.6	535	22	AA049707	Small round struct
113	5	55.6	359	16	AA072715	hisc gene product	186	5	55.6	543	20	AA0855610	Secreted protein c
114	5	55.6	370	13	AA026183	MS2-pgpD protein.	187	5	55.6	559	19	AA050909	Alteromonas fortis
115	5	55.6	371	20	AA029193	Amino acid sequenc	188	5	55.6	561	19	AA063701	Human HSK1 protein
116	5	55.6	375	21	AA09945	Arabidopsis thalia	189	5	55.6	566	20	AA049068	Amino acid sequenc
117	5	55.6	377	20	AA024072	Salmonella typhimu	190	5	55.6	566	22	AA031932	Pseudomonas fluore
118	5	55.6	382	19	AA044865	Human TP33 telomer	191	5	55.6	583	20	AA055919	Human secreted pro
119	5	55.6	384	20	AA064411	Human EDG-7 recept	192	5	55.6	588	20	AA078199	Endocarditis speci
120	5	55.6	384	20	AA064412	Human EDG-7 recept	193	5	55.6	605	16	AA079625	Lipoma preferred p
121	5	55.6	384	21	AA065500	A human G-protein	194	5	55.6	612	17	AA02123	H. pylori GHP 130
122	5	55.6	384	21	AA090862	Human edg6 protein	195	5	55.6	612	19	AA085816	Gravlin polypeptide
123	5	55.6	387	22	AA061911	R. anatisestifer o	196	5	55.6	651	19	AA053875	Amino acids 27-686
124	5	55.6	396	19	AA053868	Gravlin polypeptide	197	5	55.6	651	21	AA018410	Human gravlin PKA r
125	5	55.6	396	21	AA018408	Human gravlin PKA r	198	5	55.6	652	20	AA039225	M. tuberculosis fu
126	5	55.6	402	20	AA024475	Mouse p14. Mus sp	199	5	55.6	652	20	AA039082	M. tuberculosis fus
127	5	55.6	405	10	AA090458	Snake venom fibrol	200	5	55.6	655	14	AA031041	srnk polypeptide.
128	5	55.6	405	11	AA040482	Gene product of so	201	5	55.6	659	20	AA04497	Human delta-2 matu
129	5	55.6	410	21	AA018329	Arabidopsis thalia	202	5	55.6	659	21	AA068930	Amino acids 28-686
130	5	55.6	410	21	AA090457	Snake venom fibrol	203	5	55.6	660	21	AA068929	Amino acids 27-686
131	5	55.6	411	11	AA040481	Gene product of so	204	5	55.6	661	21	AA068928	Amino acids 26-686
132	5	55.6	421	11	AA018328	Arabidopsis thalia	205	5	55.6	662	20	AA031940	Human rad17 cell c
133	5	55.6	422	18	AA026528	Branched chain ket	206	5	55.6	662	21	AA068927	Amino acids 25-686
134	5	55.6	422	22	AA061181	Pseudomonas putida	207	5	55.6	663	20	AA031941	Human rad17 cell c
135	5	55.6	422	22	AA066454	Protein encoded by	208	5	55.6	663	21	AA068926	Amino acids 24-686
136	5	55.6	428	20	AA013450	Amino acid sequenc	209	5	55.6	664	21	AA068925	Amino acids 23-686
137	5	55.6	429	20	AA073631	Human secreted pro	210	5	55.6	669	20	AA031939	Human rad17 cell c
138	5	55.6	434	20	AA073959	Human TP33 protein	211	5	55.6	670	17	AA07869	Testis-associated
139	5	55.6	442	20	AA037457	Chlamydia trachoma	212	5	55.6	670	20	AA031937	Human rad17 cell c
140	5	55.6	453	19	AA053867	Gravlin polypeptide	213	5	55.6	671	17	AA085290	Streptococcus faec
141	5	55.6	453	21	AA018407	Human gravlin PKA r	214	5	55.6	677	21	AA068948	Amino acids 29-685
142	5	55.6	461	20	AA038793	Neisseria gonorrho	215	5	55.6	678	21	AA068947	Amino acids 28-685
143	5	55.6	461	20	AA038794	N. gonorrhoeae ant	216	5	55.6	679	21	AA068946	Amino acids 27-685
144	5	55.6	465	21	AA081676	Streptococcus pneu	217	5	55.6	680	21	AA068945	Amino acids 26-685
145	5	55.6	468	18	AA019722	Mouse p14 (muscle	218	5	55.6	681	21	AA068944	Amino acids 25-685
146	5	55.6	468	20	AA024476	Corrected mouse p1	219	5	55.6	682	21	AA068943	Nucleotide sequenc
147	5	55.6	469	17	AA087242	Protein encoded by	220	5	55.6	685	19	AA080813	Human delta-2 prot
148	5	55.6	473	20	AA068935	Alpha-factor profi	221	5	55.6	685	21	AA068912	Amino acid sequenc
149	5	55.6	478	10	AA090459	Alpha-factor profi	222	5	55.6	685	21	AA068911	Human notch ligand
150	5	55.6	478	11	AA040483	Proteinase produ	223	5	55.6	685	21	AA076912	Amino acid sequenc
151	5	55.6	480	14	AA042867	Platelet aggregati	224	5	55.6	686	21	AA068911	Amino acid sequenc
152	5	55.6	480	14	AA042867	Platelet aggregati	225	5	55.6	686	21	AA068911	Mouse notch ligand
153	5	55.6	483	21	AA079413	Southern copenhea	226	5	55.6	717	10	AA091933	BI antigen. Toxop
154	5	55.6	486	19	AA037056	HIV-1 breakthrough	227	5	55.6	730	9	AA080618	Human Bone Morphog
155	5	55.6	491	15	AA037057	HIV-1 breakthrough	228	5	55.6	730	18	AA031669	C-proteinase encod
156	5	55.6	498	15	AA044154	Human neuronal nic	229	5	55.6	739	18	AA025790	Gene 036 product d
157	5	55.6	498	18	AA090927	Neuronal nicotinic	230	5	55.6	764	21	AA068949	Fusion protein of

231	5	55.6	788	19	AAW75919	C-proteinase sequ	304	4	44.4	8	17	AAW95514	Human prostate car
232	5	55.6	797	21	AAW70963	Human Ras signal	305	4	44.4	8	20	AAW41615	Memmanian ion chan
233	5	55.6	802	21	AAW81746	M. tuberculosis fu	306	4	44.4	8	21	AAW77393	Human I-group O env
234	5	55.6	802	19	AAW64379	Mycobacterium anti	307	4	44.4	8	22	AAW31509	Amino acid sequenc
235	5	55.6	802	20	AAW32063	Mycobacterium tube	308	4	44.4	9	14	AAW44262	Residues 68-76 of
236	5	55.6	802	20	AAW39224	M. tuberculosis fu	309	4	44.4	9	14	AAW42578	HIV envelope neutr
237	5	55.6	802	20	AAW39176	M. tuberculosis fu	310	4	44.4	9	19	AAW79187	M88 murine monoclo
238	5	55.6	802	20	AAW39081	M. tuberculosis fu	311	4	44.4	9	20	AAW94619	Src homology 3 dom
239	5	55.6	802	20	AAW39033	M. tuberculosis fu	312	4	44.4	9	21	AAW98674	WT1 derived immuno
240	5	55.6	835	17	AAW96206	Trvastin protein.	313	4	44.4	9	21	AAW98680	WT1 derived immuno
241	5	55.6	843	13	AAW27744	Extracellular prot	314	4	44.4	9	21	AAW98722	WT1 derived immuno
242	5	55.6	870	21	AAW10948	L. mexicana casein	315	4	44.4	9	21	AAW98727	WT1 derived immuno
243	5	55.6	933	20	AAW21621	Ligand binding dom	316	4	44.4	9	21	AAW98780	WT1 derived immuno
244	5	55.6	933	21	AAW97292	Human progesterone	317	4	44.4	9	22	AAW31508	Amino acid sequenc
245	5	55.6	939	21	AAW53192	Maca mulatta rha	318	4	44.4	9	22	AAW76154	Tumour associated
246	5	55.6	939	21	AAW67882	Ste4p/Gdelta. Intera	319	4	44.4	10	17	AAW49590	Human leucocyte an
247	5	55.6	941	21	AAW24422	Human PRO1154 prot	320	4	44.4	10	17	AAW49591	Human leucocyte an
248	5	55.6	941	21	AAW66736	Membrane-bound pro	321	4	44.4	10	17	AAW49592	Human leucocyte an
249	5	55.6	941	22	AAW65259	Human PRO1154 (UNQ	322	4	44.4	10	17	AAW96505	Hepatitis C virus
250	5	55.6	941	22	AAW65007	Human secreted pro	323	4	44.4	10	17	AAW97522	Antigenic peptide,
251	5	55.6	954	18	AAW19752	Yeast inhibitor of	324	4	44.4	10	19	AAW76876	Fusion immunoglobu
252	5	55.6	986	19	AAW13670	C-proteinase encod	325	4	44.4	10	19	AAW76878	Fusion immunoglobu
253	5	55.6	1013	19	AAW61539	Human cardiac/brai	326	4	44.4	10	19	AAW63551	Beta (1 -> 4)-N-ac
254	5	55.6	1013	19	AAW40224	Human tollold-like	327	4	44.4	10	22	AAW31507	Amino acid sequenc
255	5	55.6	1030	19	AAW53572	Human myosin 11ght	328	4	44.4	10	22	AAW76201	Tumour associated
256	5	55.6	1030	19	AAW41378	Human protein p164	329	4	44.4	10	22	AAW76202	Tumour associated
257	5	55.6	1085	12	AAW11604	P450. 17-alpha/P450	330	4	44.4	11	10	AAW93053	HIV env protein an
258	5	55.6	1148	14	AAW43671	M. leprae rpoB gene	331	4	44.4	11	10	AAW44263	Residues 68-78 of
259	5	55.6	1189	15	AAW56496	TYFA-binding prote	332	4	44.4	11	14	AAW54624	Listeria innocua p
260	5	55.6	1213	18	AAW06086	Drosophila TYFA-bl	333	4	44.4	11	14	AAW54627	Listeria innocua p
261	5	55.6	1213	18	AAW25029	TYFA-binding prote	334	4	44.4	11	14	AAW41809	M13TMD1 mutated fr
262	5	55.6	1252	16	AAW80530	B. sphaericus SLP.	335	4	44.4	11	17	AAW97523	Antigenic peptide,
263	5	55.6	1253	13	AAW28337	SVY4 structural po	336	4	44.4	11	19	AAW50203	Peptide from a kri
264	5	55.6	1268	18	AAW58774	Human breast cance	337	4	44.4	11	21	AAW22972	Peptide from a kri
265	5	55.6	1268	18	AAW58774	Human insulin rece	338	4	44.4	11	21	AAW09549	White shrimp p62 p
266	5	55.6	1297	21	AAW36840	Human insulin rece	339	4	44.4	11	21	AAW02815	Peptide encoded by
267	5	55.6	1300	21	AAW36838	Rat insulin recept	340	4	44.4	11	21	AAW92589	BMP mutant chimeri
268	5	55.6	1315	21	AAW84046	Splice variant of	341	4	44.4	11	22	AAW31506	Peptide encoded by
269	5	55.6	1353	21	AAW84045	Splice variant of	342	4	44.4	12	13	AAW23605	Amino acid sequenc
270	5	55.6	1405	21	AAW84044	Amino acid sequenc	343	4	44.4	12	16	AAW83319	Peptide able to in
271	5	55.6	1449	21	AAW23825	Murine DEC 205 rec	344	4	44.4	12	22	AAW31505	KD-binding random
272	5	55.6	1484	21	AAW89721	Canine ribosome re	345	4	44.4	12	22	AAW31507	Amino acid sequenc
273	5	55.6	1566	16	AAW79643	Immunodominant ant	346	4	44.4	13	19	AAW70128	Human snRNP-assoc
274	5	55.6	1627	12	AAW12789	M. pneumoniae p1 c	347	4	44.4	13	19	AAW50204	Peptide produced b
275	5	55.6	1627	15	AAW47911	Mycoplasma pneumon	348	4	44.4	13	21	AAW22973	Peptide from a kri
276	5	55.6	1627	15	AAW67538	Cytadhesin p1. My	349	4	44.4	13	22	AAW31504	White shrimp p62 p
277	5	55.6	1723	17	AAW00645	Mouse DEC-205. Mu	350	4	44.4	13	22	AAW23604	Peptide able to in
278	5	55.6	1780	19	AAW53863	Human gravin polyp	351	4	44.4	14	16	AAW77855	Antigen to raise a
279	5	55.6	1780	21	AAW15380	Human gravin prote	352	4	44.4	14	17	AAW92864	Cell adhesion modu
280	5	55.6	1794	21	AAW84040	Amino acid sequenc	353	4	44.4	14	19	AAW79191	Synthetic peptide
281	5	55.6	1822	13	AAW27745	Extracellular fact	354	4	44.4	14	19	AAW55527	Antigenic HIV-1 pe
282	5	55.6	1920	22	AAW65656	Novel protein kina	355	4	44.4	14	21	AAW22974	White shrimp p62 p
283	5	55.6	2001	22	AAW20062	Arabidopsis thalia	356	4	44.4	14	21	AAW98509	Human WTI peptide
284	5	55.6	2001	22	AAW20063	Human HNRCP protei	357	4	44.4	14	21	AAW98510	Human WTI peptide
285	5	55.6	2343	21	AAW12453	Pig p105 zona pell	358	4	44.4	14	22	AAW31503	Amino acid sequenc
286	5	55.6	2476	20	AAW67738	Human down-regulat	359	4	44.4	15	10	AAW90224	Antigenic peptide
287	5	55.6	2785	21	AAW57148	Human ORFX ORF2255	360	4	44.4	15	11	AAW06576	Bovine serum album
288	5	55.6	3266	21	AAW42491	Human breast cance	361	4	44.4	15	16	AAW79629	Endocarditis speci
289	5	55.6	3418	18	AAW19211	Human breast and o	362	4	44.4	15	16	AAW79626	Endocarditis speci
290	5	55.6	3418	18	AAW23287	Human BRCA2 (om12)	363	4	44.4	15	17	AAW15317	Serum albumin whos
291	5	55.6	3418	20	AAW04355	Human BRCA2 (om11)	364	4	44.4	15	18	AAW39011	Peptide resembling
292	5	55.6	3418	20	AAW04356	Human BRCA2 (om13)	365	4	44.4	15	19	AAW78551	SH2 domain binding
293	5	55.6	3418	20	AAW04357	Human BRCA2 (om14)	366	4	44.4	15	20	AAW02215	Mutated human G-al
294	5	55.6	3418	20	AAW04358	Human BRCA2 (om15)	367	4	44.4	15	21	AAW14221	HIV US4 gp120 clea
295	5	55.6	3418	20	AAW04354	Human BRCA2 (om11)	368	4	44.4	15	22	AAW14223	Mutant HIV cleavag
296	5	55.6	3418	20	AAW04355	BRCA2 protein sequ	369	4	44.4	15	22	AAW31502	Amino acid sequenc
297	4	44.4	3418	21	AAW77819	Peptide encoded by	370	4	44.4	16	18	AAW25388	PlC gamma SH3 doma
298	4	44.4	3418	21	AAW03551	BMP mutant chimeri	371	4	44.4	16	18	AAW15570	PRN4358. Feline l
299	4	44.4	3418	21	AAW92591	Peptide encoded by	372	4	44.4	16	19	AAW76907	Fusion immunoglobu
300	4	44.4	3418	21	AAW92591	Amino acid sequenc	373	4	44.4	16	19	AAW50206	Peptide from a kri
301	4	44.4	3418	21	AAW92591	Amino acid sequenc	374	4	44.4	16	19	AAW50205	Peptide from a kri
302	4	44.4	3418	21	AAW92591	Sm B/B' epitope 16	375	4	44.4	16	21	AAW22975	White shrimp p62 p
303	4	44.4	3418	21	AAW92591	Antigenic peptide,	376	4	44.4	16	22	AAW31501	Amino acid sequenc

377	4	44.4	16	22	AAB6802	Escherichia coli K
378	4	44.4	17	22	AAB31500	Amino acid sequenc
379	4	44.4	18	19	AAW79190	Synthetic peptide
380	4	44.4	18	20	AAW94621	Src homology 3 dom
381	4	44.4	18	20	AAW84076	S. cerevisiae amin
382	4	44.4	18	22	AAB31499	Amino acid sequenc
383	4	44.4	19	16	AAW6724	gp120 epitope from
384	4	44.4	19	17	AAW02223	CD4:gamma chain fu
385	4	44.4	19	17	AAW02221	CD4:zeta chain fus
386	4	44.4	19	18	AAW33957	Vasopressin type 2
387	4	44.4	19	19	AAW35391	Bifidobacterium 10
388	4	44.4	19	22	AAB31498	Amino acid sequenc
389	4	44.4	20	12	AAW1532	Immunopeptide deri
390	4	44.4	20	14	AAW37689	Synthetic epitope.
391	4	44.4	20	16	AAW68794	Cytotoxic T lympho
392	4	44.4	20	17	AAW08052	HIV peptide #37.
393	4	44.4	20	19	AAW76943	Fusion immunoglob
394	4	44.4	20	19	AAW76875	Fusion immunoglob
395	4	44.4	20	21	AAW03854	Peptide T0120 used
396	4	44.4	20	21	AAW93365	Amino acid sequenc
397	4	44.4	20	21	AAW67262	Protein tyrosine p
398	4	44.4	20	21	AAW66445	HLA-A2-binding HIV
399	4	44.4	20	21	AAW31497	Amino acid sequenc
400	4	44.4	20	22	AAW49381	Simian immunodef
401	4	44.4	21	13	AAW3606	Peptide able to in
402	4	44.4	21	14	AAW31614	Peptide ligand for
403	4	44.4	21	14	AAW37992	Heavy chain hinge
404	4	44.4	21	19	AAW40272	K. oxytoca R-spect
405	4	44.4	21	22	AAW89251	HIV gp120 protein
406	4	44.4	21	22	AAW89252	HIV gp120 protein
407	4	44.4	21	22	AAW89253	HIV gp120 protein
408	4	44.4	21	22	AAW89254	HIV gp120 protein
409	4	44.4	21	22	AAW31496	Amino acid sequenc
410	4	44.4	22	14	AAW30539	HIV discriminatory
411	4	44.4	22	14	AAW31965	BCH-132. Syntheti
412	4	44.4	22	14	AAW41293	Peptide fragment F
413	4	44.4	22	19	AAW67032	Peptide with N-ter
414	4	44.4	22	22	AAW31495	Amino acid sequenc
415	4	44.4	23	14	AAW41294	Peptide fragment F
416	4	44.4	23	14	AAW41332	HIV gp120 epitope.
417	4	44.4	23	15	AAW63849	HIV-1 gp120-40 epi
418	4	44.4	23	16	AAW74066	Rice carbonic-anhy
419	4	44.4	23	16	AAW50207	Peptide from a xil
420	4	44.4	23	19	AAW48108	HIV gp120 residues
421	4	44.4	23	19	AAW48108	HIV gp120 residues
422	4	44.4	23	22	AAW31494	Amino acid sequenc
423	4	44.4	24	8	AAW71151	Anti-HIV peptide 6
424	4	44.4	24	9	AAW80750	Cluster of peptid
425	4	44.4	24	16	AAW33838	Sequence of peptid
426	4	44.4	24	16	AAW66432	PCUS 4-18 (476-49
427	4	44.4	24	19	AAW54953	HIV gp120 envelope
428	4	44.4	24	20	AAW08855	Expression constru
429	4	44.4	24	20	AAW08768	Expression constru
430	4	44.4	24	20	AAW05354	HIV-1 CUVAC pepi
431	4	44.4	24	21	AAW22976	White shrimp p62 p
432	4	44.4	24	22	AAW31493	Amino acid sequenc
433	4	44.4	25	7	AAW60708	HIV virus p18 prot
434	4	44.4	25	13	AAW27336	Peptide corresep. t
435	4	44.4	25	20	AAW81958	Human EMDQ-II vari
436	4	44.4	25	22	AAW31492	Amino acid sequenc
437	4	44.4	26	12	AAW1413	Hepatitis A virus
438	4	44.4	26	14	AAW30538	HIV discriminatory
439	4	44.4	26	14	AAW30755	HIV discriminatory
440	4	44.4	26	14	AAW41301	Peptide fragment F
441	4	44.4	26	16	AAW44111	HIV gp160 epitope.
442	4	44.4	26	16	AAW65044	Random bioinlylati
443	4	44.4	26	19	AAW76909	Fusion immunoglob
444	4	44.4	26	19	AAW50208	Peptide from a xil
445	4	44.4	26	19	AAW46647	Biotinylation pep
446	4	44.4	26	20	AAW29315	Biotinylation pep
447	4	44.4	26	21	AAW29277	White shrimp p62 p
448	4	44.4	26	22	AAW31491	Amino acid sequenc
449	4	44.4	27	10	AAW90819	Non-immunogenic am
	4	44.4	27	14	AAW30757	HIV discriminatory
450	4	44.4	27	19	AAW79184	HIV gp120 C5 regio
451	4	44.4	27	20	AAW38474	Human secreted pro
452	4	44.4	27	22	AAW31490	Amino acid sequenc
453	4	44.4	28	15	AAW49685	Sequence of trypti
454	4	44.4	28	18	AAW21018	Human glial fibrill
455	4	44.4	28	21	AAW38463	Fragment of human
456	4	44.4	28	21	AAW31489	Amino acid sequenc
457	4	44.4	28	21	AAW33288	Pinus radiata tran
458	4	44.4	29	21	AAW68639	Amino acid sequenc
459	4	44.4	29	21	AAW31488	Amino acid sequenc
460	4	44.4	29	22	AAW49382	Simian immunodef
461	4	44.4	29	22	AAW49383	Simian immunodef
462	4	44.4	29	22	AAW49393	Simian immunodef
463	4	44.4	30	12	AAW49394	Human tumor-asso
464	4	44.4	30	19	AAW76911	Fusion immunoglob
465	4	44.4	30	22	AAW31487	gp120 HTLV-III pep
466	4	44.4	31	17	AAW31189	Finger 2 domain of
467	4	44.4	31	18	AAW24744	Fibronectin fragme
468	4	44.4	31	18	AAW19977	HIV gp120 envelope
469	4	44.4	31	19	AAW54936	Human prostate can
470	4	44.4	31	20	AAW48370	Tomato Cu/Zn SOD e
471	4	44.4	31	20	AAW82455	Human fibronectin
472	4	44.4	31	20	AAW82988	HIV-1 group O env
473	4	44.4	31	21	AAW77377	HIV-1 group O env
474	4	44.4	31	21	AAW77378	Amino acid sequenc
475	4	44.4	31	22	AAW31486	C-terminal portion
476	4	44.4	32	10	AAW91490	WT1 derived immuno
477	4	44.4	32	21	AAW98799	Amino acid sequenc
478	4	44.4	32	22	AAW31485	Hepatitis C virus
479	4	44.4	33	16	AAW69686	Hepatitis C virus
480	4	44.4	33	17	AAW89558	Hepatitis C virus
481	4	44.4	33	17	AAW89558	Amino acid sequenc
482	4	44.4	33	22	AAW31484	Anti-GAT antibody
483	4	44.4	34	14	AAW43826	Cytochrome P450 2C
484	4	44.4	34	17	AAW89860	SEQ ID NO. 66 from
485	4	44.4	34	19	AAW22870	Human p53 proline-
486	4	44.4	34	19	AAW48443	Amino acid sequenc
487	4	44.4	34	22	AAW31481	SIV-MND gp120 V3 I
488	4	44.4	35	16	AAW67556	Peptide produced b
489	4	44.4	35	19	AAW70114	Human 5' EST secre
490	4	44.4	35	20	AAW1421	Fragment of human
491	4	44.4	35	21	AAW38462	Fragment of human
492	4	44.4	35	21	AAW67806	Peptide #206 for d
493	4	44.4	35	21	AAW67808	Peptide #208 for d
494	4	44.4	36	21	AAW67809	Peptide #209 for d
495	4	44.4	36	21	AAW38414	Fragment of human
496	4	44.4	37	18	AAW40369	Human breast cance
497	4	44.4	37	18	AAW30366	Fragment #2 of bon
498	4	44.4	37	20	AAW25880	Human secreted pro
499	4	44.4	37	21	AAW44604	Human secreted pro
500	4	44.4	37	21	AAW09516	Human Op-1 finger
501	4	44.4	37	21	AAW09559	Human Op-1 finger
502	4	44.4	37	21	AAW09562	Human Op-1 mutant
503	4	44.4	37	21	AAW09563	Human Op-1 mutant
504	4	44.4	37	21	AAW09565	Human Op-1 mutant
505	4	44.4	37	21	AAW09566	Human Op-1 mutant
506	4	44.4	37	21	AAW09573	Human Op-1 mutant
507	4	44.4	37	21	AAW84032	Amino acid sequenc
508	4	44.4	38	14	AAW41075	HIV-1 gp120 C-term
509	4	44.4	38	15	AAW58457	TSAR binding domai
510	4	44.4	38	17	AAW95453	Antigen-binding pe
511	4	44.4	38	20	AAW42830	Erythropoietin rec
512	4	44.4	38	20	AAW42835	Non-EPOR-binding c
513	4	44.4	38	20	AAW74072	Human HPT-1 bindin
514	4	44.4	38	21	AAW55741	Arabidopsis thaila
515	4	44.4	39	16	AAW66436	PCUS 4-18 (476-49
516	4	44.4	39	16	AAW66410	PCUS 4-18 (476-49
517	4	44.4	39	18	AAW19025	HIV envelope glyco
518	4	44.4	39	19	AAW75198	Human secreted pro
519	4	44.4	39	20	AAW05347	HIV-1 CUVAC pepi
520	4	44.4	39	20	AAW05340	HIV-1 CUVAC pepi
521	4	44.4	41	19	AAW59899	HIV-1 C5 region of
522	4	44.4	41	20	AAW22869	SEQ ID NO. 65 from
	4	44.4	41	20	AAW12310	Human 5' EST secre

523	4	44.4	42	18	AAW19055	596	4	44.4	69	18	AAW32366	Mycobacterium tube
524	4	44.4	42	18	AAW06501	597	4	44.4	69	18	AAW12764	A-lineage conotoxi
525	4	44.4	42	20	AAV12163	598	4	44.4	69	19	AAW81669	M. tuberculosis im
526	4	44.4	43	20	AAV12848	599	4	44.4	69	19	AAW64306	Mycobacterium tube
527	4	44.4	45	10	AAW90818	600	4	44.4	69	19	AAW39108	M. tuberculosis an
528	4	44.4	45	22	AAW87380	601	4	44.4	69	20	AAV38971	M. tuberculosis re
529	4	44.4	46	19	AAW79183	602	4	44.4	69	21	AAW55153	Arabisopsis thalia
530	4	44.4	46	21	AAW28505	603	4	44.4	70	20	AAV28247	Human secreted pro
531	4	44.4	47	20	AAV36545	604	4	44.4	70	20	AAW33960	Human 53BP2:IP-2 p
532	4	44.4	47	21	AAW45201	605	4	44.4	70	21	AAW33453	Human colon cancer
533	4	44.4	49	19	AAW46754	606	4	44.4	70	21	AAW03849	Protein fragment #
534	4	44.4	50	16	AAW1628	607	4	44.4	71	19	AAV14462	Human secreted pro
535	4	44.4	50	17	AAW98476	608	4	44.4	72	20	AAV22887	SEQ ID NO. 83 from
536	4	44.4	50	21	AAW09092	609	4	44.4	73	22	AAW70028	Mammalian CD4 IL-1
537	4	44.4	51	16	AAW77798	610	4	44.4	73	22	AAW70018	Human CD4 D4 domai
538	4	44.4	51	16	AAW77799	611	4	44.4	73	22	AAW70025	Human CD4 D4 domai
539	4	44.4	51	20	AAV48336	612	4	44.4	73	22	AAW70026	Human CD4 D4 domai
540	4	44.4	51	20	AAV36715	613	4	44.4	73	22	AAW70027	Human CD4 D4 domai
541	4	44.4	51	21	AAW16822	614	4	44.4	73	22	AAW70029	Human CD4 D4 domai
542	4	44.4	51	21	AAW09225	615	4	44.4	74	20	AAV14475	Human CD4 D4 domai
543	4	44.4	52	10	AAW91361	616	4	44.4	74	20	AAV03781	Fragment of human
544	4	44.4	52	21	AAW22970	617	4	44.4	74	21	AAW56214	S. aureus polypept
545	4	44.4	52	21	AAW22971	618	4	44.4	74	21	AAW37064	Human secreted pro
546	4	44.4	53	17	AAW88330	619	4	44.4	74	21	AAW55678	Arabisopsis thalia
547	4	44.4	53	19	AAW22898	620	4	44.4	74	21	AAW60223	Arabisopsis thalia
548	4	44.4	53	20	AAV30706	621	4	44.4	74	21	AAV50946	Human adult thymus
549	4	44.4	54	17	AAW05836	622	4	44.4	75	20	AAV35810	Chlamydia pneumoni
550	4	44.4	54	19	AAW22867	623	4	44.4	75	20	AAV12951	Amino acid sequenc
551	4	44.4	54	19	AAW22868	624	4	44.4	75	21	AAW18074	Arabisopsis thalia
552	4	44.4	54	21	AAW59095	625	4	44.4	75	21	AAV90584	Conus striatus kap
553	4	44.4	54	21	AAW00997	626	4	44.4	75	21	AAV90587	Conus sulcatus kap
554	4	44.4	54	21	AAV59595	627	4	44.4	76	21	AAW55739	Arabisopsis thalia
555	4	44.4	55	8	AAW70360	628	4	44.4	76	21	AAW01671	Human secreted pro
556	4	44.4	55	19	AAW22866	629	4	44.4	76	22	AAW58600	Murine TANGO 281 c
557	4	44.4	55	19	AAW22865	630	4	44.4	77	19	AAW68001	S. pneumoniae deri
558	4	44.4	55	20	AAW26920	631	4	44.4	77	21	AAW25354	pinus radiata cell
559	4	44.4	56	20	AAW02478	632	4	44.4	77	21	AAW46895	Arabisopsis thalia
560	4	44.4	56	21	AAW54442	633	4	44.4	78	21	AAW52108	Human secreted pro
561	4	44.4	56	22	AAW65854	634	4	44.4	78	21	AAW55152	Arabisopsis thalia
562	4	44.4	56	22	AAW65862	635	4	44.4	78	22	AAW87389	Human gene 48 enco
563	4	44.4	57	21	AAW54473	636	4	44.4	78	22	AAW87389	Human gene 48 enco
564	4	44.4	58	10	AAW91360	637	4	44.4	79	19	AAW22863	SEQ ID NO. 59 from
565	4	44.4	59	16	AAW73922	638	4	44.4	79	19	AAW22864	SEQ ID NO. 60 from
566	4	44.4	59	17	AAW04957	639	4	44.4	79	20	AAV73910	Human prostate tum
567	4	44.4	59	21	AAW58213	640	4	44.4	79	21	AAW54421	Human pancreatic c
568	4	44.4	59	21	AAW59293	641	4	44.4	80	18	AAW27747	Staphylococcus aur
569	4	44.4	59	21	AAW00608	642	4	44.4	80	18	AAW12765	A-lineage conotoxi
570	4	44.4	59	22	AAW96790	643	4	44.4	80	21	AAW60234	Arabisopsis thalia
571	4	44.4	59	22	AAW90628	644	4	44.4	81	20	AAW60234	Human endometrium
572	4	44.4	60	18	AAW15568	645	4	44.4	81	20	AAW28624	Human secreted pro
573	4	44.4	60	19	AAW20977	646	4	44.4	81	20	AAV73395	Human secreted pro
574	4	44.4	60	19	AAW27277	647	4	44.4	82	21	AAW37389	Human secreted pro
575	4	44.4	60	20	AAV11876	648	4	44.4	82	21	AAW18950	Human secreted pro
576	4	44.4	60	21	AAW46896	649	4	44.4	82	21	AAW22927	Peptide derived fr
577	4	44.4	61	14	AAW39350	650	4	44.4	82	21	AAV79629	Calreticulin Golgi
578	4	44.4	61	21	AAW09627	651	4	44.4	83	21	AAW54450	Golgi target sequ
579	4	44.4	61	21	AAW02506	652	4	44.4	84	19	AAW42038	Human pancreatic c
580	4	44.4	62	20	AAV19648	653	4	44.4	85	21	AAW02769	Mouse prococtistat
581	4	44.4	63	21	AAW51667	654	4	44.4	85	21	AAV91606	Human secreted pro
582	4	44.4	63	21	AAW59038	655	4	44.4	86	19	AAW38421	Human secreted pro
583	4	44.4	64	18	AAW11269	656	4	44.4	86	20	AAV73904	Proteolipid protei
584	4	44.4	64	20	AAV38898	657	4	44.4	86	20	AAV73929	Human prostate tum
585	4	44.4	64	21	AAW45200	658	4	44.4	86	20	AAV11815	Human 5' EST secre
586	4	44.4	64	21	AAW55463	659	4	44.4	87	21	AAW44140	Arabisopsis thalia
587	4	44.4	64	21	AAV90583	660	4	44.4	88	21	AAW40407	Arabisopsis thalia
588	4	44.4	65	21	AAW38595	661	4	44.4	88	21	AAW28504	Zea mays protein f
589	4	44.4	65	22	AAW76042	662	4	44.4	88	21	AAW33200	Zea mays protein f
590	4	44.4	65	22	AAW79213	663	4	44.4	88	21	AAW33339	Zea mays protein f
591	4	44.4	65	22	AAW55981	664	4	44.4	88	21	AAW54249	Arabisopsis thalia
592	4	44.4	67	19	AAW83944	665	4	44.4	89	20	AAV12949	Amino acid sequenc
593	4	44.4	67	19	AAW57058	666	4	44.4	89	20	AAW04406	Arabisopsis thalia
594	4	44.4	68	21	AAW53884	667	4	44.4	89	21	AAW28503	Zea mays protein f
595	4	44.4	69	18	AAW32434	668	4	44.4	89	21	AAW54248	Arabisopsis thalia

669	4	44.4	89	21	AGC01533	Human secreted pro	742	4	44.4	102	21	AB02800	Human Op-1 amino a
670	4	44.4	89	21	AGC01562	Human secreted pro	743	4	44.4	102	21	AA92569	Op-1 finger-1-heal
671	4	44.4	90	21	AA92306	Corn acid triacylg	744	4	44.4	102	22	AA63506	Human gastric can
672	4	44.4	91	20	AA11416	Human 5' EST seque	745	4	44.4	103	20	AA30835	Human secreted pro
673	4	44.4	91	21	AA40613	Human ORFX ORF377	746	4	44.4	103	21	AA40704	Human ORFX ORF46
674	4	44.4	91	21	AA42378	Human ORFX ORF2142	747	4	44.4	104	9	AA0104	Sequence encoded b
675	4	44.4	91	21	AA627140	Zea mays protein f	748	4	44.4	104	19	AA42878	SEQ ID NO. 74 from
676	4	44.4	92	20	AA60469	Human normal blad	749	4	44.4	104	21	AA41199	Human ORFX ORF63
677	4	44.4	92	21	AA63234	Zea mays protein f	750	4	44.4	104	21	AA42842	Human ORFX ORF2606
678	4	44.4	92	21	AA63234	Zea mays protein f	751	4	44.4	104	21	AA624955	Arabidopsis thalia
679	4	44.4	92	21	AA633943	Arabidopsis thalia	752	4	44.4	104	21	AA94933	Human secreted pro
680	4	44.4	92	21	AA654495	Zea mays protein f	753	4	44.4	105	19	AA122856	SEQ ID NO. 52 from
681	4	44.4	93	19	AA122860	SEQ ID NO. 56 from	754	4	44.4	105	19	AA122857	SEQ ID NO. 53 from
682	4	44.4	93	19	AAW75090	Human secreted pro	755	4	44.4	105	19	AA422858	SEQ ID NO. 54 from
683	4	44.4	93	21	AA604405	Arabidopsis thalia	756	4	44.4	105	19	AA422859	SEQ ID NO. 55 from
684	4	44.4	93	21	AA633473	Arabidopsis thalia	757	4	44.4	105	19	AA40579	Human lambda CL do
685	4	44.4	93	21	AA654347	Arabidopsis thalia	758	4	44.4	105	20	AA38473	Human secreted pro
686	4	44.4	94	17	AA89859	Cytochrome P450 2C	759	4	44.4	105	20	AA108746	Human lambda-CL do
687	4	44.4	94	19	AA122861	SEQ ID NO. 57 from	760	4	44.4	105	20	AAW92426	Human lambda-CL do
688	4	44.4	94	19	AAW75151	Human secreted pro	761	4	44.4	105	21	AA627001	Human lambda CL do
689	4	44.4	94	19	AAW75152	Human secreted pro	762	4	44.4	105	21	AA612168	Arabidopsis thalia
690	4	44.4	94	21	AA61658	Human secreted pro	763	4	44.4	106	20	AAW70803	Amino acid sequenc
691	4	44.4	94	21	AA608039	Arabidopsis thalia	764	4	44.4	106	21	AA40717	Human ORFX ORF481
692	4	44.4	94	21	AA626159	Zea mays protein f	765	4	44.4	106	21	AA637647	Arabidopsis thalia
693	4	44.4	94	21	AA637331	Arabidopsis thalia	766	4	44.4	106	21	AA601566	Human secreted pro
694	4	44.4	94	22	AA664488	Human secreted pro	767	4	44.4	106	21	AA92193	Human Iggl lambda
695	4	44.4	95	18	AAW20297	H. pylori cytoplas	768	4	44.4	107	19	AAW75784	Human lymphocyte s
696	4	44.4	95	20	AAW74161	Human prostate tum	769	4	44.4	107	21	AA642526	Human ORFX ORF2290
697	4	44.4	95	21	AA641126	Zea mays protein f	770	4	44.4	107	21	AA609358	Arabidopsis thalia
698	4	44.4	95	21	AA657203	Arabidopsis thalia	771	4	44.4	108	20	AA129241	Amino acid sequenc
699	4	44.4	95	21	AA659156	Arabidopsis thalia	772	4	44.4	108	20	AA105478	C. albicans Rbt1 p
700	4	44.4	95	21	AA916121	Human secreted pro	773	4	44.4	108	21	AA618536	Zea mays protein f
701	4	44.4	96	21	AA632768	Eucalyptus grandis	774	4	44.4	108	21	AA603520	Human secreted pro
702	4	44.4	96	21	AA606013	Arabidopsis thalia	775	4	44.4	109	14	AA639729	First type III fib
703	4	44.4	96	21	AA608038	Arabidopsis thalia	776	4	44.4	109	18	AAW37348	Human fibronectin
704	4	44.4	96	21	AA637330	Arabidopsis thalia	777	4	44.4	109	19	AAW57189	Fibronectin first
705	4	44.4	97	14	AA653359	Osteogenic protein	778	4	44.4	109	19	AAW42034	Mouse preprocortis
706	4	44.4	97	14	AA653387	Murine osteogenic	779	4	44.4	109	20	AA428574	Secreted peptide c
707	4	44.4	97	19	AA638643	Streptococcus pneu	780	4	44.4	109	20	AA34593	Chlamydia pneumoni
708	4	44.4	97	20	AAW27248	C. elegans CED-6 p	781	4	44.4	109	20	AA688817	Polypeptide fragme
709	4	44.4	97	20	AAW89696	Human osteogenic p	782	4	44.4	109	20	AAW82982	Human fibronectin
710	4	44.4	97	20	AAW95444	Conserved 6 cystei	783	4	44.4	110	12	AA612387	Amplified human ap
711	4	44.4	97	21	AA633109	Pinus radiata trun	784	4	44.4	110	21	AA624425	Human PRO1274 prot
712	4	44.4	97	21	AA633072	Arabidopsis thalia	785	4	44.4	110	21	AA615654	Arabidopsis thalia
713	4	44.4	97	21	AA648926	Arabidopsis thalia	786	4	44.4	110	21	AA618889	Zea mays protein f
714	4	44.4	97	21	AAW90944	Commomora testoste	787	4	44.4	110	21	AA699380	Human PRO1274 (UNQ
715	4	44.4	97	22	AA665852	Human OSTG0281 cy	788	4	44.4	110	21	AA687273	Human signal pepti
716	4	44.4	98	10	AA695681	Human osteogenic p	789	4	44.4	110	22	AA666129	Protein of the Inv
717	4	44.4	99	21	AA641554	Arabidopsis thalia	790	4	44.4	111	16	AA666317	Human Immunoglobul
718	4	44.4	100	15	AA647238	Wild-type feline H	791	4	44.4	111	18	AAW28276	Amino acid sequenc
719	4	44.4	100	21	AA627328	Arabidopsis thalia	792	4	44.4	111	21	AA612314	Zea mays protein f
720	4	44.4	100	21	AA636857	Human secreted pro	793	4	44.4	111	21	AA603420	Human secreted pro
721	4	44.4	100	21	AA600536	Human secreted pro	794	4	44.4	111	21	AA692027	Human bone morphog
722	4	44.4	100	22	AA681811	Streptococcus pneu	795	4	44.4	112	21	AA619019	Zea mays protein f
723	4	44.4	100	22	AA631970	Rice glutamate 1-s	796	4	44.4	112	21	AA637235	Arabidopsis thalia
724	4	44.4	101	20	AA135775	Chlamydia pneumoni	797	4	44.4	113	17	AA696560	Hepatitis C virus
725	4	44.4	101	20	AA612050	Human 5' EST seque	798	4	44.4	113	17	AA696561	Hepatitis C virus
726	4	44.4	102	10	AA695682	Human osteogenic p	799	4	44.4	113	17	AA696562	Hepatitis C virus
727	4	44.4	102	14	AA653360	Osteogenic protein	800	4	44.4	113	17	AA696564	Hepatitis C virus
728	4	44.4	102	18	AA656889	Human osteogenic p	801	4	44.4	113	21	AA640765	Human ORFX ORF529
729	4	44.4	102	18	AA656897	Mutant human osteo	802	4	44.4	113	21	AA615925	Arabidopsis thalia
730	4	44.4	102	18	AAW36872	Human osteogenic p	803	4	44.4	113	21	AA660083	Arabidopsis thalia
731	4	44.4	102	18	AAW36873	Mouse osteogenic p	804	4	44.4	113	21	AA660682	Arabidopsis thalia
732	4	44.4	102	19	AAW78901	Human UNC-5 homolo	805	4	44.4	113	21	AA600281	Human secreted pro
733	4	44.4	102	20	AAW36828	Chlamydia trachoma	806	4	44.4	114	14	AA653361	N-terminally trunc
734	4	44.4	102	20	AA116708	WO9914235 Seq ID N	807	4	44.4	114	20	AAW34698	Chlamydia pneumoni
735	4	44.4	102	20	AA119744	SEQ ID NO 462 from	808	4	44.4	114	20	AAW95454	N-terminally trunc
736	4	44.4	102	20	AAW89697	Human osteogenic p	809	4	44.4	114	21	AA608037	Arabidopsis thalia
737	4	44.4	102	20	AAW95443	Conserved 7 cystei	810	4	44.4	114	21	AA637329	Arabidopsis thalia
738	4	44.4	102	21	AAW54387	Human pancreatic c	811	4	44.4	114	21	AAW75983	Murine skin cell p
739	4	44.4	102	21	AA606012	Arabidopsis thalia	812	4	44.4	114	21	AAW76033	Murine skin cell p
740	4	44.4	102	21	AA644007	Zea mays protein f	813	4	44.4	114	22	AAW55822	Skin cell protein,
741	4	44.4	102	21	AAW09534	Human Op-1 C-termi	814	4	44.4	114	22	AAW55972	Skin cell protein,

815	4	44.4	115	18	AAW12437	OP-1 based morphon
816	4	44.4	115	20	AAV42461	Rat guanlylin prepr
817	4	44.4	115	20	AAV39287	Human phosphodiester
818	4	44.4	115	20	AAI12133	Human 5' EST secre
819	4	44.4	115	21	AAW97653	Wheat SUG1 polypep
820	4	44.4	115	20	AAW58270	Arabidopsis thalia
821	4	44.4	116	14	AAW53362	N-terminally trunc
822	4	44.4	116	16	AAW8728	Rmf gene product d
823	4	44.4	116	20	AAW5453	N-terminally trunc
824	4	44.4	116	21	AAW56080	Human secreted pro
825	4	44.4	117	14	AAW53363	N-terminally trunc
826	4	44.4	117	18	AAV11162	S. pneumoniae prot
827	4	44.4	117	20	AAV74203	Human prostate tum
828	4	44.4	117	20	AAV66146	Human bladder tumo
829	4	44.4	117	20	AAV37327	Amino acid sequenc
830	4	44.4	117	20	AAV35533	Chlamydia pneumoni
831	4	44.4	117	20	AAW92252	BIL72 polypeptide
832	4	44.4	117	20	AAW95452	N-terminally trunc
833	4	44.4	117	21	AAW24952	Arabidopsis thalia
834	4	44.4	117	21	AAW09548	Trypsin truncated
835	4	44.4	117	21	AAW02814	Human trypsin trun
836	4	44.4	117	21	AAV25595	Trypsin truncated
837	4	44.4	117	21	AAV70526	Maize plastid targ
838	4	44.4	118	16	AAW71184	Chimeric protein g
839	4	44.4	118	21	AAW57065	Human prostate can
840	4	44.4	118	21	AAW57234	Arabidopsis thalia
841	4	44.4	119	14	AAW53364	N-terminally trunc
842	4	44.4	119	20	AAV34585	Chlamydia pneumoni
843	4	44.4	119	20	AAW95451	N-terminally trunc
844	4	44.4	119	21	AAW03931	Human secreted pro
845	4	44.4	119	22	AAW08893	Human secreted pro
846	4	44.4	119	22	AAW20301	Arabidopsis apopto
847	4	44.4	119	22	AAW62005	B-myb protein frag
848	4	44.4	120	21	AAW36031	Zea mays protein f
849	4	44.4	120	21	AAW36653	Arabidopsis thalia
850	4	44.4	120	22	AAW47126	CDIFF-4, Incyte ID
851	4	44.4	121	19	AAW68979	Human microtubule
852	4	44.4	121	21	AAW53900	Human colon cancer
853	4	44.4	121	21	AAW33951	Arabidopsis thalia
854	4	44.4	122	10	AAW3697	Protein encoded by
855	4	44.4	122	13	AAW22381	Antigen tg-3e. EI
856	4	44.4	122	16	AAW75407	HIV-3 strain AMT70
857	4	44.4	122	20	AAW38835	Neisseria meningit
858	4	44.4	122	21	AAW42096	Human ORFX ORF1860
859	4	44.4	122	21	AAW17953	Arabidopsis thalia
860	4	44.4	123	21	AAW40679	Human ORFX ORF43
861	4	44.4	123	21	AAW50920	Human fetal brain
862	4	44.4	124	15	AAW54336	Anti-HIV gp120 imm
863	4	44.4	124	17	AAW01310	VH region of HIV n
864	4	44.4	124	18	AAW33607	Human secreted pro
865	4	44.4	124	19	AAW56732	Nicellus specific
866	4	44.4	124	20	AAW74122	Human prostate tum
867	4	44.4	124	20	AAV60074	Human endometrium
868	4	44.4	124	21	AAW10230	Human fetal kidney
869	4	44.4	124	21	AAW27327	Arabidopsis thalia
870	4	44.4	124	21	AAW34082	Zea mays protein f
871	4	44.4	124	21	AAW41932	Arabidopsis thalia
872	4	44.4	124	21	AAW58520	Zea mays protein f
873	4	44.4	124	21	AAW00852	Human secreted pro
874	4	44.4	124	21	AAW95162	Anti-gp120 HCl3 he
875	4	44.4	124	21	AAV98271	Anti-gp120 HCl3 he
876	4	44.4	125	20	AAV04704	Mouse Rpppa amino
877	4	44.4	125	22	AAW74775	Human MPJ3 protein
878	4	44.4	125	22	AAW35230	M. tuberculosis RV3
879	4	44.4	126	10	AAW90479	Chimeric monoclonal
880	4	44.4	126	21	AAW03617	Human secreted pro
881	4	44.4	127	13	AAW29010	p146-k3 protein pr
882	4	44.4	127	18	AAW08945	Kappa light chain
883	4	44.4	127	19	AAW44176	Monoclonal antibod
884	4	44.4	127	21	AAW28002	Arabidopsis thalia
885	4	44.4	127	21	AAW41891	Arabidopsis thalia
886	4	44.4	127	22	AAW88497	Haemophilus influe
887	4	44.4	128	20	AAW78449	H. annuus pollen al
888	4	44.4	128	20	AAW78450	H. annuus pollen al
889	4	44.4	128	20	AAW78451	H. annuus pollen al
890	4	44.4	128	20	AAW78448	H. annuus pollen al
891	4	44.4	128	21	AAW05701	Arabidopsis thalia
892	4	44.4	128	21	AAW22977	Arabidopsis thalia
893	4	44.4	128	21	AAW32977	Arabidopsis thalia
894	4	44.4	128	21	AAW34081	Zea mays protein f
895	4	44.4	128	21	AAW35338	Zea mays protein f
896	4	44.4	128	21	AAW42644	Arabidopsis thalia
897	4	44.4	128	21	AAW52278	Arabidopsis thalia
898	4	44.4	129	21	AAW01792	Rice M10 homologue
899	4	44.4	129	21	AAW36652	Arabidopsis thalia
900	4	44.4	130	9	AAW70377	Corresponds to p14
901	4	44.4	130	19	AAW70377	Anti-human CD23 6G
902	4	44.4	130	20	AAV73825	Human prostate tum
903	4	44.4	130	21	AAW33140	Arabidopsis thalia
904	4	44.4	130	21	AAW38587	Arabidopsis thalia
905	4	44.4	130	21	AAW02970	Human secreted pro
906	4	44.4	130	22	AAW81654	Streptococcus pneu
907	4	44.4	131	22	AAW70790	N. magdali bacter
908	4	44.4	131	21	AAW10968	Arabidopsis thalia
909	4	44.4	131	21	AAW36856	Arabidopsis thalia
910	4	44.4	131	22	AAW64639	Human secreted pro
911	4	44.4	132	14	AAW53365	N. alata arabinoaga
912	4	44.4	132	16	AAW75510	Human Rpppa amino
913	4	44.4	132	20	AAV04697	Human 5' EST secre
914	4	44.4	132	20	AAW5450	N-terminally trunc
915	4	44.4	132	21	AAW41063	Human ORFX ORF27
916	4	44.4	132	21	AAW08058	Arabidopsis thalia
917	4	44.4	132	21	AAW32226	Arabidopsis thalia
918	4	44.4	133	20	AAV60073	Human endometrium
919	4	44.4	133	20	AAV37947	Amino acid sequenc
920	4	44.4	133	20	AAW78447	H. annuus pollen al
921	4	44.4	133	20	AAW78441	H. annuus pollen al
922	4	44.4	133	21	AAW41454	Human ORFX ORF1218
923	4	44.4	133	21	AAW04077	Human secreted pro
924	4	44.4	134	21	AAW41939	Human ORFX ORF1703
925	4	44.4	134	22	AAW46970	M. jannaschl EF-P
926	4	44.4	134	22	AAW79820	Corynebacterium gl
927	4	44.4	135	19	AAW62642	Flea serine protea
928	4	44.4	135	21	AAW41247	Human ORFX ORF1011
929	4	44.4	135	21	AAW10861	Arabidopsis thalia
930	4	44.4	135	21	AAW26078	Zea mays protein f
931	4	44.4	135	21	AAW03345	Human secreted pro
932	4	44.4	136	20	AAV37091	Amino acid sequenc
933	4	44.4	136	21	AAW33199	Arabidopsis thalia
934	4	44.4	136	21	AAW33942	Zea mays protein f
935	4	44.4	136	21	AAW36651	Arabidopsis thalia
936	4	44.4	137	20	AAW29171	Amino acid sequenc
937	4	44.4	137	20	AAV37129	Amino acid sequenc
938	4	44.4	137	21	AAW10860	Arabidopsis thalia
939	4	44.4	137	21	AAW57233	Arabidopsis thalia
940	4	44.4	138	19	AAW47361	Human ORFX ORF116
941	4	44.4	138	19	AAW42019	Arabidopsis thalia
942	4	44.4	138	20	AAW08297	Zea mays protein f
943	4	44.4	138	20	AAV04923	Osteogenic protein
944	4	44.4	138	21	AAW43352	Arabidopsis thalia
945	4	44.4	138	21	AAW12821	Human ORFX ORF116
946	4	44.4	138	21	AAW33233	Arabidopsis thalia
947	4	44.4	138	21	AAW36403	Zea mays protein f
948	4	44.4	139	13	AAW23187	Osteogenic protein
949	4	44.4	139	13	AAW27285	Arabidopsis thalia
950	4	44.4	139	13	AAW27286	Arabidopsis thalia
951	4	44.4	139	14	AAW53366	Mature murine oste
952	4	44.4	139	14	AAW53386	N-terminally trunc
953	4	44.4	139	14	AAW53386	Murine osteogenic
954	4	44.4	139	14	AAW33398	Human mature OP-1
955	4	44.4	139	14	AAW33399	Mouse mature OP-1
956	4	44.4	139	14	AAW33392	Morphogen hOP-1
957	4	44.4	139	14	AAW33922	Morphogen mop-1
958	4	44.4	139	15	AAW31467	Mature p3 OR 31-34
959	4	44.4	139	15	AAW46724	Human mature osteo
960	4	44.4	139	15	AAW46733	Mouse osteogenic p
	4	44.4	139	15	AAW60967	Mature human OP-1

961	4	44.4	139	15	AAR60968	Murine OP-1. Mus
962	4	44.4	139	16	AAR71974	BMP-7. Homo sapie
963	4	44.4	139	17	AAW00222	Mouse mature osteo
964	4	44.4	139	17	AAW00221	Human mature osteo
965	4	44.4	139	18	AAW40180	Human hOP1 mature
966	4	44.4	139	18	AAW40181	Mouse hOP1 mature
967	4	44.4	139	18	AAW36871	Mature protein anl
968	4	44.4	139	19	AAW63003	Mouse OP1 protein
969	4	44.4	139	19	AAW54064	Bone morphogenetic
970	4	44.4	139	20	AAV13210	Human secreted pro
971	4	44.4	139	20	AAW95449	Mature human osteo
972	4	44.4	139	20	AAW84215	Bone morphogenetic
973	4	44.4	139	20	AAW84215	Arabidopsis thalia
974	4	44.4	139	21	AAW23992	Arabidopsis thalia
975	4	44.4	139	21	AAW9547	Mature OP-1 mutant
976	4	44.4	139	21	AAW92594	Human mature H223
977	4	44.4	139	21	AAW92594	Mature mutant OP-1
978	4	44.4	139	21	AAW70755	Mature modified hu
979	4	44.4	139	21	AAW57218	Human osteogenic p
980	4	44.4	139	21	AAW57219	Mouse osteogenic p
981	4	44.4	140	19	AAW98699	H. pylori GHP0 693
982	4	44.4	140	20	AAW06111	Nelson Bay virus P
983	4	44.4	140	21	AAW18399	Arabidopsis thalia
984	4	44.4	140	21	AAW33950	Arabidopsis thalia
985	4	44.4	140	21	AAW39677	Arabidopsis thalia
986	4	44.4	140	21	AAW02053	Human secreted pro
987	4	44.4	140	21	AAW92593	Mutant OP-1 constr
988	4	44.4	141	22	AAW78968	C. glutamicum SMT
989	4	44.4	141	21	AAW03951	Human mesenchymal
990	4	44.4	141	21	AAW43355	Human ORFX ORF3119
991	4	44.4	141	21	AAW18094	Arabidopsis thalia
992	4	44.4	141	21	AAW28000	Arabidopsis thalia
993	4	44.4	141	21	AAW41890	Arabidopsis thalia
994	4	44.4	141	21	AAW95429	Human calcium chan
995	4	44.4	142	13	AAW28985	Thyroid N-acetyl-g
996	4	44.4	142	21	AAW41796	Human ORFX ORF1560
997	4	44.4	142	21	AAW12791	Clostridium cellu
998	4	44.4	142	21	AAW08989	Arabidopsis thalia
999	4	44.4	142	21	AAW53843	Arabidopsis thalia
1000	4	44.4	142	22	AAW74776	Rat MP3 protein.

ALIGNMENTS

RESULT 1

AAW45168 standard; protein: 9 AA.

AC AAR45168:

DT 16-JUN-1994 (first entry)

XX Listeria p60 peptide epitope.

DE Listeria monocytogenes: antibodies; immunoassay; conjugate.

XX Listeria monocytogenes: antibodies; immunoassay; conjugate.

OS Synthetic.

PN DE4318450-A.

PD 16-DEC-1993.

XX 03-JUN-1993: 93DE-4318450.

PF 11-JUN-1992: 92DE-4319111.

PR 25-NOV-1992: 92DE-4339567.

XX (MERE) MERCK PATENT GMBH.

PA Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;

PI Hofmann G, Bubert A, Goebel W, Koehler S;

XX

DR WPI; 1993-406956/51.

XX New primers for PCR detection of Listeria - including individual

PT species, also new peptide(s) for raising antibodies for

PT immunochemical detection

XX

PS Disclosure; Fig 2; 19pp; German.

XX

CC The sequence is that of a Listeria p60 peptide epitope which

CC which may be used in the prodn. of antibodies for the detection

CC of Listeria by immunoassay (partic. ELISA). It may be used as

CC part of a method that allows determination of individual Listeria

CC species, esp. L. monocytogenes.

XX

SQ Sequence 9 AA:

Query Match 100.0%; Score 9; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 3.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSPVPAPTO 9

Db 1 vstpvapctg 9

RESULT 2

AAW73891 standard; peptide: 21 AA.

AC AAR73891:

DT 05-DEC-1995 (first entry)

XX Listeria monocytogenes protein P60 precursor peptide 144-164.

DE Listeria monocytogenes: protein P60 precursor; vaccine;

XX meningitis related homologous antigenic sequence; MRHAS; RV-1;

KW immunoassay; diagnosis; treatment; prophylactic; bacterial;

KM viral; peptide 144-164.

XX

OS Listeria monocytogenes.

XX

PN WO9509232-A.

XX

PD 06-APR-1995.

XX

PF 28-SEP-1994: 94WO-CA00516.

XX

PR 28-SEP-1993: 93US-0127499.

XX

PA (SHAR) SHARMA L R.

PA (VALS) VAN ALSTYNE D.

XX

XX Sharma LR, Van Alstyne D;

XX

DR WPI; 1995-147431/19.

XX

PT New peptide(s) and corresp. antibodies for the treatment of

PT meningitis - the peptide(s) corresp. to homologous antigenic

PT sites on bacterial and viral agents and on chemokine(s), used for

PT detecting and preventing meningitis

XX

PS Claim 34; Page 74; 98pp; English.

XX

CC AAR7913 is the Listeria monocytogenes protein P60 precursor. It

CC contains the meningitis related antigenic sequences (MRHAS) claimed

CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a

CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The

CC claimed MRHAS peptides may be used in immunoassays to diagnose the

CC presence of bacterial and/or viral meningitis agents in a sample,

CC or in prophylactic and therapeutic meningitis treatments. The

CC peptides may also be used as vaccines against meningitis.

XX Sequence 21 AA;
SQ

Query Match 100.0%; Score 9; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPPTG 9
| | | | | | | | | | |
DB 2 vstpvapptg 10

RESULT 3

AAR45178
ID AAR45178 standard; Protein; 478 AA.

AC AAR45178;

DT 16-JUN-1994 (first entry)

DE Listeria p60 protein.

KW Immunogenic polypeptide; antibodies; immunoassay; conjugate.

OS Listeria monocytogenes.

PN DE4318450-A.

PD 16-DEC-1993.

PF 03-JUN-1993; 93DE-4318450.

PR 11-JUN-1992; 92DE-4219111.

PR 25-NOV-1992; 92DE-4239567.

PA (MERE) MERCK PATENT GMBH.

PI Schubert P, Neumann S, Pawelzik W, Linxweiler W, Burger C;

PI Hofmann G, Bubert A, Goedel W, Koehler S;

DR WPI: 1993-406956/51.

PT New primers for PCR detection of Listeria - including individual

PT species, also new peptide(s) for raising antibodies for

PT immunochemical detection

PS Disclosure: Fig 4; 19pp; German.

CC The sequence is that of the Listeria p60 protein. Antibodies

CC generated against the protein can be used in the detection

CC of Listeria by immunoassay (partic. ELISA). The detection method

CC allows determination of individual Listeria species, esp.

CC L. monocytogenes.

SQ Sequence 478 AA;

RESULT 4

AAR73913
ID AAR73913 standard; Protein; 484 AA.

AC AAR73913;

XX

DT 05-DEC-1995 (first entry)

DE Listeria monocytogenes protein p60 precursor.

XX Listeria monocytogenes; protein p60 precursor; vaccine;

KW meningitis related homologous antigenic sequence; MRHAS; RV-1;

KW immunoassay; diagnosis; treatment; prophylactic; bacterial;

OS Listeria monocytogenes.

PN WO9509232-A.

PD 06-APR-1995.

PF 28-SEP-1994; 94WO-CA00516.

PR 28-SEP-1993; 93US-0127499.

PA (SHAR/) SHARMA L R.

PA (VALS/) VAN ALSTYNE D.

PI Sharma LR, Van Alstyne D;

DR WPI: 1995-147431/19.

PT New peptide(s) and corresp. antibodies for the treatment of

PT meningitis - the peptide(s) corresp. to homologous antigenic

PT sites on bacterial and viral agents and on chemokine(s), used for

PT detecting and preventing meningitis

PS Claim 47; Fig 7/10; 98pp; English.

CC AAR73913 is the Listeria monocytogenes protein p60 precursor. It

CC contains the meningitis related antigenic sequences (MRHAS) claimed

CC in AAR73891-R73894 and AAR73903-R73906, which are recognised by a

CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The

CC claimed MRHAS peptides may be used in immunoassays to diagnose the

CC presence of bacterial and/or viral meningitis agents in a sample,

CC or in prophylactic and therapeutic meningitis treatments. The

CC peptides may also be used as vaccines against meningitis.

CC NB: Identified by matching corresponding MRHAS peptides.

SQ Sequence 484 AA;

OY 1 VSTPVAPPTG 9
| | | | | | | | | | |
DB 145 vstpvapptg 153

DT 16-JUN-1994 (first entry)

DE Listeria p60 peptide epitope.

KW Listeria monocytogenes; antibodies; immunoassay; conjugate.

OS Synthetic.

PN DE4318450-A.

PD 16-DEC-1993.

XX

PF 03-JUN-1993: 93DE-4318450.
 XX 11-JUN-1992: 92DE-4219111.
 PR 25-NOV-1992: 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure: Fig 2; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 SQ Sequence 12 AA:

Query Match 88.9%; Score 8; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 STPVAPTO 9
 |||||
 Db 1 stpvaptg 8

RESULT 6
 AAR54615 standard; Protein: 6 AA.
 ID AAR54615
 XX
 AC AAR54615;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria p60 peptide epitope.
 XX
 KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993: 93DE-4318450.
 XX
 PR 11-JUN-1992: 92DE-4219111.
 PR 25-NOV-1992: 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure: Page 3; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which

CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 SQ Sequence 6 AA:

Query Match 66.7%; Score 6; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPTO 9
 |||||
 Db 1 pvaptg 6

RESULT 7
 AAR45173 standard; Protein: 10 AA.
 ID AAR45173
 XX
 AC AAR45173;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria p60 peptide epitope.
 XX
 KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993: 93DE-4318450.
 XX
 PR 11-JUN-1992: 92DE-4219111.
 PR 25-NOV-1992: 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure: Fig 2; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 SQ Sequence 10 AA:

Query Match 66.7%; Score 6; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPTO 9
 |||||
 Db 1 pvaptg 6

RESULT 8
 AAR45159

```

ID  AAR45159 standard; Protein: 20 AA.
XX
AC  AAR45159;
XX
DT  16-JUN-1994 (first entry)
XX
DE  Listeria p60 peptide epitope.
XX
KW  Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX
OS  Synthetic.
XX
FH  Key
FT  Region
FT  Location/Qualifiers
FT  1..7
FT  /note= "opt. 0-7 amino acid residues"
FT  14..20
FT  /note= "opt. 0-7 amino acid residues"
XX
DE  DE4318450-A.
XX
PD  16-DEC-1993.
XX
PE  03-JUN-1993; 93DE-4318450.
XX
PR  11-JUN-1992; 92DE-4219111.
PR  25-NOV-1992; 92DE-4239567.
XX
PA  (MERE ) MERCK PATENT GMBH.
XX
PI  Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
PI  Hofmann G, Bubert A, Goebel W, Koehler S;
XX
DR  WPI: 1993-406956/51.
XX
XX
PT  New primers for PCR detection of Listeria - including individual
PT  species, also new peptide(s) for raising antibodies for
PT  immunochemical detection
XX
PS  Claim 3; Page 4; 19pp; German.
XX
CC  The sequence is that of a Listeria p60 peptide epitope which
CC  which may be used in the prodn. of antibodies for the detection
CC  of Listeria by immunoassay (partic. ELISA). It may be used as
CC  part of a method that allows determination of individual Listeria
CC  species, esp. L. monocytogenes.
XX
SQ  Sequence 20 AA:

Query Match 66.7%; Score 6; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  4 PVAPRG 9
DB  8 pvpapcg 13

```

```

OS  Chlamydia trachomatis.
XX
PN  W09928475-A2.
XX
PD  10-JUN-1999.
XX
PE  27-NOV-1998; 98WO-IB01939.
XX
PR  04-NOV-1998; 98US-0107077.
PR  28-NOV-1997; 97ER-0015041.
PR  17-DEC-1997; 97ER-0016034.
XX
PA  (GEST ) GENSET.
XX
PI  Griffais R;
XX
DR  WPI: 1999-371125/31.
XX
XX
PT  Genome sequence of Chlamydia trachomatis
XX
PS  Disclosure: Page 1323-1324; 1755pp; English.
XX
CC  AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome
CC  of Chlamydia trachomatis (see A4201425). The polypeptides can be used as
CC  vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC  can also be used to control growth of the microorganism. Chlamydia
CC  trachomatis is responsible for a large number of diseases, e.g. eye
CC  diseases such as conventional trachoma, nongonococcal urethritis,
CC  paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC  nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC  peritphalitis, bartolinitis; pneumonia in breast feeding infants;
CC  and venereal lymphogranulomatosis. The polypeptides of the invention
CC  may be of use in treating these diseases.
XX
SQ  Sequence 157 AA:

Query Match 66.7%; Score 6; DB 20; Length 157;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2 SRPVAP 7
DB  14 srpvap 19

RESULT 10
AAB41666
ID  AAB41666 standard; Protein: 343 AA.
XX
AC  AAB41666;
XX
DT  08-FEB-2001 (first entry)
XX
DE  Human ORFX ORF1430 polypeptide sequence SEQ ID NO:2860.
XX
XX
KW  Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW  vulnerrary; antiproliferative; antiparkinsonian; neuroprotective;
KW  anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW  immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW  hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW  antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KW  antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW  neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW  cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW  cholesterol ester storage; systemic lupus erythematosus; infection;
KW  severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW  allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW  bone damage; cartilage damage; antinflammatory disease; coagulation;
KW  thrombosis; contraceptive.
XX
OS  Homo sapiens.
XX

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PN WO200058473-A2.
 PD 05-OCT-2000.
 XX
 XX 31-MAR-2000; 2000WO-US08621.
 PE
 XX 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2000-602362/57.
 DR N-PSDB; AAC75875.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 11; Page 2100-2101; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
 CC antiparasitic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antihypertoid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 SQ Sequence 343 AA;
 Query Match 66.7%; Score 6; DB 21; Length 343;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 TPVAPT 8
 |||||
 Db 289 tpvapt 294
 RESULT 11
 ID AAY05477
 AAY05477 standard; Protein; 750 AA.
 XX
 AC AAY05477;
 XX
 DT 07-JUL-1999 (first entry)
 XX
 DE C. albicans Rbt1 protein sequence.
 XX
 KM Rbt1; detection; TUP1 gene function; pathogenic potential; vaccine;
 KM virulence inhibitor; infection; diagnosis; filamentous growth;
 KM antibiotic resistance.
 XX
 OS Candida albicans.

XX
 PN WO918115-A1.
 XX
 PD 15-APR-1999.
 XX
 XX 02-OCT-1998; 98WO-US20655.
 PE
 XX 01-OCT-1998; 98US-0165239.
 PR 02-OCT-1997; 97US-0061058.
 PR 18-DEC-1997; 97US-0068065.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Braun B, Johnson AD;
 XX
 DR WPI; 1999-263994/22.
 DR N-PSDB; AAX36552.
 XX
 PT Nucleic acid encoding Rbt1 polypeptides of Candida albicans
 XX
 PS Claim 28; Fig 3b; 82pp; English.
 XX
 CC This sequence is the Candida albicans Rbt1 protein of the invention.
 CC The Rbt1 gene and its fragments are useful for detecting or quantifying
 CC C. albicans nucleic acid in hybridization or amplification methods; as
 CC therapeutic agents; as indicators of TUP1 gene function (and thus of
 CC pathogenic potential); as a polypeptide processing signal or template for
 CC various functional domains of Rbt1. Plasmids containing the Rbt1 gene can
 CC be used as vaccines. Rbt1 is used to detect or quantify specific
 CC antibodies against Rbt1, while antibodies against Rbt1 can be used to
 CC detect Rbt1 in standard immunoassays. Rbt1 can also be used for drug
 CC screening, rational drug design and identification of proteins that
 CC interact physically with Rbt1. Cells that express Rbt1 can be used to
 CC screen for agents that control virulence in C. albicans. Antibodies
 CC against Rbt1 may be used to purify Rbt1 and to raise anti-idiotypic
 CC antibodies. Modulation of Rbt1 function, specifically by disrupting the
 CC corresponding gene, is used to inhibit virulence of C. albicans. The Rbt1
 CC gene and protein allow diagnosis of infection without the need for
 CC culturing and microscopic examination. The presence of Rbt1 indicates
 CC lack of TUP1 activity and/or filamentous growth, and also the degree of
 CC virulence and/or resistance/susceptibility to particular antibiotics, for
 CC prognosis or selection of appropriate treatments.
 CC
 SQ Sequence 750 AA;
 Query Match 66.7%; Score 6; DB 20; Length 750;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 STPVAP 7
 |||||
 Db 650 stpvap 655
 RESULT 12
 ID AAB59817
 AAB59817 standard; Protein; 999 AA.
 XX
 AC AAB59817;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE TutD protein #8.
 XX
 KM Toluene degradation; enzyme; waste degradation; TutD.
 XX
 OS Thauera aromatica.
 OS Xanthomonas maltophilia.
 OS Geobacter metallireducens.
 OS Azarcus toluilyticus.
 XX
 PN WO200072650-A2.

XX 07-DEC-2000.
PD 24-MAY-2000; 2000WO-US14298.
XX
XX 01-JUN-1999; 99US-0323872.
XX
XX (UYOH-) UNIV OHIO.
XX
XX Coschigano PW;
XX WPI: 2001-041080/05.
XX N-PSDB; AAF23625; AAF23627.
XX
XX Composition comprising toluene degrading enzyme useful for biological
PT treatment of organic compounds, especially for degrading toluene or its
PT analogs -
XX
XX Disclosure: Fig 5; 122pp; English.
XX
XX The present invention relates to toluene degrading enzyme genes and
CC proteins tuth (see AAF23629 and AAB59831), tuti (AAF23630 and AAB59832),
CC tutf (AAF23631 and AAB59833) and turg (AAF23632 and AAB59834). The
CC toluene degrading enzymes are homologues of pyruvate formate lyase. The
CC toluene degrading enzymes are useful for biological treatment of organic
CC compounds and in particular for the degradation of toluene and its
CC analogs contained in liquid or solid waste source. The present sequence
CC is a protein sequence for toluene degrading enzyme, tuth.
XX
XX Sequence 999 AA;
SQ

Query Match 66.7%; Score 6; DB 22; Length 999;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVA 6
|||||
Db 757 vstpva 762

RESULT 13
AAB59827
ID AAB59827 standard; Protein: 1592 AA.
XX
AC AAB59827;
XX
DT 04-APR-2001 (first entry)
XX
DE Protein #4 encoded by tuth/E gene.
XX
KW Toluene degradation; enzyme: waste degradation; Tute; Tuth.
XX
XX Thauera aromatica.
OS Xanthomonas maltophilia.
OS Geobacter metallireducens.
OS Azorarcus toluyticus.
XX
XX WO200072650-A2.
PN
XX
XX 07-DEC-2000.
PD
XX 24-MAY-2000; 2000WO-US14298.
XX
XX 01-JUN-1999; 99US-0323872.
XX
XX (UYOH-) UNIV OHIO.
XX
XX Coschigano PW;
XX
XX WPI: 2001-041080/05.
XX N-PSDB; AAF23627.
XX

PT Composition comprising toluene degrading enzyme useful for biological
PT treatment of organic compounds, especially for degrading toluene or its
PT analogs -
XX
XX Disclosure: Fig 12; 122pp; English.
XX
XX The present invention relates to toluene degrading enzyme genes and
CC proteins tuth (see AAF23629 and AAB59831), tuti (AAF23630 and AAB59832),
CC tutf (AAF23631 and AAB59833) and turg (AAF23632 and AAB59834). The
CC toluene degrading enzymes are homologues of pyruvate formate lyase. The
CC toluene degrading enzymes are useful for biological treatment of organic
CC compounds and in particular for the degradation of toluene and its
CC analogs contained in liquid or solid waste source. The present sequence
CC is a protein sequence encoded by toluene degrading enzyme gene, Tuth/E.
XX
XX Sequence 1592 AA;
SQ

Query Match 66.7%; Score 6; DB 22; Length 1592;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVA 6
|||||
Db 1350 vstpva 1355

RESULT 14
AAV21365
ID AAV21365 standard; Protein: 7 AA.
XX
XX AAV21365;
XX
XX 22-JUL-1999 (first entry)
XX
XX Human HUPF-I mutant protein fragment 17.
DE
XX

KW Human: beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMG-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9845322-A2.
PN
XX
XX 15-OCT-1998.
PD
XX 02-APR-1998; 98WO-IB00705.
XX
XX 10-APR-1997; 97US-0043163.
XX
XX (UYUT-) RIJKSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACADEMY OF SCI.
XX (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
XX Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX
XX WPI: 1998-609901/51.
XX N-PSDB; AAX75768.
XX

PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA

XX Disclosure: Figure 17: 258pp: English.

PS

XX

CC This invention describes a novel method for the diagnosis of a disease

CC caused by, or associated with, an RNA molecule that has a frameshift

CC mutation. The method is used to diagnose age-related diseases, especially

CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's

CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,

CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II

CC and many others listed) or susceptibility to these disorders. The method

CC allows a definitive diagnosis of Alzheimer's disease in living patients,

CC at an early stage. It is based on the observation that disease may be

CC caused by mutations in RNA rather than DNA. The invention describes the

CC use of neuronal system RNA molecules, specifically proteins including

CC beta-amyloid precursor protein (beta-Ap), the microtubule associated

CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule

CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,

CC neurofilament-F, presentin I, presentin II, glial fibrillary acidic

CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma

CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group

CC protein-C (HMGp-C) and neuroendocrine specific protein A.

XX

XQ

Sequence 7 AA:

Query Match	55.6%	Score 5:	DB 19:	length 7:
Best Local	Similarity 100.0%	Pred. No.	3.4e+05:	
Matches	5:	Conservative	0:	Mismatches 0:
				Indels 0:
				Gaps 0

Qy	4	PVAPT	8
Db	2	PVAPT	6

RESULT 15

ID AAW70120 standard; peptide; 9 AA.

AC AAW701203

DT 07-DEC-1998 (flrst entry)

DE Peptide produced by subtilisin digestion of 45 kDa MPT 32 glycoprotein.

KW Glycopeptide; subtilisin; reversed-phase HPLC; Edman degradation; FAB-MS;

KW antigen.

OS Mycobacterium tuberculosis.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
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40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
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53	53	53
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57	57	57
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62	62	62
63	63	63
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84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

/note= "O-glycosylated with an alpha-mannose residue"

PN W09829132-A1

PD 09-JUL-1998.

PF 29-DEC-1997; 97WO-US24189.

PR 31-DEC-1996; 96US-0034003.

PA (UYNX) UNIV NEW YORK STATE.

PI Belisle JT, Laal S, Zolla-Pazner S;

DR WPI; 1998-387787/33.

PT Early detection of mycobacterial infection - by testing a biological
PT fluid sample from a subject for the presence of antibodies reactive
PT with *Mycobacterium tuberculosis* antigens
XX
XX
Example 3; Page 71; 170pp; English.

XX Sequences AAM70109, AAM70115-W70141 are N-terminal amino acid sequences of glycopeptides, or non-glycosylated peptides generated by subtilisin digestion of the 45 kDa MPr 32 glycoprotein. These sequences were obtained by purifying the 45 kDa protein, digesting it with subtilisin, and then separating the products by reversed-phase HPLC on a column. CC This digestion yielded 26 peptides, of which five were found to be CC glycosylated (AAM70109, AAM70115, AAM70120, AAM70126, and AAM70128). CC All CC of the peptides were subjected to both Fast Atom Bombardment-Mass Spectrometry (FAB-MS), and automated Edman degradation to determine their CC molecular weight and N-terminal amino acid sequence, respectively. The CC discovery of the complete primary structure of MPr 32 glycoprotein CC enables further work to be performed and the possibility of it being used CC as an antigen for the early detection of mycobacterial disease.

Sequence	9 AA
5Q	

Query Match	55.6%;	Score 5;	DB 19;	Length 9;
Best Local	Similarity	100.0%;	Pred. No. 3.4e+05;	
Matches	5;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0

QY	3	TPVAP	7
Db	1	tpvap	5

RESULT 16

ID AAW70126 standard; peptide; 11 AA

AC AAW70126;

DT 07-DEC-1998 (first entry)

DE Peptide produced by subtilisin digestion of 45 kDa MPT 32 glycoprotein.

KW Glycopeptide; subtlisin; reversed-phase HPLC; Edman degradation; FAB-MS;

KW antlgen.

OS Mycobacterium tuberculosis

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
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80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT /note= "O-glycosylated with an alpha-mannose residue"

PN W09829132-A1

PD 09-JUL-1998.

PF 29-DEC-1997; 97WO-US24189.

PR 31-DEC-1996; 96US-0034003.

PA (UYNX) UNIV NEW YORK STATE.

PI Belisle JT, Laal S, Zolla-Pazner S;

DR WPI; 1998-387787/33

PT Early detection of mycobacterial infection - by testing a biological
PT fluid sample from a subject for the presence of antibodies reactive
PT with Mycobacterium tuberculosis antigens

PS Example 3; Page 71; 170pp; English.

CC Sequences AAW70109, AAW70115-W70141 are N-terminal amino acid sequences of glycopeptides, or non-glycosylated peptides generated by subtilisin digestion of the 45 kDa MPR 32 glycoprotein. These sequences were CC obtained by purifying the 45 kDa protein, digesting it with subtilisin, CC and then separating the products by reversed-phase HPLC on a column. CC This digestion yielded 26 peptides, of which five were found to be

CC glycosylated (AAW70109, AAW70115, AAW70120, AAW70126, and AAW70128). All
 CC of the peptides were subjected to both Fast Atom Bombardment-Mass
 CC Spectrometry (FAB-MS), and automated Edman degradation to determine their
 CC molecular weight and N-terminal amino acid sequence, respectively. The
 CC discovery of the complete primary structure of MPT 32 glycoprotein
 CC enables further work to be performed and the possibility of it being used
 CC as an antigen for the early detection of mycobacterial disease.

SQ Sequence 11 AA:

Query Match 55.6%; Score 5; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVPAP 7
 11111
 Db 1 tpvap 5

RESULT 17
 AAB72848
 ID AAB72848 standard; Protein; 11 AA.

AC AAB72848;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Human p53 A76T mutated peptide.

XX Human; p53 mutation; mutant; muten; gene therapy; supertransactivating;
 KM cancer.

OS Homo sapiens.
 OS Synthetic.

PN WO200109325-A2.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-US20538.

PR 30-JUL-1999; 99US-014634.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Resnick MA, Inga A;

DR WPI; 2001-123321/13.

XX New isolated mutated human p53 polypeptides for inducing toxicity in a
 PT cell, treating cancer and identifying compounds that mimic toxic or
 PT supertransactivating mutations -

PS Claim 6; Page -; 144pp; English.

CC The present invention provides a number of peptides derived from the
 CC human p53 protein and containing specific mutations. These are useful for
 CC isolating supertransactivating and toxic p53 mutants, and for inhibiting
 CC cell growth and treating cancer. The present sequence is a peptide
 CC derived from the wild-type human p53 protein shown in AAB72878.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from that given in Genbank acc. no. X02469 (see AAB72878).

SQ Sequence 11 AA:

Query Match 55.6%; Score 5; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
 11111

Db 3 pvapt 7

RESULT 18

AAW82295
 ID AAW82295 standard; Peptide; 20 AA.

AC AAW82295;

DT 15-MAR-1999 (first entry)

DE Dynamin 41.20 zelan120 peptide.

XX Targeting agent; gastrointestinal tract; brain; drug delivery;
 KM drug targeting; phage display; dynamin II; human.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 1 /note="N-terminal dansyl group"

PN WO951825-A1.

PD 19-NOV-1998.

PF 15-MAY-1998; 98WO-US10079.

PR 15-MAY-1997; 97US-0857046.

PA (CYNO-) CYTOGEN CORP.

PA (ELAN-) ELAN CORP PLC.

PI Alvarez VL, O'Mahony DJ, Seveso M;

DR WPI; 1999-009778/01.

XX New targeting agents enabling transport of active agents through
 PT human/animal tissue, or their uptake - useful in the treatment and
 PT prevention of diseases, especially of the gastro-intestinal tract
 PT (GIT)

PS Example 4; Page 53; 83pp; English.

XX This dansylated peptide, termed dynamin 41.20 zelan120 peptide,
 CC is a truncated fragment of dynamin 41.2 zelan086 peptide (see
 CC AAW82294). Dynamin 41.2 is derived from human dynamin II and shows
 CC homology to peptide 41.1 (see AAW82293), which was isolated from a
 CC phage display library and shown to have the ability to enhance
 CC transport of active agents from the gastrointestinal tract (GIT) to
 CC brain. Dynamin 41.2 and peptide fragments of it (see AAW82295-97)
 CC were compared with peptide 41.1 for their ability to enhance
 CC transport of PLGA particles in vivo and in vitro. The invention
 CC relates to targeting agents capable of permitting or facilitating
 CC transport of an active agent through human or animal GIT tissue.
 CC The targeting agents are peptides (see AAW82286-93), or their
 CC derivatives (e.g. fragments, see AAW82300-10) and peptidomimetics,
 CC and the nucleotide sequences coding for them (see AAV73312-19). They
 CC have use in facilitating transport of active agents from the GIT
 CC lumen into the systemic blood system and/or in targeting active
 CC agents to the GIT. Preferably, the active agent is a drug or
 CC drug-containing nanoparticle or microparticle.

SQ Sequence 20 AA:

Query Match 55.6%; Score 5; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 11111

Db 5 vslpv 9

RESULT 19
AAW82310
ID AAW82310 standard; Peptide: 23 AA.
XX
AC AAW82310;
XX
DT 15-MAR-1999 (first entry)
XX
DE Transport peptide fragment.
XX
KM Targetting agent; gastrointestinal tract; brain; drug delivery;
KW drug targetting; dynamini; human; transport peptide.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9851825-A1.
XX
PD 19-NOV-1998.
XX
PF 15-MAY-1998; 98WO-US10079.
XX
PR 15-MAY-1997; 97US-0857046.
XX
PA (CYTO-) CYTOGEN CORP.
PA (ELAN-) ELAN CORP PLC.
XX
PI Alvarez VL, O'Mahony DJ, Seveso M;
XX
DR WPI; 1999-009778/01.
XX
PT New targetting agents enabling transport of active agents through
PT human/animal tissue, or their uptake - useful in the treatment and
PT prevention of diseases, especially of the gastro-intestinal tract
PT (GIT)
XX
PS Claim 10; Page 66; 83pp; English.
XX
CC This is a fragment of dynamin 41.2 (see AAW82294), a peptide derived
CC from human dynamin II. Claimed transport or uptake targetting
CC agents can include this, or other, claimed peptide fragments (see
CC AAW82300-10). Such transport or targetting agents permit or
CC facilitate the transport of an active agent through a human or
CC animal tissue such as gastrointestinal tract lumen, or uptake of
CC the active agent into the human or animal tissue. The active agent
CC is preferably a drug or drug-containing nanoparticle or
CC microparticle. Therapeutic methods of administration,
CC pharmaceutical compositions and formulations based of the
CC targetting peptides are also provided.
XX
SQ Sequence 23 AA:

Query Match 55.6%; Score 5; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
XX |||||
DB 5 vslpv 9

RESULT 20
AAW79982
ID AAW79982 standard; peptide: 25 AA.
XX
AC AAW79982;
XX
DT 01-MAY-1996 (first entry)
XX

DE Signal transduction regulatory tyrosine kinase SH3 binding peptide.
XX
KW Signal transduction; src-family thymidine kinase; lipid kinase;
KW tyrosine kinase; adaptor; inhibition; regulation; immunodeficiency;
KW allergy; inflammation; cancer; autoimmune disease; Epstein-Barr virus;
KW immunoproliferative disease; bovine leukaemia virus; EBV; BLV;
KW chronic fatigue syndrome; infectious mononucleosis.
XX
OS Homo sapiens.
XX
PN WO9524915-A1.
XX
PD 21-SEP-1995.
XX
PF 17-MAR-1995; 95WO-US03438.
XX
PR 17-MAR-1994; 94US-0215116.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Cambler JC, Clark MR, Pleiman CM;
XX
DR WPI; 1995-336809/43.
XX
PT Regulation of signal transduction pathways, esp. involving
PT src-family thymidine kinase - useful for treatment of allergic and
PT inflammatory responses
XX
PS Claim 10; Page 101; 131pp; English.
XX
CC AAW79982-83 are signal transduction regulatory ARH1 peptides. They
CC bind the SH3 domain of src family tyrosine kinases. ARH1 regulatory
CC peptides are capable of regulating the activity of tyrosine kinases,
CC lipid kinases, thymidine kinases and adaptor molecules. They can be
CC used in a method to regulate signal transduction in such cells as
CC B cells, T cells, macrophages, dendritic cells and pluripotent stem
CC cells. The method allows regulation and treatment of allergic and
CC inflammatory responses, autoimmune disease, immunodeficiency and
CC immunoproliferative diseases, cancer and disease caused by
CC Epstein-Barr and bovine leukaemia viruses.
XX
SQ Sequence 25 AA:

Query Match 55.6%; Score 5; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
XX |||||
DB 16 tpvap 20

RESULT 21
AAW78130
ID AAW78130 standard; Protein: 27 AA.
XX
AC AAW78130;
XX
DT 13-APR-1999 (first entry)
XX
DE Human secreted protein encoded by gene 5 clone HPBD36.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.

```

XX Key Location/Qualifiers
FH Misc-difference 27
FT /label= unknown
XX
XX MO9856804-A1.
XX
XX 17-DEC-1998.
XX
XX 11-JUN-1998; 98WO-US12125.
XX
XX 02-OCT-1997; 97US-0061060.
XX 13-JUN-1997; 97US-0049547.
XX 13-JUN-1997; 97US-0049548.
XX 13-JUN-1997; 97US-0049549.
XX 13-JUN-1997; 97US-0049550.
XX 13-JUN-1997; 97US-0049606.
XX 13-JUN-1997; 97US-0049607.
XX 13-JUN-1997; 97US-0049608.
XX 13-JUN-1997; 97US-0049609.
XX 13-JUN-1997; 97US-0049610.
XX 13-JUN-1997; 97US-0049611.
XX 13-JUN-1997; 97US-0050366.
XX 13-JUN-1997; 97US-0050901.
XX 08-JUL-1997; 97US-0052989.
XX 18-AUG-1997; 97US-0055984.
XX 12-SEP-1997; 97US-0058665.
XX 12-SEP-1997; 97US-0058666.
XX 12-SEP-1997; 97US-0058669.
XX 12-SEP-1997; 97US-0058750.
XX 12-SEP-1997; 97US-0058971.
XX 12-SEP-1997; 97US-0058972.
XX 12-SEP-1997; 97US-0060834.
XX 02-OCT-1997; 97US-0060841.
XX 02-OCT-1997; 97US-0060844.
XX 02-OCT-1997; 97US-0060865.
XX 02-OCT-1997; 97US-0061059.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;
PI Moore PA, NI J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
PI Yu GL;
XX WPI: 1999-080881/07.
XX N-PSDB; AAX04315.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 11; Page 266; 380pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin Fc
XX portion (e.g. AAX04302) for increasing the stability of the fused
XX protein as compared to the human protein only.
XX The invention relates to 86 novel genes and their fragments (nucleic
XX acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 86
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAX04311 for described uses).
XX
XX Sequence 27 AA:
SQ

```

Query Match 55.6%; Score 5; DB 20; Length 27;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
 |||||
 Db 9 pvapt 13

RESULT 22

AAW82294
 ID AAW82294 standard; Peptide; 43 AA.

AC AAW82294;

DT 15-MAR-1999 (first entry)

DE Dynamin 41.2 Zelman086 peptide.

KW Targetting agent; gastrointestinal tract; brain; drug delivery;
 KW drug targetting; phage display; dynamin II; human.

XX Homo sapiens.
 OS Synthetic.

FT Key. Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal dansyl group"

PN MO9851825-A1.

PD 19-NOV-1998.

PF 15-MAY-1998; 98WO-US10079.

PR 15-MAY-1997; 97US-0857046.

XX (CYTO-) CYTOGEN CORP.

PA (ELAN-) ELAN CORP PLC.

XX Alvarez VL, O'Mahony DJ, Seveso M;

DR WPI: 1999-009778/01.

PT New targetting agents enabling transport of active agents through
 PT human/animal tissue, or their uptake - useful in the treatment and
 PT prevention of diseases, especially of the gastro-intestinal tract
 PT (GIT)

PS Example 4; Page 53; 83pp; English.

XX This dansylated peptide, termed dynamin 41.2 Zelman086 peptide,
 CC is derived from human dynamin II. It shows homology to peptide
 CC 41.1 (see AAW82293), which was isolated from a phage display
 CC library and shown to have the ability to enhance transport of
 CC active agents from the gastrointestinal tract (GIT) to brain.
 CC Dynamin 41.2 and peptide fragments of it (see AAW82295-97) were
 CC compared with peptide 41.1 for their ability to enhance transport
 CC of PLGA particles in vivo and in vitro. The invention relates to
 CC targeting agents capable of permitting or facilitating transport
 CC of an active agent through human or animal GIT tissue. The
 CC targeting agents are peptides (see AAW82286-93), or their derivatives
 CC (e.g. fragments, see AAW82300-10) and peptidomimetics, and the
 CC nucleotide sequences coding for them (see AAV73312-19). They have
 CC use in facilitating transport of active agents from the GIT lumen
 CC into the systemic blood system and/or in targetting active agents
 CC to the GIT. Preferably, the active agent is a drug or
 CC drug-containing nanoparticle or microparticle.

XX Sequence 43 AA:

Query Match 55.6%; Score 5; DB 20; Length 43;

Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSRPV 5
|||||
DB 5 vsrpv 9

RESULT 23
AAV01143
ID AAV01143 standard; Protein; 45 AA.

XX AAV01143;

DT 18-MAY-1999 (first entry)

DE Secreted protein encoded by gene 9 clone HSIDY06.

XX Human; secreted protein; gene therapy; protein therapy; tissue; cancer;
KW tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS;
KW developmental abnormality; foetal deficiency; Alzheimer's disease;
KW cognitive disorder; schizophrenia; immunological disorder; mood disorder;
KW immune deficiency disease; respiratory disorder; arthritis; skeletal;
KW haematopoietic disorder; neural; osteoporosis; metabolic disorders;
KW cardiovascular; endocrine; gastrointestinal; asthma; diagnosis.

XX Homo sapiens.

PN W09901020-A2.

XX 14-JAN-1999.

PF 30-JUN-1998; 98WO-US13608.

XX 12-SEP-1997; 97US-0058663.

PR 01-JUL-1997; 97US-0051381.

PR 01-JUL-1997; 97US-0051480.

PR 12-SEP-1997; 97US-0058598.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Carter KC, Endress GA, Feng P, Rosen CA, Ruben SM;

DR WPI: 1999-105663/09.

DR N-PSDB; AAX22119.

XX New isolated human genes and the secreted polypeptides they encode -

PT useful for diagnosis and treatment of e.g. cancers, neurological

PT disorders, immune diseases, immune deficiency diseases or blood

PT disorders

XX Claim 11; Page 146; 179pp; English.

XX The invention relates to nucleic acid sequences (AAX22111 to AAX22134)

XX encoding human secreted proteins (AAV01135 to AAV01158). The secreted

XX protein gene sequences are deposited with the ATCC under deposit number

XX ATCC 209118. Host cells comprising recombinant vectors containing the

XX nucleic acid sequences are used for the recombinant production of the

XX secreted proteins. The polynucleotide and amino acid sequences are useful

XX for are useful for preventing, treating or ameliorating medical

XX conditions e.g. by protein or gene therapy. Pathological conditions can

XX be also diagnosed by determining the amount of the new polypeptides in a

XX sample or by determining the presence of mutations in the new

XX polynucleotides. Specific uses are described for each of the

XX polynucleotides, based on which tissues they are most highly expressed

XX in, and include developing products for the diagnosis or treatment of

XX cancer, tumours, developmental abnormalities and foetal deficiencies,

XX autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders,

XX schizophrenia, immunological disorders, immune deficiency diseases

XX (AIDS), mood disorders, respiratory disorders, arthritis, asthma,

XX haematopoietic disorders, neural disorders, skeletal disorders,

XX osteoporosis, metabolic disorders, cardiovascular disorders, endocrine

XX disorders or gastrointestinal disorders. The polypeptides are also useful

CC for identifying their binding partners. The present sequence represents a
CC human secreted protein (see descriptor line for gene number and clone
CC identification).

XX Sequence 45 AA;

Query Match 55.6%; Score 5; DB 20; Length 45;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
DB 33 tpvap 37

RESULT 24

AAAB33087
ID AAB33087 standard; Protein; 48 AA.

XX AAB33087;

DT 25-JAN-2001 (first entry)

DE Pinus radiata transcription factor protein sequence #214.

XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;

XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;

XX basic helix-loop-helix zipper; homeotic; homeobox; MADS;

XX homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain;

XX type 2 Cys2His2; CCAAT box element; MYB.

XX Pinus radiata.

XX WO200053724-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US06112.

XX 11-MAR-1999; 99US-0266513.

XX 18-AUG-1999; 99US-0149485.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX WOOD M, McGrath A, Shenk MA, Glenn M;

XX WPI: 2000-579369/54.

XX New isolated polynucleotide encoding a plant transcription factor for

XX producing a plant e.g. a woody plant, preferably eucalyptus or pine,

XX having modified gene expression or modified activity of a polypeptide

XX -

XX Claim 8; Page 422; 747pp; English.

XX The present invention relates to novel plant transcription factors from

XX Eucalyptus grandis or Pinus radiata. The present sequence is one such

XX transcription factor. The transcription factor may be used to produce a

XX plant having modified gene expression such as a woody plant e.g. a

XX eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or

XX to modify the activity of a polypeptide in a plant. The transcription

XX factors of the present invention are members from the following families

XX of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic

XX helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain

XX zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2

XX Cys2His2, CCAAT box elements and MYB.

XX Sequence 48 AA;

Query Match 55.6%; Score 5; DB 21; Length 48;

Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
|||||
Db 24 stpva 28

RESULT 25

AAB44975
ID AAB44975 standard; Protein: 57 AA.

XX AAB44975;

DT 12-FEB-2001 (first entry)

DE Human secreted protein encoded by gene 7 homologue.

XX Secreted protein: human; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; gene therapy; treatment; autoimmune disease; infection;
KW cardiovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; epithelial cell proliferation; skin aging; mental state;
KW transplantation; metabolism modulation.

XX Homo sapiens.

XX WO200055200-A1.

XX 21-SEP-2000.

PD 09-MAR-2000; 2000WO-US06042.

PE 12-MAR-1999; 99US-0124143.

PR 03-DEC-1999; 99US-0168663.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

DR WPI; 2000-656008/63.

PT Isolated human secretory proteins, nucleic acids encoding them and
PT antibodies directed against them, useful for diagnosing and treating
PT disorders related to the proteins such as cancer, Alzheimer's disease
PT and Parkinsons -

PS Disclosure; Page 405-406; 453pp; English.

XX This invention describes a novel isolated polypeptide (I) and its
CC encoding nucleic acid molecule (II) which have immunosuppressive,
CC antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant,
CC vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,
CC virucide, fungicide and ophthalmological activity and which can be used
CC for gene therapy. (I) and (II) are used to prevent, treat or ameliorate
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. (I) and (II) are also used in diagnosing a
CC pathological condition or susceptibility to a pathological condition. The
CC antibodies to (II) can also be used in alleviating symptoms associated
CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays
CC or enzyme linked immunosorbent assays (ELISA). Disorders which are
CC diagnosed or treated include autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides are used to
CC modulate mammalian metabolism, to change mammal's mental state or

CC physical state by influencing biorhythms circadian rhythms, depression
CC tendency for violence tolerance for pain, reproductive capabilities,
CC hormonal or endocrine levels, appetite, libido, memory, stress or other
CC cognitive qualities, as a food additive or preservative, such as to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrates, vitamins, minerals, cofactors or other nutritional
CC components.

XX Sequence 57 AA;

Query Match 55.6%; Score 5; DB 21; Length 57;

Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
|||||
Db 29 vstpv 33

RESULT 26

AAB44976
ID AAB44976 standard; Protein: 59 AA.

XX AAB44976;

DT 12-FEB-2001 (first entry)

DE Human secreted protein encoded by gene 7 homologue.

XX Secreted protein: human; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; gene therapy; treatment; autoimmune disease; infection;
KW cardiovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; epithelial cell proliferation; skin aging; mental state;
KW transplantation; metabolism modulation.

XX Homo sapiens.

XX WO200055200-A1.

XX 21-SEP-2000.

PD 09-MAR-2000; 2000WO-US06042.

PE 12-MAR-1999; 99US-0124143.

PR 03-DEC-1999; 99US-0168663.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

DR WPI; 2000-656008/63.

PT Isolated human secretory proteins, nucleic acids encoding them and
PT antibodies directed against them, useful for diagnosing and treating
PT disorders related to the proteins such as cancer, Alzheimer's disease
PT and Parkinsons -

PS Disclosure; Page 406; 453pp; English.

XX This invention describes a novel isolated polypeptide (I) and its
CC encoding nucleic acid molecule (II) which have immunosuppressive,
CC antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant,
CC vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,
CC virucide, fungicide and ophthalmological activity and which can be used
CC for gene therapy. (I) and (II) are used to prevent, treat or ameliorate
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. (I) and (II) are also used in diagnosing a
CC pathological condition or susceptibility to a pathological condition. The
CC antibodies to (II) can also be used in alleviating symptoms associated
CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays

or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides are used to modulate mammalian metabolism, to change mammal's mental state or physical state by influencing biorythms circadian rhythms, depression tendency for violence tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, stress or other cognitive qualities, as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrates, vitamins, minerals, cofactors or other nutritional components.

Sequence 59 AA:

Query Match 55.6%; Score 5; DB 21; Length 59;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSRPV 5
|||||
DB 31 vsrpv 35

RESULT 27
AAB39069
ID AAB39069 standard; Protein; 72 AA.

AC AAB39069;
DT 02-FEB-2001 (first entry)
XX Human secreted protein BLAST search protein SEQ ID NO: 159.
DE Human secreted protein BLAST search protein SEQ ID NO: 159.
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vlnenar; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW candidant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX Homo sapiens.
OS Homo sapiens.
PN WO200056880-A1.
XX 28-SEP-2000.
PD 16-MAR-2000; 2000WO-US06781.
XX 19-MAR-1999; 99US-0125363.
PR 08-DEC-1999; 99US-0169617.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Ruben SM, Komatsoulis G;
XX WPI; 2000-602220/57.
DR Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating disorders such as Parkinson's and
PT Alzheimer's diseases, cancers and infections -
XX Disclosure; Pages 409-410; 422pp; English.
PS The invention relates to the isolation of genes AAC59679-C59728 encoding
CC the human secreted proteins AAB38971-B39020. This sequence represents a

peptide fragment homologous to the protein encoded by the gene isolated in the present invention. The sequence is a search result from a BLASTX CC homology search. The genes and proteins are useful for preventing, CC ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed CC in the specification. The nucleic acids, proteins, antibodies and CC (ant)agonists are useful in the diagnosis, treatment and prevention of: CC (a) cancer, e.g. breast and ovarian cancer, and other cancers of the CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, CC lung, or urogenital; (b) immune disorders e.g. Addison's disease, CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid CC arthritis and ulcerative colitis; (c) cardiovascular disorders such CC as myocardial ischaemias; (d) wound healing; (e) neurological diseases CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such CC as viral, bacterial, fungal and parasitic infections.

Sequence 72 AA:

Query Match 55.6%; Score 5; DB 21; Length 72;
Best Local Similarity 100.0%; Pred. No. 12e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSRPV 5
|||||
DB 34 vsrpv 38

RESULT 28
AAV27569
ID AAV27569 standard; Protein; 87 AA.

AC AAV27569;
DT 30-JUL-1999 (first entry)
XX Human secreted protein encoded by gene No. 3.
DE Human secreted protein encoded by gene No. 3.
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX Homo sapiens.
OS Homo sapiens.
PN WO924836-A1.
XX 20-MAY-1999.
PD 04-NOV-1998; 98WO-US23435.
XX 17-NOV-1997; 97US-0066100.
PR 07-NOV-1997; 97US-0064900.
PR 07-NOV-1997; 97US-0064908.
PR 07-NOV-1997; 97US-0064911.
PR 07-NOV-1997; 97US-0064912.
PR 07-NOV-1997; 97US-0064983.
PR 07-NOV-1997; 97US-0064984.
PR 07-NOV-1997; 97US-0064985.
PR 07-NOV-1997; 97US-0064987.
PR 07-NOV-1997; 97US-0064988.
PR 17-NOV-1997; 97US-0066090.
PR 17-NOV-1997; 97US-0066094.
PR 17-NOV-1997; 97US-0066095.
PR 17-NOV-1997; 97US-0066089.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX

PI Carter KC, Ebner R, Endress GA, Feng P, Janat F;
 PI Kyaw H, Lafleur DM, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Wei Y;
 XX WPI: 1999-337740/28.
 DR N-PSDB; AAX84935.
 XX
 PT New human secreted proteins and coding sequences useful for treating
 PT disorders of the immune system and hyperproliferative disorders
 PS
 XX Claim 11: Page 350; 507pp: English.
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAX84924) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 125 novel genes and their fragments (nucleic
 CC acid sequences: AAX84933-85057; amino acid sequences AAY27567-Y27933)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 125
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAX84933 for described uses).
 CC
 XX Sequence 87 AA:
 S0
 Query Match 55.6%; Score 5; DB 20; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PVAPT 8
 |||||
 Db 60 pvapt 64
 RESULT 29
 AAB41518
 ID AAB41518 standard; Protein: 89 AA.
 XX
 AC AAB41518:
 XX
 DT -08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF1282 polypeptide sequence SEQ ID NO:2564.
 XX
 KW Human: open reading frame; ORFX: detection; cytosolic; hepatotropic;
 KW vulnery; antiparasitic; antiparkinsonian; noctropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antineoplastic;
 KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antineoplastic disease; coagulation;
 KW thrombosis; contraceptive.
 KW
 XX Homo sapiens.
 OS
 XX
 PN MO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000MO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 XX

PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI: 2000-602362/57.
 DR N-PSDB; AAC75727.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 PS
 XX Claim 11: Page 1830; 5507pp: English.
 CC AACT74446 to AACT77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytosolic; hepatotropic; vulnery;
 CC antiparasitic; antiparkinsonian; noctropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antineoplastic; antibacterial; antiviral; antifungal; antineumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antineoplastic disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 XX Sequence 89 AA:
 S0
 Query Match 55.6%; Score 5; DB 21; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSTPV 5
 |||||
 Db 19 vstpv 23
 RESULT 30
 AAR47117
 ID AAR47117 standard; peptide: 94 AA.
 XX
 AC AAR47117:
 XX
 DT 30-JUN-1994 (first entry)
 XX
 DE Complete sequence of human prostatic inhibin peptide.
 XX
 KW Prosthetic inhibin peptide; cancer; adenocarcinoma; breast cancer;
 KW hyperplasia; PIF; follicle stimulating hormone; FSH; tumour;
 KW inhibition; prostate cancer; gastrointestinal tract.
 KW
 XX Homo sapiens.
 OS
 XX
 PN MO9325224-A.
 XX
 PD 23-DEC-1993.
 XX
 PF 16-JUN-1993; 93MO-CA00252.
 XX

PR 16-JUN-1992; 9205-0899535.
XX
XX (VETR-) VETROGEN CORP.
XX
PI Garde S, Panchal CJ, Sheth AR;
XX WPI: 1994-007191/01.
XX
PT Prepn. contg. prostatic inhibin peptide or analogues - used for
PT treating benign prostatic hyperplasia, adenocarcinoma or diseases
PT with high FSH levels
PS Disclosure; Figure 1; 48pp; English.
XX
XX Peptides or analogues of prostatic inhibin peptide (PIP) are used
CC in a pharmaceutical preparation for treating patients with benign
CC prostatic hyperplasia or adenocarcinoma, particularly adenocarcinoma
CC of the prostate or gastrointestinal tract or breast cancer. The
CC preparation can also be used to treat patients with diseases
CC characterised by elevated levels of follicle stimulating hormone
CC (FSH). The PIP and its analogues inhibit tumour growth and decrease
CC FSH levels without adversely affecting testosterone levels.
XX
SQ Sequence 94 AA:

Query Match 55.68; Score 5; DB 15; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTRPV 5
| | | | |
DB 53 vslpv 57

RESULT: 31
AAG54394
ID AAG54394 standard; Protein; 98 AA.
XX
AC AAG54394;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69351.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
PD 06-SEP-2000.
XX
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123588.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.

PR 30-APR-1999; 9905-0132407.
PR 04-MAY-1999; 9905-0132484.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 06-MAY-1999; 9905-0132487.
PR 07-MAY-1999; 9905-0132683.
PR 11-MAY-1999; 9905-0134256.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 14-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 10-JUN-1999; 9905-0138847.
PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 26-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144884.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.

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PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 27-AUG-1999; 99US-0151303.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.

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PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 55.6%; Score 5; DB 21; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 2 SRPVA 6
DB 69 SRPVA 73

RESULT 32
AAV82898
ID AAV82898 standard; Protein; 101 AA.
XX
AC AAV82898;
XX
DT 24-JUL-2000 (first entry)
XX
DE CUB domain from BMP-1 protein of mouse.
XX
KM BPC-1; oncogene; oncogenic; cancer; prostate; bladder; antibody;
KM antisenese; vaccine; detection; prognosis; drug screening; BMP-1;
KM mouse.
XX
OS Mus musculus.
XX
PN WO200009691-A2.
XX
PD 24-FEB-2000.
XX
PF 10-AUG-1999; 99WO-US18250.
XX
PR 10-AUG-1999; 98US-0095982.
XX
PA (UROG-) UROGENESYS INC.
PA (AFAR/) AFAR D E.
PA (HUBE/) HUBERT R S.
PA (LEON/) LEONG K.
PA (RATT/) RATTANO A B.
PA (SAFE/) SAFEFAN D C.
PA (JAKO/) JAKOBOVITS A.
XX
PI Afar DE, Hubert RS, Leong K, Rattano AB, Safiran DC, Jakobovits A;
XX
XX WPI, 2000-206006/18.
XX
XX New isolated BPC-1 polypeptides, useful for developing products for the
XX diagnosis, staging, prognosis and treatment of cancers, particularly
XX prostate or bladder cancer
XX
XX Disclosure: Figure 3; 79pp; English.
XX
XX BPC-1 polypeptides and polynucleotides can be used for the detection
XX of BPC-1 polypeptides and polynucleotides in biological samples, this
XX is particularly useful for detecting cancers expressing BPC-1, e.g.

```

CC prostate cancer or bladder cancer. Antibodies directed against BPC-1
CC or antisense polynucleotides can be used for treating such cancers.
CC The BPC-1 polypeptides can also be used in vaccines for treating or
CC inhibiting the development of a cancer expressing BPC-1. The
CC polypeptides and polynucleotides can also be used for detection,
CC prognosis, drug screening and predicting susceptibility to developing
CC cancer. In normal human tissues BPC-1 is only expressed in certain
CC tissues of the brain, however, it is expressed at high levels in
CC prostate cancer cells and bladder cancer cells. The BPC-1 polypeptide
CC comprises a CUB domain which is expressed in prostate and bladder
CC carcinoma cells and which shows sequence similarity with CUB domains
CC from other known proteins. This is a CUB domain from the BMP-1
CC protein of a mouse. It shows 36.3% identity with the
CC BPC-1 CUB domain 3 in 102 residues overlap.
XX
XX

SO Sequence 101 AA;

Query Match 55.6%; Score 5; DB 21; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPRO 9
| | | | |
Db 23 vapro 27

RESULT 33

AAB72875
ID AAB72875 standard; Protein: 102 AA.

XX AAB72875;

DT 09-MAY-2001 (first entry)

XX Human p53 A76T/V122A mutated peptide.

DE Human p53 mutation; mutant; mutelin; gene therapy; supertransactivating;
XX cancer.

XX Homo sapiens.

OS Synthetic.

XX WO200109325-A2.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-US20538.

XX 30-JUL-1999; 99US-0146634.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Resnick MA, Inga A;

XX WPI; 2001-123321/13.

PT New isolated mutated human p53 polypeptides for inducing toxicity in a
PT cell, treating cancer and identifying compounds that mimic toxic or
PT supertransactivating mutations -
XX

PS Claim 33; Page -: 144pp; English.

CC The present invention provides a number of peptides derived from the
CC human p53 protein and containing specific mutations. These are useful for
CC isolating supertransactivating and toxic p53 mutants, and for inhibiting
CC cell growth and treating cancer. The present sequence is a peptide
CC derived from the wild-type human p53 protein shown in AAB72878.
CC Note: The present sequence is not shown in the specification but is
CC derived from that given in Genbank acc. no. X02469 (see AAB72878).
XX

SO Sequence 102 AA;

Query Match 55.6%; Score 5; DB 22; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
| | | | |
Db 23 pvapt 27

RESULT 34

AAW56088
ID AAW56088 standard; Protein: 104 AA.

XX AAW56088;

DT 17-AUG-1998 (first entry)

XX Murine monocytic chemoattractant protein 5.

DE Murine; mouse; monocytic chemoattractant protein; MCP-4; MCP-5; chemokine;
XX immune response; cancer; AIDS; malaria; parasitic infection.
XX

XX Mus spretus.

XX WO9814573-A1.

XX 09-APR-1998.

XX 30-SEP-1997; 97WO-US17900.

XX 30-SEP-1996; 96US-0027128.

XX (GEHO) GEN HOSPITAL CORP.

XX Garcia-Zepeda E, Luster AD, Sarafi M;

XX WPI; 1998-240080/21.

XX N-PSDB; AAV28592.

PT Monocyte chemoattractant proteins, MCP-4 and MCP-3 - used to develop
PT products for treating e.g. cancers, infections, asthma, cystic
PT fibrosis, rhinitis, atherosclerosis or inflammatory bowel disease
XX
XX Claim 25; Page 54; 106pp; English.

CC The present sequence represents murine monocytic chemoattractant protein 5
CC (MCP-5). The MCP-4 and MCP-5 have activity in stimulating chemotactic
CC activity. The proteins can be used for treating cancers, e.g. a
CC lymphoma (e.g. Hodgkin's lymphoma), a plasmacytoma, a melanoma, a
CC sarcoma, a tumour within the lung or gastrointestinal tract, or
CC infectious disease such as AIDS or malaria. Antagonists to the proteins
CC can be used for treating e.g. asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis, sinusitis, rhinitis, atherosclerosis,
CC glomerulonephritis, multiple sclerosis, inflammatory bowel disease,
CC arthritis or adult respiratory distress syndrome. Infections such as
CC parasitic infections may also be treated with a molecule that inhibits
CC MCP-4 or MCP-5 expression.
XX

SO Sequence 104 AA;

Query Match 55.6%; Score 5; DB 19; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
| | | | |
Db 27 vstpv 31

RESULT 35

AAW57322

ID AAW57322 standard; Protein; 104 AA.
XX
AC AAW57322;
XX
DT 11-AUG-1998 (first entry)
XX
DE Mouse monocytic chemotactic protein 5.
XX
KM Mouse; murine; monocytic chemotactic protein 5; MCP-5; mMCP-5; diagnosis;
KM Immune system disorder; Infection; Inflammation; allergy; tumour;
KW cardiovascular disease.
XX
OS Mus sp.
XX
PN WO9812324-A1.
XX
PD 26-MAR-1998.
XX
PF 11-SEP-1997; 97WO-US16105.
XX
PR 08-NOV-1996; 96US-0744419.
PR 18-SEP-1996; 96US-0026882.
XX
PA (BLOO-) CENT BLOOD RES INC.
XX
PI Gonzalo J, Gutierrez-Ramos J;
XX
DR WPI: 1998-217264/19.
DR N-PSDB: AAV30789, AAV30790.
XX
XX
PT Monocyte chemotactic protein-5 - used to develop products for
PT treating e.g. immune system disorders, infections, inflammation,
PT allergy, cardiovascular disease or tumours
XX
XX
PS Claim 28; Page 79; 101pp; English.
XX
XX
CC The present sequence represents monocytic chemotactic protein 5 (MCP-5).
CC The MCP-5 protein stimulates chemotaxis of eosinophils, monocytes and
CC lymphocytes, but not neutrophils, and so is likely to be involved with
CC eosinophil-, monocyte- and/or lymphocyte-mediated inflammations.
CC Products of the present invention can be used for treating e.g.
CC bacterial, fungal or parasitic infections of for tumour cell killing,
CC or for promoting wound healing. The products can also be used for
CC limiting an unwanted inflammatory response or an allergic response,
CC e.g. in inflammatory bowel disease, glomerular inflammation, lupus,
CC membranous nephropathy, glomerulo-sclerosis, chronic hepatic
CC inflammation, fibrotic lung disease, idiopathic pulmonary disease,
CC adult respiratory distress syndrome, sarcoidosis, pleural effusions
CC which occur secondary to various diseases, respiratory allergies,
CC asthma, atherosclerosis, cardiovascular disease, arthritis,
CC endometriosis, gingivitis inflammation, inflammatory skin conditions,
CC delayed-type hypersensitivity responses, or allergic inflammation.
CC The products can also be used for detection, diagnosis and drug
CC screening.
XX
SQ Sequence 104 AA:

Query Match 55.6%; Score 5; DB 19; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSRPV 5
Db 27 vscpv 31

RESULT 36
AAG54393
ID AAG54393 standard; Protein; 112 AA.
XX
AC AAG54393;
XX

DT 18-OCT-2000 (first entry)
XX
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69350.
XX
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 27-AUG-1999; 99US-0151066.
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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 55.6%; Score 5; DB 21; Length 112;
Best Local Similarity 100.0%; Pred: No. 1 Be+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
|||||
Db 83 stpva 87

RESULT 37
ID AAY1113 standard; Protein: 114 AA.
XX AAY1113;
AC AAY1113;
XX 08-JUN-1999 (first entry)
DT
DT
XX H. pylori ORF hp6e10363_30517031_f3_3 secreted protein.
DE
XX
XX Vaccine; probe; diagnostic; ORF; cell envelope protein;
KW secreted protein; cytoplasmic protein; cellular protein.
KW
XX

```

OS Helicobacter pylori.
XX
XX MO9824475-A1.
XX
XX 11-JUN-1998.
XX
XX 05-DEC-1997; 97WO-US22104.
XX
XX 14-JUL-1997; 97US-0891928.
XX
XX 05-DEC-1996; 96US-0759625.
XX
XX 25-MAR-1997; 97US-0823745.
XX
XX (ASTR ) ASTRA AB.
XX
XX Alm RA, Castriotta LM, Dolg PC, Kabok Z, Smith D;
XX
XX WPI: 1998-333051/29.
XX
XX N-PSDB; AAX30642.
XX
XX New isolated Helicobacter pylori nucleic acids - used to develop
XX products for the diagnosis, prevention and treatment of infection by
XX H. pylori and other Helicobacter species
XX
XX Claims 37, 41: Page 278-279; 339pp: English.
XX
XX Recombinant or substantially pure preparations of H. pylori polypeptides
XX are disclosed, together with the nucleic acids encoding them. In all,
XX 97 ORFs are shown. The proteins are variously cell envelope proteins,
XX cytoplasmic proteins, secreted proteins or other cellular proteins.
XX Vaccines containing the nucleic acids or proteins are claimed, as are
XX probes containing at least 8 nucleotides from the nucleic acid
XX sequences. The vaccines are useful for treating or reducing the risk of
XX H. pylori infections, and the probes can be used diagnostically for
XX detecting the presence of Helicobacter in a sample. The products are
XX also of use in screening for compounds having the ability to interfere
XX with the H. pylori life cycle or to inhibit H. pylori infection.
XX
XX Sequence 114 AA:
SQ

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Query Match 55.6%; Score 5; DB 19; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 SRPVA 6
   11111
DB 99 srpva 103

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RESULT 38
 AAG03726
 ID AAG03726 standard; Protein; 114 AA.
 XX
 AC AAG03726;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 7807.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.

```

XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI: 2000-500381/45.
XX
XX N-PSDB; AAC03732.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 7807; 71pp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
XX of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
XX were prepared from total human RNAs or polyA+ RNAs derived from 30
XX different tissues. EST sequences usually correspond mainly to the 3'
XX untranslated region (UTR) of the mRNA because they are often obtained
XX from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
XX isolating cDNA sequences derived from the 5' ends of mRNAs and even in
XX those cases where longer cDNA sequences have been obtained, the full 5'
XX UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
XX ends and can therefore be used to obtain full length cDNAs and genomic
XX DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
XX chromosome mapping procedures. They are used to obtain upstream
XX regulatory sequences and to design expression and secretion vectors.
XX
XX Sequence 114 AA:
SQ

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Query Match 55.6%; Score 5; DB 21; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VSTRPV 5
   11111
DB 73 vstrpv 77

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RESULT 39
 AAG54455
 ID AAG54455 standard; Protein; 121 AA.
 XX
 AC AAG54455;
 XX
 DT 18-OCT-2000 (first entry)
 XX
 DE Zea mays protein fragment SEQ ID NO: 69435.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence; corn.
 XX
 OS Zea mays subsp. mays.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
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 PR 05-MAR-1999; 99US-0123180.
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 PR 09-MAR-1999; 99US-0123548.
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 PR 23-MAR-1999; 99US-0125788.
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 PR 25-MAR-1999; 99US-0126264.
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 PR 01-APR-1999; 99US-0127462.
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 PR 06-APR-1999; 99US-0128234.
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 PR 19-APR-1999; 99US-0130077.
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PR 23-APR-1999; 99US-0130891.
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PR 30-AUG-1999; 99US-0151303.
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PR 29-OCT-1999; 99US-0162142.

Query Match 55.6%; Score 5; DB 21; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVPAP 8
Db 64 pvpap 68

RESULT 40
AAB40264
ID AAB40264 standard; Protein: 125 AA.

AC AAB40264;
XX
DT 08-FEB-2001 (first entry)
XX

DE Human ORFX ORF28 polypeptide sequence SEQ ID NO:56.

XX Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
XX vulnerability; antiproliferative; antiparkinsonian; noctropic; neuroprotective;
XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
XX hypotensive; dermatological; immunosuppressive; antineoplastic; antithyroid;
XX antiviral; antibacterial; antifungal; antirheumatic; antihypertensive;
XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
XX cholesterol ester storage; systemic lupus erythematosus; infection;
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
XX bone damage; cartilage damage; antiinflammatory disease; coagulation;
XX thrombosis; contraceptive.

OS Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000MO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach M;
XX

DR WPI, 2000-602362/57.
DR N-PSDB: AAC74473.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
PS
XX Claim 11; Page 449; 5507pp; English.

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytosolic; hepatotropic; vulnerability;
CC antiproliferative; antiparkinsonian; noctropic; neuroprotective;
CC osteopathic; anticonvulsant; antirheumatic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antineoplastic; antithyroid; antiviral; antifungal; antirheumatic;
CC antihypertensive; antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.

SO Sequence 125 AA;

Query Match 55.6%; Score 5; DB 21; Length 125;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
Db 14 tpvap 18

RESULT 41

AAG54454
ID AAG54454 standard; Protein: 125 AA.

XX AAG54454;

XX 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 69434.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence; corn.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 23-APR-1999; 9905-0130891.
PR 28-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.
PR 30-APR-1999; 9905-0132407.
PR 04-MAY-1999; 9905-0132484.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 06-MAY-1999; 9905-0132487.
PR 07-MAY-1999; 9905-0132863.
PR 11-MAY-1999; 9905-0134256.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 14-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 10-JUN-1999; 9905-0138847.
PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140635.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 12-JUL-1999; 9905-0142920.
PR 13-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143562.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.

PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144884.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 02-AUG-1999; 9905-0146389.
PR 03-AUG-1999; 9905-0147038.
PR 04-AUG-1999; 9905-0147204.
PR 04-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147192.
PR 05-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 06-AUG-1999; 9905-0147416.
PR 09-AUG-1999; 9905-0147493.
PR 09-AUG-1999; 9905-0147935.
PR 10-AUG-1999; 9905-0148171.
PR 11-AUG-1999; 9905-0148319.
PR 12-AUG-1999; 9905-0148341.
PR 13-AUG-1999; 9905-0148565.
PR 16-AUG-1999; 9905-0148684.
PR 17-AUG-1999; 9905-0149175.
PR 18-AUG-1999; 9905-0149426.
PR 20-AUG-1999; 9905-0149722.
PR 20-AUG-1999; 9905-0149723.
PR 20-AUG-1999; 9905-0149929.
PR 23-AUG-1999; 9905-0149902.
PR 23-AUG-1999; 9905-0149930.
PR 25-AUG-1999; 9905-0150566.
PR 26-AUG-1999; 9905-0150884.
PR 27-AUG-1999; 9905-0151085.
PR 27-AUG-1999; 9905-0151086.
PR 27-AUG-1999; 9905-0151080.
PR 30-AUG-1999; 9905-0151303.
PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151930.
PR 07-SEP-1999; 9905-0152363.
PR 10-SEP-1999; 9905-0153070.
PR 15-SEP-1999; 9905-0153758.
PR 16-SEP-1999; 9905-0154018.
PR 16-SEP-1999; 9905-0154039.
PR 20-SEP-1999; 9905-0154779.
PR 22-SEP-1999; 9905-0155139.
PR 23-SEP-1999; 9905-0155486.
PR 24-SEP-1999; 9905-0155659.
PR 28-SEP-1999; 9905-0156458.
PR 29-SEP-1999; 9905-0156566.
PR 04-OCT-1999; 9905-0157117.
PR 05-OCT-1999; 9905-0157753.
PR 06-OCT-1999; 9905-0157865.
PR 07-OCT-1999; 9905-0158029.
PR 08-OCT-1999; 9905-0158232.
PR 12-OCT-1999; 9905-0158369.
PR 13-OCT-1999; 9905-0159293.
PR 13-OCT-1999; 9905-0159294.

PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159337.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 55.6%; Score 5; DB 21; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
 |||||
 Db 68 vPAPT 72

RESULT 42

AAM77657
 ID AAM77657 standard; Protein; 130 AA.

AC AAM77657;

DT 30-OCT-1998 (first entry)

DE Staphylococcus aureus protein of unknown function.

KW Staphylococcus aureus protein; immune response induction; eye infection;
 antibody production; T-cell immune response; gastrointestinal infection;
 respiratory infection; inhibitor; bacterial infection; cardiac infection;
 central nervous system; kidney infection; urinary tract infection;
 antimicrobial compound identification; broad spectrum antibiotic;
 therapy.

KM Staphylococcus aureus.

OS Staphylococcus aureus.

FT Key Location/Qualifiers
 FT Misc-difference 1.130 /note="residues designated X are unspecified, and
 represented as Xaa in the specification"

PN EP841394-A2.

PD 13-MAY-1998.

PF 24-SEP-1997; 97EP-0307485.

PR 24-SEP-1996; 96US-0027032.

PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Black MT, Burnham MKR, Hodgson JE, Knowles DJC;
 Lonetto MA, Nicholas RO, Pratt JM, Relchard RM, Rosenberg M;

PI Ward JM;
 XX
 DR WPI: 1998-252940/23.
 DR N-PSDB: AAV53451.
 XX
 PT New nucleic acid sequences from Staphylococcus aureus MCHU29 -
 useful in vaccines and for treatment of bacterial infections of e.g.
 respiratory tract and central nervous system
 XX
 PS Claim 11; Page 312; 390pp; English.
 XX
 CC This sequence represents a Staphylococcus aureus protein of unknown
 function, and is encoded by a DNA sequence of the invention.
 CC The DNA sequences were isolated from Staphylococcus aureus MCHU29
 (NCIMB 40771). Host cells containing the DNA sequences are used to
 produce polypeptides or fragments. The proteins are used in the treatment
 of disease, for inducing an immune response by administering them, to
 produce antibody and/or T-cell immune response. Antagonists of the
 CC proteins are used for the inhibition of bacterial polypeptides.
 CC Conditions which may be treated include bacterial infections, especially
 respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
 CC urinary tract, skin, bones and joints. The proteins can also be used to
 CC identify antimicrobial compounds which are broad spectrum antibiotics,
 especially useful in the treatment of H. pylori infection.
 XX
 SQ Sequence 130 AA;

Query Match 55.6%; Score 5; DB 19; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPTQ 9
 |||||
 Db 108 vAPTQ 112

RESULT 43

AAB53631
 ID AAB53631 standard; Protein; 130 AA.

AC AAB53631;

DT 09-MAR-2001 (first entry)

DE Human colon cancer antigen protein sequence SEQ ID NO:1171.

KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 identification; cytostatic; cardioactive; neuroprotective; vulnerary;
 immunomodulatory; muscular; gynaecological; gastrointestinal;
 immunomodulatory; muscular; gynaecological; gastrointestinal;
 nephrotoxic; anti-infective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.

KM Homo sapiens.

OS Homo sapiens.

PN WO200055351-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US05883.

PR 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI: 2000-587534/55.
 DR N-PSDB: AAC98388.
 PT Colon cancer associated gene sequences, referred to as colon cancer

PT antigens, useful for the treatment, prevention, and diagnosis of colon
XX disorders such as colon cancer -
PS Claim 11; Page 1753; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardiostatic, muscular;
CC neuroprotective, immunomodulatory, gynaecological and antibacterial activities,
CC vulnertropic, nephrotropic, antinfecitive and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAB54007 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 130 AA;
XX
XX
Query Match 55.6%; Score 5; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VSTPV 5
| | | | |
Db 63 vslpv 67
XX
RESULT 44
AAB56449
ID AAB56449 standard; Protein: 132 AA.
XX
AC AAB56449;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1027.
XX
XX Human prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardiostatic; immunomodulatory; muscular;
KW vulnertropic; gastrointestinal; nephrotropic; antinfecitive; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
XX Homo sapiens.
OS
XX
XX WO200055174-A1.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000WO-US05988.
PF
XX
XX 12-MAR-1999; 99US-0124270.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2000-587513/55.
DR
XX
XX N-PSDB; AAF15652.
DR
XX
XX Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX

PS Claim 11; Page 1457; 2338pp; English.
XX
XX AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardiostatic, immunomodulatory, muscular, vulnertropic, gastrointestinal,
CC nephrotropic, antinfecitive, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 132 AA;
XX
XX
Query Match 55.6%; Score 5; DB 21; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VSTPV 5
| | | | |
Db 91 vslpv 95
XX
RESULT 45
AAB43699
ID AAB43699 standard; Protein: 151 AA.
XX
XX
AC AAB43699;
XX
DT 08-FEB-2001 (first entry)
XX
XX
DE Human cancer associated protein sequence SEQ ID NO:1144.
XX
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnertropic; immunomodulatory;
KW antidiabetic; antitumour; antineuritic; antiallergic; antiviral;
KW antinflamatory; antihypoid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nocertropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX
XX Homo sapiens.
OS
XX
XX WO200055350-A1.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000WO-US05882.
PF
XX
XX 12-MAR-1999; 99US-0124270.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2000-587533/55.
DR
XX
XX N-PSDB; AAC77908.
DR
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer -
XX
PS Claim 11; Page 1760-1761; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given
CC

CC In ABA4398 to ABA44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerary; immunomodulator;
CC antidiabetic; antiasmatic; antirheumatic; antarthritic;
CC antiinflammatory; antihypertoid; antiallergic; antibacterial; antiviral;
CC dermatologic; vasotropic; antiproliferative; cardiant; thrombolytic; coagulant;
CC nootropic; vasotropic; antiproliferative; cardiant; thrombolytic; coagulant;
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and ABA44240 represent sequences used in the exemplification of
CC the present invention.

XX Sequence 151 AA:

Query Match 55.6%; Score 5; DB 21; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVPAP 7
| | | | |
DB 50 tpvap 54

RESULT 46

AAG54453
ID AAG54453 standard; Protein; 152 AA.

AC AAG54453;

XX 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 69433.

XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.

XX Zea mays subsp. mays.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 29-MAR-1999; 99US-0126264.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0128845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131445.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
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 DT 30-APR-2001 (first entry)
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 fine chemical production; microorganism; organic acid; nucleoside;
 nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
 lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
 carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
 XX
 OS Corynebacterium glutamicum.
 XX
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XX	(BADI) BASF AG.	
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XX	WPI: 2001-137957/14.	
DR	N-PSDB; AAF72092.	
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PT	pathway proteins, useful for producing fine chemicals in	
PT	microorganisms, including organic acids, nonproteolnogenic amino acids,	
PT	and purine and pyrimidine bases -	
XX		
PS	Claim 20; Page 1107; 1737pp; English.	
XX		
CC	AAE71753 to AAE72330 encode the Corynebacterium glutamicum metabolic	
CC	pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum	
CC	MP nucleic acids are useful for the production of fine chemicals	
CC	in microorganisms, including organic acids, nonproteolnogenic amino	
CC	acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,	
CC	saturated and unsaturated fatty acids, diols, carbohydrates, aromatic	
CC	compounds, vitamins, cofactors, polyketides and enzymes.	
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 PR 09-MAR-2000; 2000US-0187970.
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 PA (BADI) BASF AG.
 PI Pompeius M, Kroegeer B, Schroeder H, Zeider O, Haberhauer G;
 XX WPI; 2001-137957/14.
 DR N-PSDB; AAF72100.
 XX
 PT Nucleic acids from *Corynebacterium glutamicum* encoding metabolic
 PT pathway proteins, useful for producing fine chemicals in
 PT microorganisms, including organic acids, nonproteinogenic amino acids,
 PT and purine and pyrimidine bases -
 PT
 PS Claim 20; Page 1123-1124; 1737pp; English.
 XX
 CC AAF71753 to AAF72330 encode the *Corynebacterium glutamicum* metabolic
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum
 CC MP nucleic acids are useful for the production of fine chemicals
 CC in microorganisms, including organic acids, nonproteinogenic amino
 CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
 CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, cofactors, polyketides and enzymes.
 CC
 XX Sequence 152 AA;
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 Query Match 55.6%; Score 5; DB 22; Length 152;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 115 vslpv 119
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 DT 30-APR-2001 (first entry)
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 KM fine chemical production; microorganism; organic acid; nucleoside;
 KM nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
 KM lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
 KM carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
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 PF 23-JUN-2000; 2000MO-IB00923.
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 PR 14-JUL-1999; 99DE-1033005.
 PR 14-JUL-1999; 99DE-1033006.
 PR 14-JUL-1999; 99US-0148613.
 PR 27-AUG-1999; 99DE-1040764.
 PR 27-AUG-1999; 99DE-1040765.
 PR 27-AUG-1999; 99DE-1040766.
 PR 27-AUG-1999; 99DE-1040832.
 PR 31-AUG-1999; 99DE-1041378.
 PR 31-AUG-1999; 99DE-1041379.
 PR 31-AUG-1999; 99DE-1041380.
 PR 31-AUG-1999; 99DE-1041394.
 PR 31-AUG-1999; 99DE-1041396.
 PR 03-SEP-1999; 99DE-1042076.
 PR 03-SEP-1999; 99DE-1042077.
 PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042086.
 PR 03-SEP-1999; 99DE-1042087.
 PR 03-SEP-1999; 99DE-1042088.
 PR 03-SEP-1999; 99DE-1042095.
 PR 03-SEP-1999; 99DE-1042124.
 PR 03-SEP-1999; 99DE-1042129.
 PR 09-MAR-2000; 2000US-0187970.
 XX
 PA (BADI) BASF AG.
 XX
 PI Pompeius M, Kroegeer B, Schroeder H, Zeider O, Haberhauer G;
 XX WPI; 2001-137957/14.
 DR N-PSDB; AAF72106.
 XX
 PT Nucleic acids from *Corynebacterium glutamicum* encoding metabolic
 PT pathway proteins, useful for producing fine chemicals in
 PT microorganisms, including organic acids, nonproteinogenic amino acids,
 PT and purine and pyrimidine bases -
 PT
 PS Claim 20; Page 1141-1142; 1737pp; English.
 XX
 CC AAF71753 to AAF72330 encode the *Corynebacterium glutamicum* metabolic
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum
 CC MP nucleic acids are useful for the production of fine chemicals
 CC in microorganisms, including organic acids, nonproteinogenic amino
 CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
 CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, cofactors, polyketides and enzymes.
 CC
 XX

SQ Sequence 152 AA;

DB 55 vstpv 59

Query Match 55.6%; Score 5; DB 22; Length 152;

Best Local Similarity 100.0%; Pred. No. 2.4e+02; Search completed: August 15, 2001, 12:35:31

Job time: 156 sec

OY 1 VSTPV 5
|||||
DB 115 vstpv 119

RESULT 50

AAB24690

ID AAB24690 standard; Peptide: 158 AA.

AC AAB24690;

DT 27-NOV-2000 (first entry)

DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:122.

KW Plant; corn; Arabidopsis thaliana; sequence-determined DNA fragment;
SDF; genetic mapping; identification; promoter; structural gene; UTR;
untranslated region; expression control.

OS Plant.

PN WO200040695-A2.

PD 13-JUL-2000.

PE 07-JAN-2000; 2000WO-US00466.

PR 08-JAN-1999; 99US-0115293.

PA (CERE-) CERES INC.

PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L;

DR WPI: 2000-465970/40.

PT New corn plant and Arabidopsis thaliana sequence-determined DNA
PT fragments, useful for expressing gene products and for controlling
PT expression of a target gene -

PS Claim 14; Page 381-382; 673pp; English.

CC The present invention describes polynucleotides, such as complete cDNA
CC sequences and/or sequences of genomic DNA encompassing complete genes,
CC portions of genes, and/or intergenic regions, collectively referred to
CC as sequence-determined DNA fragments (SDFs), from corn plants and
CC Arabidopsis thaliana. The SDFs are promoters, structural genes, and
CC untranslated regions (UTRs), or 3' termination sequences. They can be
CC used for expressing a gene product and controlling expression of a
CC target gene, either as a promoter, a structural gene, an UTR or as a
CC 3' termination sequence. They are also useful as tools for genetic
CC mapping, and identification of a particular individual plant or for
CC clustering a group of plants with a common trait. AAA78433 to AAA78630
CC and AAB24605 to AAB25099 represent the specifically claimed
CC polynucleotide sequences and polypeptides encoded by them given in the
CC present invention.

SQ Sequence 158 AA;

Query Match 55.6%; Score 5; DB 21; Length 158;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 1 VSTPV 5
|||||

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2001, 12:32:55 ; Search time 33.87 Seconds
(without alignments)
20.241 Million cell updates/sec

Title: US-09-372-036-26
Perfect score: 9
Sequence: 1 VSRPVAPTQ 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	484	2 A41487	protein p60 precu
2	6	66.7	102	2 F83231	hypothetical prote
3	6	66.7	155	2 S35162	SRH-21 protein - p
4	6	66.7	187	2 JC4806	core protein G - p
5	6	66.7	218	2 C86847	transcription regu
6	6	66.7	288	2 F71504	hypothetical prote
7	6	66.7	293	2 F75466	hypothetical prote
8	6	66.7	447	2 T34992	probable lipoprote
9	6	66.7	453	1 F64623	amidase - Helicoba
10	6	66.7	453	1 A71891	glu-tRNA amidotran
11	6	66.7	460	2 T23087	hypothetical prote
12	6	66.7	637	2 S66953	hypothetical prote
13	6	66.7	748	2 T49633	glycan 1,4-alpha-g
14	6	66.7	748	2 H84913	probable ATP-depen
15	6	66.7	865	2 A47282	calcium-binding pr
16	6	66.7	1093	2 T50652	AP-3 complex beta3
17	6	66.7	1094	2 T50651	AP-3 complex beta3
18	6	66.7	1105	2 T18295	AP-3 adaptor compl
19	5	55.6	75	2 F75264	hypothetical prote
20	5	55.6	82	2 T29802	hypothetical prote
21	5	55.6	88	2 T34429	hypothetical prote
22	5	55.6	103	1 K4RB	Ig kappa-B4 chain
23	5	55.6	104	2 F53275	beta-microseminopr
24	5	55.6	114	2 A34567	methylnalonyl-CoA
25	5	55.6	115	2 B49094	conserved hypotnet
26	5	55.6	117	2 A72293	hypothetical prote
27	5	55.6	123	2 G71189	lymphocyte antigen
28	5	55.6	126	2 I54454	hypothetical 13.4K
29	5	55.6	128	2 JN0727	

30	5	55.6	132	2 T03397	hypothetical prote
31	5	55.6	134	2 B60497	MHC class II histo
32	5	55.6	141	2 E22580	hypothetical prote
33	5	55.6	147	2 T15036	photosystem I chal
34	5	55.6	161	2 C96568	hypothetical prote
35	5	55.6	162	2 B84018	hypothetical prote
36	5	55.6	165	2 S61230	cytochrome-c blosy
37	5	55.6	170	2 S11770	lama protein - Lis
38	5	55.6	170	2 B83871	hypothetical prote
39	5	55.6	175	2 T50849	hypothetical prote
40	5	55.6	177	1 S57789	hypothetical prote
41	5	55.6	178	1 KRRT	kappa-casein precu
42	5	55.6	178	2 S56300	hypothetical prote
43	5	55.6	179	2 S01400	H+-transporting AT
44	5	55.6	179	2 G84789	hypothetical prote
45	5	55.6	181	2 A05080	kappa-casein precu
46	5	55.6	185	2 D96572	protein P12M16.6 I
47	5	55.6	193	2 H86404	probable lipid tra
48	5	55.6	197	2 D85875	probable minor fil
49	5	55.6	199	2 F86832	hypothetical prote
50	5	55.6	201	2 S69748	hypothetical prote
51	5	55.6	206	2 H83587	conserved hypotnet
52	5	55.6	211	2 T22122	hypothetical prote
53	5	55.6	217	2 S10212	late 33K protein -
54	5	55.6	218	2 G71260	probable ribulose-
55	5	55.6	223	2 G82478	hypothetical prote
56	5	55.6	224	2 A31459	MHC class II histo
57	5	55.6	225	2 F72642	probable shikimate
58	5	55.6	228	2 F75390	hypothetical prote
59	5	55.6	229	1 LCBO	prolactin precurs
60	5	55.6	229	1 LCSH	prolactin - goat
61	5	55.6	229	2 T83982	hypothetical prote
62	5	55.6	241	2 T17798	probable muramidase
63	5	55.6	245	2 F71474	succinate dehydrog
64	5	55.6	251	2 C84036	hypothetical prote
65	5	55.6	252	2 A86449	hypothetical prote
66	5	55.6	260	2 T18909	MHC class II histo
67	5	55.6	261	1 HLH0DB	MHC class II histo
68	5	55.6	261	1 HLH0IC	MHC class II histo
69	5	55.6	261	1 B37044	MHC class II histo
70	5	55.6	261	2 I54480	HLA DQ-beta - huma
71	5	55.6	261	2 T51222	hypothetical prote
72	5	55.6	264	2 C37386	hypothetical prote
73	5	55.6	264	2 S01922	hypothetical prote
74	5	55.6	267	2 T32063	hypothetical prote
75	5	55.6	268	2 D29312	MHC class II histo
76	5	55.6	269	2 I54432	MHC class II histo
77	5	55.6	271	2 T16421	hypothetical prote
78	5	55.6	273	2 F84242	imidazoleglycerol-
79	5	55.6	276	2 S75249	esterase A110992 -
80	5	55.6	276	2 T29894	hypothetical prote
81	5	55.6	282	2 E71662	protein export pro
82	5	55.6	288	2 A81009	hypothetical prote
83	5	55.6	293	2 T35621	hypothetical prote
84	5	55.6	296	2 G84747	AT-hook DNA-bindin
85	5	55.6	298	2 T36900	probable integral
86	5	55.6	299	2 A82063	uroporphyrin-III C
87	5	55.6	302	2 A86841	hypothetical prote
88	5	55.6	303	2 S39611	phosphoprotein pho
89	5	55.6	305	2 B55346	phosphoprotein pho
90	5	55.6	307	1 S75769	hypothetical prote
91	5	55.6	307	2 T24423	hypothetical prote
92	5	55.6	311	2 H8746	hypothetical prote
93	5	55.6	314	2 S22513	ethylene-forming e
94	5	55.6	315	2 T25171	hypothetical prote
95	5	55.6	315	2 T26422	hypothetical prote
96	5	55.6	318	2 T00112	glycosyltransferas
97	5	55.6	319	2 T46145	hypothetical prote
98	5	55.6	321	2 J50772	37K glycoprotein -
99	5	55.6	323	2 A31351	probable transmemb
100	5	55.6	324	2 C83695	quinone oxidoreduc
101	5	55.6	324	2 T24465	hypothetical prote
102	5	55.6	325	1 A45470	hydroxymethylgluta

103	5	55.6	325	2	D70666	probable modb prot	176	5	55.6	471	2	JC1403	glutamate--ammonia
104	5	55.6	331	2	T28694	hypothetical prote	177	5	55.6	473	2	S75141	glutamate--ammonia
105	5	55.6	332	2	T26145	hypothetical prote	178	5	55.6	473	2	H69761	conserved hypochet
106	5	55.6	335	2	T31559	hypothetical prote	179	5	55.6	474	2	T10271	capsid-associated
107	5	55.6	335	2	T31560	hypothetical prote	180	5	55.6	475	2	T44597	conserved hypochet
108	5	55.6	335	2	T31561	hypothetical prote	181	5	55.6	475	2	D86209	protein P2265.18
109	5	55.6	335	2	H75518	probable cytochrom	182	5	55.6	475	2	A85923	hypothetical prote
110	5	55.6	336	1	B38274	y box-binding prot	183	5	55.6	476	2	B44997	merozoite surface
111	5	55.6	337	2	C69124	ribosomal protein	184	5	55.6	476	2	T25736	hypothetical prote
112	5	55.6	339	1	G75529	peptide ABC transp	185	5	55.6	477	2	G71319	hypothetical prote
113	5	55.6	342	2	T45456	probable membrane	186	5	55.6	478	2	JC4880	fibrinolytic metal
114	5	55.6	343	2	T14245	NADH dehydrogenase	187	5	55.6	478	2	A43296	atrolysin E (EC 3.
115	5	55.6	356	1	XNECHC	histidinol-phospha	188	5	55.6	478	2	A32555	major merozoite su
116	5	55.6	356	1	D85827	histidinol-phospha	189	5	55.6	480	1	A30065	trigramin precursor
117	5	55.6	358	2	T35104	probable two-compo	190	5	55.6	481	2	S43125	trigramin precursor
118	5	55.6	359	1	XNEBHC	histidinol-phospha	191	5	55.6	481	2	JC4342	fibrinolytic prote
119	5	55.6	362	2	S24551	protein-tyrosine k	192	5	55.6	482	2	A44997	merozoite surface
120	5	55.6	366	1	MNXRSD	sigma NS protein -	193	5	55.6	482	2	T32564	hypothetical prote
121	5	55.6	366	1	MNXRST	sigma NS protein -	194	5	55.6	488	1	QOBEHS	alkaline exonuclea
122	5	55.6	366	1	MNXRST	sigma NS protein -	195	5	55.6	488	2	T44030	alkaline exonuclea
123	5	55.6	366	2	C27401	sigma NS protein -	196	5	55.6	488	2	T44215	protein P22G5.14
124	5	55.6	366	2	S53073	hypothetical prote	197	5	55.6	488	2	F86209	hypothetical prote
125	5	55.6	367	1	A46355	site-specific DNA-	198	5	55.6	488	2	T30976	hypothetical prote
126	5	55.6	367	2	T18185	probable site-spec	199	5	55.6	498	2	G02421	hypothetical prote
127	5	55.6	368	2	S06058	NADH dehydrogenase	200	5	55.6	500	2	S77243	hypothetical prote
128	5	55.6	368	2	G84769	hypothetical prote	201	5	55.6	501	2	T27513	hypothetical prote
129	5	55.6	372	2	G01425	nucleolar 75K auto	202	5	55.6	504	2	T34995	probable integral
130	5	55.6	375	2	T51333	transcription fact	203	5	55.6	504	2	G02474	interferon regulat
131	5	55.6	376	2	S04497	surface antigen PA	204	5	55.6	505	2	B46629	mucin 6, gastric
132	5	55.6	379	2	A45443	tubulin--tyrosine	205	5	55.6	508	2	T19350	hypothetical prote
133	5	55.6	380	2	B69523	succinyl-CoA synth	206	5	55.6	509	1	S04346	steroid 17alpha-mo
134	5	55.6	380	2	D84214	NADH dehydrogenase	207	5	55.6	509	1	S36572	protein L1
135	5	55.6	383	2	S32975	gene BCRP2 protein	208	5	55.6	510	2	S53970	amido-phosphoribosy
136	5	55.6	386	2	S64614	probable membrane	209	5	55.6	510	2	A45338	conexin-56 - chic
137	5	55.6	390	2	F85048	multidrug resistan	210	5	55.6	512	2	T33463	probable serine ca
138	5	55.6	390	2	F85916	multidrug resistan	211	5	55.6	513	2	D72753	probable xyulose
139	5	55.6	391	2	T51097	thyroid hormone re	212	5	55.6	514	1	P1WL8	L1 protein - human
140	5	55.6	394	2	F69888	alanine racemase h	213	5	55.6	516	1	P1WL5	L1 protein - human
141	5	55.6	394	2	T18752	hypothetical prote	214	5	55.6	517	2	S36496	L1 protein - human
142	5	55.6	402	2	C64895	hypothetical prote	215	5	55.6	517	2	S36496	L1 protein - human
143	5	55.6	402	2	G86117	probable virulence	216	5	55.6	517	2	S36496	L1 protein - human
144	5	55.6	402	2	G85882	probable virulence	217	5	55.6	518	2	S36472	L2 protein - human
145	5	55.6	402	2	JH0403	procollagen I C-pr	218	5	55.6	525	1	P1WL85	L1 protein - human
146	5	55.6	404	2	T35050	hypothetical prote	219	5	55.6	530	1	D83291	probable MFS trans
147	5	55.6	407	2	S66260	metalloproteinase	220	5	55.6	534	2	C69146	hypothetical prote
148	5	55.6	408	2	T37929	probable major fac	221	5	55.6	537	2	E96606	hypothetical prote
149	5	55.6	410	2	D70599	hypothetical prote	222	5	55.6	542	2	T29707	hypothetical prote
150	5	55.6	414	1	HYRSNC	atrolysin C (EC 3.	223	5	55.6	543	2	T00513	cytochrome P450 ho
151	5	55.6	414	2	S41608	atrolysin B (EC 3.	224	5	55.6	543	2	S19933	glycine-rich prote
152	5	55.6	414	2	S41609	atrolysin C (EC 3.	225	5	55.6	543	2	T49892	glycine-rich prote
153	5	55.6	415	2	T20335	hypothetical prote	226	5	55.6	544	2	T20741	hypothetical prote
154	5	55.6	416	2	G69748	conserved hypochet	227	5	55.6	546	2	S36490	carbamoyl-phosphat
155	5	55.6	418	2	F83986	transducer BH2694	228	5	55.6	547	2	B56573	probable enzyme 24
156	5	55.6	420	2	B84788	hypothetical prote	229	5	55.6	550	2	C86704	hypothetical prote
157	5	55.6	421	2	D81098	gcpe protein NMB13	230	5	55.6	553	2	C75318	conserved hypochet
158	5	55.6	421	2	H81843	conserved hypochet	231	5	55.6	556	2	D86262	hypothetical prote
159	5	55.6	422	2	G70984	probable papas pro	232	5	55.6	557	2	T47511	probable transport
160	5	55.6	423	1	XXPS2M	dihydroallopsamide s	233	5	55.6	557	2	A70480	carbamoyl-phosphat
161	5	55.6	423	1	H84257	Hrli3 transducer l	234	5	55.6	558	2	E86016	probable enzyme 24
162	5	55.6	423	2	T44358	transducer protein	235	5	55.6	559	2	C75286	hypothetical prote
163	5	55.6	423	2	S73020	hypothetical prote	236	5	55.6	570	2	F70332	proline-tRNA synth
164	5	55.6	428	1	E83365	branched-chain alp	237	5	55.6	573	2	S66710	probable membrane
165	5	55.6	432	1	A41056	brachyury homolog	238	5	55.6	579	2	S54872	penicillin-binding
166	5	55.6	442	2	D71481	probable trigger f	239	5	55.6	581	2	E75383	conserved hypochet
167	5	55.6	444	2	B84292	hypothetical prote	240	5	55.6	585	2	F85809	hypothetical prote
168	5	55.6	448	2	B56558	retinoic acid rece	241	5	55.6	587	2	F85084	probable athlia-11
169	5	55.6	451	2	G83916	hypocotate oxidase	242	5	55.6	599	2	D81367	probable pyruvate
170	5	55.6	453	2	S40943	hypocotate prote	243	5	55.6	601	1	A64222	heat shock protein
171	5	55.6	455	2	H83494	probable 2-isoprop	244	5	55.6	603	2	S06059	gene NDI introm 4
172	5	55.6	456	2	H85574	hypothetical prote	245	5	55.6	604	2	S54032	probable amino acil
173	5	55.6	459	2	A41977	retinoic acid rece	246	5	55.6	604	2	S25203	srmr protein - Str
174	5	55.6	462	2	B86262	hypothetical prote	247	5	55.6	605	2	E69153	cadmium efflux ATP
175	5	55.6	464	2	A56558	retinoic acid rece	248	5	55.6	609	2	E72012	glutamine--fructos

249	5	55.6	609	2	S45930	probable amino aci
250	5	55.6	612	2	G71972	threonine--tRNA li
251	5	55.6	612	2	C64535	threonine--tRNA li
252	5	55.6	613	2	G82762	penicillin binding
253	5	55.6	614	2	A56614	acetate--CoA ligas
254	5	55.6	622	2	A64980	hypothetical 68.5k
255	5	55.6	634	1	W1ML51	E1 protein - human
256	5	55.6	634	2	I49642	estrogen-responsiv
257	5	55.6	637	2	S74677	hypothetical prote
258	5	55.6	643	1	DJEC36	DNA-directed DNA p
259	5	55.6	643	2	G85344	hypothetical prote
260	5	55.6	648	2	F85845	unknown protein en
261	5	55.6	648	2	T37581	probable serine-th
262	5	55.6	649	2	PC4395	myosin 3 - human
263	5	55.6	649	2	JN0809	drebrin E (clone g
264	5	55.6	651	2	T15624	hypothetical prote
265	5	55.6	651	2	T14763	hypothetical prote
266	5	55.6	662	2	T18233	probable transcript
267	5	55.6	670	2	T34548	hypothetical prote
268	5	55.6	671	2	A38109	autolysin - Entero
269	5	55.6	682	2	T47473	receptor-like prot
270	5	55.6	682	2	C84295	UDP-sugar hydrolas
271	5	55.6	683	2	E86358	hypothetical prote
272	5	55.6	685	3	JC7570	Delta-4 protein -
273	5	55.6	686	3	JC7569	hypothetical prote
274	5	55.6	700	2	D85582	hypothetical prote
275	5	55.6	700	2	T33577	hypothetical prote
276	5	55.6	701	1	S33709	DHR39--short protei
277	5	55.6	707	2	JC2218	procollagen C-endo
278	5	55.6	711	2	A85352	cadmium-transporti
279	5	55.6	730	1	BMHUI	procollagen C-endo
280	5	55.6	748	2	S54505	hypothetical prote
281	5	55.6	750	1	H70628	probable pkng prot
282	5	55.6	753	2	T24869	hypothetical prote
283	5	55.6	755	2	S42462	structural polypyo
284	5	55.6	763	2	T44735	serine/threonine-s
285	5	55.6	767	2	S63220	probable membrane
286	5	55.6	768	2	T37601	probable transcript
287	5	55.6	781	1	S64576	hypothetical prote
288	5	55.6	781	2	A86205	hypothetical prote
289	5	55.6	790	2	S27458	SM2 protein - yea
290	5	55.6	794	2	T37989	DNA mismatch repai
291	5	55.6	796	2	T03746	hypothetical prote
292	5	55.6	806	2	H70647	probable NADH dehy
293	5	55.6	808	1	S33708	nuclear steroid/th
294	5	55.6	811	2	PN0689	connectin I - chic
295	5	55.6	811	2	S76690	hypothetical prote
296	5	55.6	817	2	S51342	verprolin - yeast
297	5	55.6	823	1	A58788	procollagen C-endo
298	5	55.6	823	2	T02812	probable membrane
299	5	55.6	829	2	T33283	hypothetical prote
300	5	55.6	834	2	E69380	hypothetical prote
301	5	55.6	835	2	S11442	methyI-accepting C
302	5	55.6	835	2	C86444	invasin - Yersinia
303	5	55.6	842	2	S49124	carbon-monoxide de
304	5	55.6	843	2	S33442	EF protein - Strept
305	5	55.6	845	1	PRXSIA	RNA-directed RNA p
306	5	55.6	866	1	JC4305	dynamin II - human
307	5	55.6	868	1	A36878	dynamin 2 - rat
308	5	55.6	870	2	A53165	dynamin II isoform
309	5	55.6	870	2	B53165	dynamin II isoform
310	5	55.6	873	2	A47283	calphotin - fruit
311	5	55.6	899	2	S51341	SGP1 protein - yea
312	5	55.6	900	1	GNNMYV	genome polyprotein
313	5	55.6	920	2	T33263	cell division prot
314	5	55.6	929	2	G72677	hypothetical prote
315	5	55.6	929	2	G71420	hypothetical prote
316	5	55.6	930	2	A25923	progesterone recep
317	5	55.6	931	2	D86222	protein F7G19.9 li
318	5	55.6	933	1	ORHUP	progesterone recep
319	5	55.6	939	2	S28394	probable serine/th
320	5	55.6	940	2	T01834	hypothetical prote
321	5	55.6	951	2	T08987	probable cadmium-t

322	5	55.6	954	2	S57108	hypothetical prote
323	5	55.6	964	2	T15342	hypothetical prote
324	5	55.6	964	2	A75634	McRB-related prote
325	5	55.6	986	1	B58788	procollagen C-endo
326	5	55.6	990	2	I51618	nucleolar phosphop
327	5	55.6	991	2	I49540	procollagen C-endo
328	5	55.6	1001	2	T00532	probable cadmium-t
329	5	55.6	1004	2	H70673	probable mbp prot
330	5	55.6	1009	1	DJBEM2	DNA-directed DNA p
331	5	55.6	1018	1	S73720	cyathierence acces
332	5	55.6	1027	1	GNLJST	pol polyprotein -
333	5	55.6	1047	2	T46489	hypothetical prote
334	5	55.6	1057	2	S45801	probable membrane
335	5	55.6	1070	2	T25836	hypothetical prote
336	5	55.6	1108	2	T38673	probable transcript
337	5	55.6	1113	2	H84105	hypothetical prote
338	5	55.6	1119	2	T50995	related to cytoke
339	5	55.6	1123	2	S36846	myosin-binding pro
340	5	55.6	1138	2	S24614	myosin-binding pro
341	5	55.6	1159	2	T43461	probable phosphodi
342	5	55.6	1171	1	QOKRFP	pyruvate (flavodox
343	5	55.6	1172	2	F70535	probable pr08 prot
344	5	55.6	1172	2	F84572	probable cadmium-t
345	5	55.6	1179	2	S31145	DNA-directed RNA p
346	5	55.6	1182	2	T29097	pro-pol-dutPase po
347	5	55.6	1199	2	S20969	Na+/Ca2+, K+-exchan
348	5	55.6	1211	2	T42230	AR4 protein - mous
349	5	55.6	1213	2	A54063	TARA-binding prote
350	5	55.6	1217	2	T25894	hypothetical prote
351	5	55.6	1224	2	T42625	AF-4 protein - mou
352	5	55.6	1224	2	T40765	webl protein homol
353	5	55.6	1228	2	S59681	webl protein membrane
354	5	55.6	1240	2	T04193	hypothetical prote
355	5	55.6	1253	1	VHWV	structural polypyo
356	5	55.6	1254	2	JC7185	chromosome 1 Clorf
357	5	55.6	1268	2	B36502	insulin receptor-r
358	5	55.6	1268	2	T31420	C-terminal domain-
359	5	55.6	1276	2	T18526	SREBP cleavage act
360	5	55.6	1300	2	A36502	insulin receptor-r
361	5	55.6	1331	2	A72647	probable surface I
362	5	55.6	1337	2	A53824	nuclear pore membr
363	5	55.6	1341	2	T17285	hypothetical prote
364	5	55.6	1415	2	T21244	zysg-9 protein - Ca
365	5	55.6	1418	2	T37264	phospholipase C (E
366	5	55.6	1473	2	A35186	salivary agglutini
367	5	55.6	1534	2	A56734	ritosome receptor,
368	5	55.6	1566	2	A43607	cell surface antlg
369	5	55.6	1582	2	T15308	hypothetical prote
370	5	55.6	1616	2	T47801	hypothetical prote
371	5	55.6	1627	1	IUYMAP	adhesin PI precurs
372	5	55.6	1635	2	A41480	adhesin PI, group
373	5	55.6	1670	1	CGHU3B	collagen alpha 3(I
374	5	55.6	1684	2	JW0057	gravin - human
375	5	55.6	1687	2	T30244	phosphodiesterase
376	5	55.6	1694	2	A83512	hypothetical prote
377	5	55.6	1706	2	T30175	exoribonuclease, v
378	5	55.6	1711	2	T31337	1,4-beta-glucanase
379	5	55.6	1719	2	T30174	exoribonuclease, v
380	5	55.6	1723	2	S58880	receptor DEC-205 -
381	5	55.6	1736	2	A47747	light junction pro
382	5	55.6	1785	2	A45546	major merizolite su
383	5	55.6	1794	2	T38459	hypothetical diver
384	5	55.6	1822	2	S33441	EF protein - strep
385	5	55.6	1829	2	T34239	hypothetical prote
386	5	55.6	1846	2	T10670	hypothetical prote
387	5	55.6	1963	2	T49914	callose synthase c
388	5	55.6	2144	2	S71490	asII protein - fru
389	5	55.6	2254	2	D86215	protein T6D22.14 l
390	5	55.6	2287	2	T21312	hypothetical prote
391	5	55.6	2290	1	GNNYE	genome polyprotein
392	5	55.6	2292	1	GNNYED	genome polyprotein
393	5	55.6	2292	1	GNNYEB	genome polyprotein
394	5	55.6	2292	2	S35961	capsid polyprotein

395	5	55.6	2292	2	S55401	capsid polypoteine
396	5	55.6	2447	2	T16870	hypothetical prote
397	5	55.6	2476	2	T34022	zonadhesin - pig
398	5	55.6	2500	1	WMHUE2	HIV-EP2 enhancer-b
399	5	55.6	2796	2	JC4743	fatty-acid synthas
400	5	55.6	3131	2	S39842	emulatin synthetas
401	5	55.6	3133	2	S52093	hemocytin - silkw
402	5	55.6	3418	1	G02394	breast cancer tumo
403	5	55.6	4162	2	T42633	connectin/titin -
404	5	55.6	4957	2	T03455	ALR protein - huma
405	5	55.6	5262	2	T03454	ALR protein - huma
406	5	55.6	6839	2	S57242	twlctnln [similar]
407	5	55.6	7160	2	T27935	hypothetical prote
408	4	44.4	15	2	A40634	orf19 3' of eryk -
409	4	44.4	23	2	F61491	seed protein ws-6
410	4	44.4	25	2	T40692	cena protein (Igal
411	4	44.4	30	2	B60281	30k serine protein
412	4	44.4	32	2	S13897	alkaline phosphata
413	4	44.4	33	2	T22565	R-phycoerythrin ga
414	4	44.4	38	2	S40096	chlorophyll a/b-bl
415	4	44.4	41	2	B54357	muconate cyclolom
416	4	44.4	41	4	I68632	hypothetical myeli
417	4	44.4	43	2	H82712	hypothetical prote
418	4	44.4	45	2	T35464	hypothetical prote
419	4	44.4	47	2	E47395	histone H1 II-1 (c
420	4	44.4	48	1	T242R2	toxin RpiI - sea a
421	4	44.4	48	2	JN0355	neurotoxin I - sea
422	4	44.4	49	2	PC4007	hypothetical prote
423	4	44.4	50	2	B60718	phospholipase A2 h
424	4	44.4	51	2	S47401	outer membrane pro
425	4	44.4	52	2	A57336	ropA protein - Rhl
426	4	44.4	53	2	I53394	Soluble interleuk1
427	4	44.4	53	2	F47395	histone H1 II-1 (c
428	4	44.4	53	2	B47395	histone H1 II-1 (c
429	4	44.4	53	2	C47395	histone H1 II-1 (c
430	4	44.4	53	2	D47395	histone H1 II-1 (c
431	4	44.4	53	2	G47395	histone H1 II-2 (c
432	4	44.4	53	2	A72614	hypothetical prote
433	4	44.4	56	2	I56605	17 alpha-hydroxyla
434	4	44.4	60	2	S53364	mucin 5AC (clone J
435	4	44.4	62	1	CCBO17	ubiquinol--cytochr
436	4	44.4	62	2	T26847	hypothetical prote
437	4	44.4	63	2	B31075	antifreeze protein
438	4	44.4	64	2	D31075	antifreeze protein
439	4	44.4	65	2	S35024	hypothetical prote
440	4	44.4	66	2	S65971	yycd protein - Bac
441	4	44.4	66	2	PN0644	hypothetical prote
442	4	44.4	67	2	I47395	histone H1 I-1 (cl
443	4	44.4	67	2	G72372	hypothetical prote
444	4	44.4	67	2	A64321	archaeal histone -
445	4	44.4	67	2	A64457	archaeal histone -
446	4	44.4	67	2	D64416	archaeal histone -
447	4	44.4	67	2	D64513	archaeal histone,
448	4	44.4	68	1	A55457	lactocin S precurs
449	4	44.4	69	2	PC7068	synapotaegmin II p
450	4	44.4	69	2	A82489	cold shock DNA-bin
451	4	44.4	70	2	S74243	6-phosphofructo-2-
452	4	44.4	70	2	A47395	histone H1 I-1 (N-
453	4	44.4	71	2	T45384	ribosomal protein
454	4	44.4	71	2	C82537	hypothetical prote
455	4	44.4	72	2	S30980	gene 35 protein -
456	4	44.4	72	2	T48971	hypothetical prote
457	4	44.4	73	2	H69035	conserved hypotnet
458	4	44.4	73	2	T20911	hypothetical prote
459	4	44.4	73	2	E82788	hypothetical prote
460	4	44.4	75	2	C44196	orf13 protein - Mar
461	4	44.4	76	2	T17673	hypothetical prote
462	4	44.4	76	2	A75309	hypothetical prote
463	4	44.4	76	2	I39960	hypothetical prote
464	4	44.4	77	2	S48322	SNP2 protein - yea
465	4	44.4	77	2	E82612	hypothetical prote
466	4	44.4	78	2	S72745	B1177_F2-71 protei
467	4	44.4	78	2	T35377	hypothetical prote
468	4	44.4	78	2	T00719	hypothetical prote
469	4	44.4	79	2	T30118	hypothetical prote
470	4	44.4	80	1	RHIDS	gonadoliberin I pr
471	4	44.4	80	2	T07273	photosystem II pho
472	4	44.4	81	2	T29888	hypothetical prote
473	4	44.4	82	2	T29889	hypothetical prote
474	4	44.4	82	2	T29893	hypothetical prote
475	4	44.4	82	2	T29891	hypothetical prote
476	4	44.4	82	2	T33088	hypothetical prote
477	4	44.4	84	2	A53012	serum response fac
478	4	44.4	84	2	T09540	polline rich prote
479	4	44.4	87	1	FDFICP	antifreeze protein
480	4	44.4	87	2	B31075	antifreeze protein
481	4	44.4	87	2	C31075	antifreeze protein
482	4	44.4	87	2	T27141	hypothetical prote
483	4	44.4	88	2	F85713	hypothetical prote
484	4	44.4	88	2	A85743	hypothetical prote
485	4	44.4	91	2	D86503	hypothetical prote
486	4	44.4	91	2	C72119	hypothetical prote
487	4	44.4	92	2	T34744	hypothetical prote
488	4	44.4	92	2	T51187	small zinc finger-
489	4	44.4	93	2	T53642	insulin-like growt
490	4	44.4	93	2	A86491	CT001 hypothetical
491	4	44.4	93	2	T45593	small zinc finger-
492	4	44.4	93	2	F72130	conserved hypotnet
493	4	44.4	94	2	B84539	hypothetical prote
494	4	44.4	95	2	A56644	inverted repeat co
495	4	44.4	96	2	T16179	hypothetical prote
496	4	44.4	98	2	T49562	alpha-1 type III c
497	4	44.4	99	2	C29826	hypothetical prote
498	4	44.4	100	2	B72540	hypothetical prote
499	4	44.4	100	2	S65724	extracellular hemo
500	4	44.4	101	1	MNVUMB	nonstructural prot
501	4	44.4	101	1	MNVUBV	nonstructural prot
502	4	44.4	101	2	B72079	hypothetical prote
503	4	44.4	101	2	F86544	hypothetical prote
504	4	44.4	101	2	T19560	hypothetical prote
505	4	44.4	102	1	W7WLEP	E7 protein - deer
506	4	44.4	102	1	PH1076	Ig light chain V r
507	4	44.4	102	2	C81682	conserved hypotnet
508	4	44.4	102	2	F84709	probable glutaredo
509	4	44.4	102	2	B26167	Ig lambda chain C
510	4	44.4	103	2	G75513	conserved hypotnet
511	4	44.4	103	2	G75513	gastirin precursor
512	4	44.4	104	1	J00863	hypothetical 11.6k
513	4	44.4	104	2	I2HU	Ig lambda chain C
514	4	44.4	105	1	S47430	protein kinase (EC
515	4	44.4	105	2	A05188	hypothetical prote
516	4	44.4	105	2	T36213	spcd protein - Str
517	4	44.4	105	2	S27493	nocd protein - Bra
518	4	44.4	105	2	S44838	R02D0.3 protein -
519	4	44.4	105	2	D82734	outer membrane pro
520	4	44.4	105	1	K4RBBS	Ig kappa-2 chain C
521	4	44.4	106	1	B48354	nonstructural prot
522	4	44.4	106	1	S20774	Ig heavy chain V r
523	4	44.4	106	2	G20907	Ig kappa-B4 chain
524	4	44.4	106	2	G72632	hypothetical prote
525	4	44.4	106	2	S64649	Rbl2 protein - yea
526	4	44.4	106	2	T45621	hypothetical prote
527	4	44.4	107	2	B64845	hypothetical prote
528	4	44.4	107	2	A82653	hypothetical prote
529	4	44.4	107	2	S51687	protein-tyrosine-P-
530	4	44.4	108	2	D72662	hypothetical prote
531	4	44.4	108	2	F84479	En/Spm-like transp
532	4	44.4	108	2	A72704	hypothetical prote
533	4	44.4	108	2	G72708	hypothetical prote
534	4	44.4	108	2	D71279	hypothetical prote
535	4	44.4	109	2	T34639	hypothetical prote
536	4	44.4	109	2	T17325	hypothetical prote
537	4	44.4	109	2	D70610	probable PE protei
538	4	44.4	110	2	T46071	hypothetical prote
539	4	44.4	110	2	G72696	hypothetical prote
540	4	44.4	110	2	G72696	hypothetical prote

541	4	44.4	111	2	T16302	hypothetical prote	614	4	44.4	127	2	G83870	inner spore coat p
542	4	44.4	111	2	A81673	conserved hypotet	615	4	44.4	128	2	D72481	hypothetical prote
543	4	44.4	111	2	S17200	protein kinase (Ec	616	4	44.4	128	2	H84223	hypothetical prote
544	4	44.4	111	2	D72646	hypothetical prote	617	4	44.4	128	2	T05635	hypothetical prote
545	4	44.4	112	2	E82540	conserved hypotet	618	4	44.4	128	2	T32789	hypothetical prote
546	4	44.4	112	2	S30269	protein hdeb precu	619	4	44.4	129	2	B71350	probable ribosomal
547	4	44.4	112	2	F66023	hypothetical prote	620	4	44.4	130	1	R3MX8	ribosomal protein
548	4	44.4	112	2	A71515	hypothetical prote	621	4	44.4	130	2	S08079	Ig kappa chain pre
549	4	44.4	112	2	T01515	hypothetical prote	622	4	44.4	130	2	G70813	probable lpgs prot
550	4	44.4	112	2	C83938	hypothetical prote	623	4	44.4	130	2	D70966	probable phage pro
551	4	44.4	113	2	PC1281	NS protein - hepa	624	4	44.4	130	2	T29887	hypothetical prote
552	4	44.4	113	2	S11640	hypothetical prote	625	4	44.4	130	2	D84363	hypothetical prote
553	4	44.4	113	2	D83220	hypothetical prote	626	4	44.4	130	2	T51879	hypothetical prote
554	4	44.4	113	2	T49533	hypothetical prote	627	4	44.4	130	2	A72553	hypothetical prote
555	4	44.4	113	2	B71088	hypothetical prote	628	4	44.4	131	2	T35341	hypothetical prote
556	4	44.4	114	2	S07898	endothelin 3 - tab	629	4	44.4	131	2	S60913	hypothetical prote
557	4	44.4	115	1	JN0318	guanylin precursor	630	4	44.4	131	2	H75320	hypothetical prote
558	4	44.4	115	1	KVMSL7	Ig kappa chain pre	631	4	44.4	131	2	E72649	hypothetical prote
559	4	44.4	115	2	E45213	Ca2+-transporting	632	4	44.4	131	2	T19134	hypothetical prote
560	4	44.4	115	2	G72568	hypothetical prote	633	4	44.4	131	2	E70920	probable moab prot
561	4	44.4	115	2	B70702	hypothetical prote	634	4	44.4	131	2	B67882	unknown protein F2
562	4	44.4	115	2	B84684	hypothetical prote	635	4	44.4	131	2	T24051	hypothetical prote
563	4	44.4	115	2	D84501	hypothetical prote	636	4	44.4	132	2	S49160	hypothetical prote
564	4	44.4	116	1	B46279	guanylin precursor	637	4	44.4	132	2	B70312	hypothetical prote
565	4	44.4	116	2	I51733	beta-2-microglobul	638	4	44.4	132	2	T17822	hypothetical prote
566	4	44.4	116	2	G70831	hypothetical prote	639	4	44.4	133	1	SXADE1	hexon-associated p
567	4	44.4	116	2	S70726	replication activa	640	4	44.4	133	2	S49487	long-chain-fatty-a
568	4	44.4	116	2	S70313	hypothetical prote	641	4	44.4	133	2	D69107	ribosomal protein
569	4	44.4	116	2	H72489	hypothetical prote	642	4	44.4	133	2	G75432	hypothetical prote
570	4	44.4	117	2	T02872	probable lipid tra	643	4	44.4	133	2	G75432	hypothetical prote
571	4	44.4	117	2	S21668	Ig kappa chain v r	644	4	44.4	134	2	B37476	E3 gene encoding h
572	4	44.4	117	2	B82614	hypothetical prote	645	4	44.4	134	2	JC4772	hypothetical prote
573	4	44.4	117	2	E75537	conserved hypotet	646	4	44.4	134	2	S74701	hypothetical prote
574	4	44.4	118	2	S12440	Ig lambda chain (M	647	4	44.4	134	2	A83296	hypothetical prote
575	4	44.4	118	2	S12441	Ig lambda chain (K	648	4	44.4	134	2	F75416	hypothetical prote
576	4	44.4	118	2	S12442	Ig lambda chain (K	649	4	44.4	135	2	A48491	twisting motility
577	4	44.4	118	2	D72000	hypothetical prote	650	4	44.4	135	2	C64453	translacion initia
578	4	44.4	118	2	T35747	hypothetical prote	651	4	44.4	135	2	T31260	hypothetical prote
579	4	44.4	118	2	T07905	low-carbon dioxide	652	4	44.4	135	2	G72714	hypothetical prote
580	4	44.4	118	2	G66623	hypothetical prote	653	4	44.4	136	2	T35335	hypothetical prote
581	4	44.4	118	2	S34346	hypothetical prote	654	4	44.4	137	2	T06390	histone H2B-3 - to
582	4	44.4	119	2	S08077	Ig kappa chain pre	655	4	44.4	137	2	B28534	lucC 5'-region hyp
583	4	44.4	119	2	E72526	hypothetical prote	656	4	44.4	138	2	B45244	transcription regu
584	4	44.4	120	2	S21667	Ig kappa chain v r	657	4	44.4	138	2	T04560	hypothetical prote
585	4	44.4	120	2	S21666	Ig kappa chain v r	658	4	44.4	138	2	B83366	hypothetical prote
586	4	44.4	120	2	T23978	hypothetical prote	659	4	44.4	138	2	G85806	hypothetical prote
587	4	44.4	120	2	G86402	hypothetical prote	660	4	44.4	138	2	T29558	hypothetical prote
588	4	44.4	120	2	A72539	hypothetical prote	661	4	44.4	139	2	T34633	hypothetical prote
589	4	44.4	121	2	E70313	histidine triad-li	662	4	44.4	139	2	T23471	hypothetical prote
590	4	44.4	121	2	JC4622	ribosomal phospho	663	4	44.4	140	2	H64664	conserved hypotet
591	4	44.4	121	2	T32888	hypothetical prote	664	4	44.4	140	2	JU0041	hypothetical 14.5k
592	4	44.4	121	2	S75660	hypothetical prote	665	4	44.4	141	1	S34067	H+-transporting AT
593	4	44.4	122	2	T22096	hypothetical prote	666	4	44.4	141	2	T36028	probable iron sulf
594	4	44.4	123	2	G71143	hypothetical prote	667	4	44.4	142	1	S42722	interleukin-3 prec
595	4	44.4	123	2	H75059	hypothetical prote	668	4	44.4	142	1	S42721	interleukin-3 prec
596	4	44.4	123	2	B75546	hypothetical prote	669	4	44.4	142	1	D69510	oxaloacetate decar
597	4	44.4	123	2	C71423	hypothetical prote	670	4	44.4	142	2	A53624	microtubule-associ
598	4	44.4	123	2	T20279	hypothetical prote	671	4	44.4	142	2	T10483	reca-associated pr
599	4	44.4	124	1	MMIHMS	nonstructural prot	672	4	44.4	142	2	A70757	hypothetical prote
600	4	44.4	124	2	H72263	conserved hypotet	673	4	44.4	142	2	E83975	hypothetical prote
601	4	44.4	124	2	T36292	hypothetical prote	674	4	44.4	143	1	S04230	H+-transporting AT
602	4	44.4	125	2	S78697	probable export pr	675	4	44.4	143	1	H65243	yJL protein - Esc
603	4	44.4	125	2	C70977	hypothetical prote	676	4	44.4	143	2	S34065	H+-transporting AT
604	4	44.4	125	2	B72610	hypothetical prote	677	4	44.4	143	2	T15722	hypothetical prote
605	4	44.4	125	2	T38537	probable single-st	678	4	44.4	144	1	SXAD12	hexon-associated p
606	4	44.4	126	2	T24181	hypothetical prote	679	4	44.4	144	2	S66570	biotin carboxyl ca
607	4	44.4	126	2	H75433	hypothetical prote	680	4	44.4	144	2	PC1110	riboflavin synthas
608	4	44.4	126	2	G84215	hypothetical prote	681	4	44.4	144	2	C75376	hypothetical prote
609	4	44.4	127	1	C64140	probable glycyI ra	682	4	44.4	144	2	JC2102	lectin-related pro
610	4	44.4	127	2	E72263	flagellar basal-bo	683	4	44.4	144	2	T46334	hypothetical prote
611	4	44.4	127	2	S00653	chlorophyll a/b-bi	684	4	44.4	144	2	B83069	hypothetical prote
612	4	44.4	127	2	C85091	arabinogalactan-pr	685	4	44.4	144	2	A57362	gytb protein - Str
613	4	44.4	127	2	F64039	hypothetical prote	686	4	44.4	145	2	A82619	pilus protein Xf19

687	4	44.4	145	2	C70328	conserved hypot	760	4	44.4	160	2	F84350	hypothetical prote
688	4	44.4	145	2	S63134	probable membrane	761	4	44.4	161	1	AFKTA	allophycocyanin al
689	4	44.4	145	2	G70424	pillin - Aquifex ae	762	4	44.4	161	2	S44757	ribosomal protein
690	4	44.4	146	1	H8TR1	hemoglobin I beta	763	4	44.4	161	2	S43260	heliix-loop-helix p
691	4	44.4	146	2	T03368	histone H2B1 - com	764	4	44.4	161	2	C36810	hypothetical prote
692	4	44.4	146	2	S76168	hypothetical prote	765	4	44.4	161	2	H82782	hypothetical prote
693	4	44.4	146	2	G73544	hypothetical prote	766	4	44.4	161	2	T37105	probable integr
694	4	44.4	146	2	F82418	cytochrome c554 VC	767	4	44.4	162	2	H69504	hypothetical prote
695	4	44.4	147	2	T33327	hypothetical prote	768	4	44.4	162	2	C72699	hypothetical prote
696	4	44.4	147	2	T49624	hypothetical prote	769	4	44.4	162	2	G96671	hypothetical prote
697	4	44.4	147	2	T02273	hypothetical prote	770	4	44.4	162	2	C72665	hypothetical prote
698	4	44.4	148	2	G83613	probable acetyltra	771	4	44.4	163	1	YC6C3H	hypothetical prote
699	4	44.4	148	2	C84690	probable membrane	772	4	44.4	163	2	S15940	acetylactate synth
700	4	44.4	148	2	T21488	hypothetical prote	773	4	44.4	163	2	B64131	acetylactate synth
701	4	44.4	148	2	B96721	probable thioredox	774	4	44.4	163	2	B85490	hypothetical prote
702	4	44.4	149	2	C72611	hypothetical prote	775	4	44.4	163	2	F83059	acetylactate synth
703	4	44.4	149	2	F75509	hypothetical prote	776	4	44.4	163	2	H81066	acetylactate synth
704	4	44.4	150	2	G72660	hypothetical prote	777	4	44.4	164	1	TVBE11	transfoming prote
705	4	44.4	150	2	G84173	archaeal histone A	778	4	44.4	164	2	H71850	flavodoxin - Heli
706	4	44.4	151	1	S76566	hypothetical prote	779	4	44.4	164	2	A64665	flavodoxin - Heli
707	4	44.4	151	2	T09256	heat shock protein	780	4	44.4	164	2	T38684	mitochondrial inne
708	4	44.4	151	2	F82427	hypothetical prote	781	4	44.4	164	2	S35021	nolB protein - Rhl
709	4	44.4	151	2	B45696	23-28k immunoreact	782	4	44.4	164	2	B70922	hypothetical prote
710	4	44.4	151	2	D72706	hypothetical prote	783	4	44.4	164	2	S44659	ZK353.3 protein -
711	4	44.4	151	2	S33205	proteinase 5 - but	784	4	44.4	164	2	S18038	homeotic protein S
712	4	44.4	152	2	S08350	superoxide dismuta	785	4	44.4	164	2	JC4675	transcriptlon fact
713	4	44.4	152	2	B71119	probable aspartate	786	4	44.4	165	2	A31635	neural cell adhesi
714	4	44.4	152	2	S57422	cysteine proteinas	787	4	44.4	165	2	T39187	probable arylalkyl
715	4	44.4	152	2	T09253	heat shock protein	788	4	44.4	165	2	T47011	hypothetical prote
716	4	44.4	152	2	T30753	hypothetical prote	789	4	44.4	166	2	H83630	hypothetical prote
717	4	44.4	152	2	T31054	hypothetical prote	790	4	44.4	167	1	S32716	ribosome releasing
718	4	44.4	152	2	A84303	hypothetical prote	791	4	44.4	167	1	UYPWF3	nonstructural prot
719	4	44.4	152	2	T08401	hypothetical prote	792	4	44.4	167	2	S73043	hypothetical prote
720	4	44.4	152	2	T494126	hypothetical prote	793	4	44.4	168	2	S67993	amylogenin - maize
721	4	44.4	152	2	T11658	mitochondrial impo	794	4	44.4	168	2	S52994	arabinogalactan-11
722	4	44.4	152	2	S35206	serine proteinase	795	4	44.4	168	2	S60970	hypothetical prote
723	4	44.4	153	2	B49854	probable reca regu	796	4	44.4	169	2	T30684	probable dual spec
724	4	44.4	153	2	F83192	conserved hypot	797	4	44.4	169	2	T29283	peptidylprolyl iso
725	4	44.4	153	2	S29277	hypothetical prote	798	4	44.4	169	2	H72611	hypothetical prote
726	4	44.4	153	2	E72506	hypothetical prote	799	4	44.4	169	2	D72347	hypothetical prote
727	4	44.4	153	2	S73143	photosystem I chal	800	4	44.4	170	2	T35957	hypothetical prote
728	4	44.4	153	2	JC5854	polyetide synthas	801	4	44.4	171	2	A45562	mezoecite surface
729	4	44.4	154	2	T28434	transcription regu	802	4	44.4	171	2	H69997	conserved hypot
730	4	44.4	154	2	B69105	hypothetical prote	803	4	44.4	171	2	T41803	AcMNPV ori58 - Bom
731	4	44.4	154	2	A85551	hypothetical prote	804	4	44.4	171	2	S41642	hypothetical prote
732	4	44.4	154	2	PC4031	hypothetical 154 p	805	4	44.4	171	2	H70527	probable PE protei
733	4	44.4	154	2	S55017	hypothetical prote	806	4	44.4	171	2	T37090	probable secreted
734	4	44.4	154	2	F72741	hypothetical prote	807	4	44.4	172	2	T21753	hypothetical prote
735	4	44.4	155	1	SNF82	pathogenesis-relat	808	4	44.4	173	1	RUPSEO	tubredoxin II - Ps
736	4	44.4	155	2	T11670	pathogenesis relat	809	4	44.4	173	2	F73932	peptidylprolyl iso
737	4	44.4	155	2	E64105	acetyl-CoA carboxy	810	4	44.4	174	2	F70674	hypothetical prote
738	4	44.4	155	2	H86721	hypothetical prote	811	4	44.4	174	2	A45356	neuromedin U precu
739	4	44.4	155	2	A81065	sigma-54 dependant	812	4	44.4	175	2	C83141	inorganic pyrophos
740	4	44.4	155	2	H75302	conserved hypot	813	4	44.4	175	2	S49992	ribulose-1,5-bisph
741	4	44.4	156	1	SNF81	pathogenesis-relat	814	4	44.4	175	2	E56271	long polar flmbria
742	4	44.4	156	2	C84027	molybdoplerin conv	815	4	44.4	175	2	S71560	early light-induce
743	4	44.4	156	2	D81343	probable integr	816	4	44.4	175	2	T39781	hypothetical prote
744	4	44.4	157	2	D70541	hypothetical prote	817	4	44.4	175	2	D75514	hypothetical prote
745	4	44.4	157	2	S04939	heat shock 22K pro	818	4	44.4	175	2	A26882	pilZ hypot
746	4	44.4	157	2	H72751	hypothetical prote	819	4	44.4	176	2	D45213	Ca2+-transporting
747	4	44.4	157	2	S31634	hypothetical prote	820	4	44.4	176	2	I53630	cell surface glyco
748	4	44.4	157	2	F83464	flagellar motor sw	821	4	44.4	176	2	D71434	hypothetical prote
749	4	44.4	157	2	S49793	hypothetical prote	822	4	44.4	176	2	T45308	hypothetical prote
750	4	44.4	157	2	T25638	hypothetical prote	823	4	44.4	176	2	S02210	con-8 protein - Ne
751	4	44.4	158	2	S20518	hypothetical prote	824	4	44.4	176	2	F72651	hypothetical prote
752	4	44.4	158	2	S20517	hypothetical prote	825	4	44.4	177	2	T06306	hypothetical prote
753	4	44.4	158	2	T30379	biotin carboxyl ca	826	4	44.4	177	2	D83111	transcription anti
754	4	44.4	158	2	D64365	hypothetical prote	827	4	44.4	177	2	D81392	probable transcrip
755	4	44.4	159	2	H65478	ybak protein - Esc	828	4	44.4	177	2	A83064	hypothetical prote
756	4	44.4	159	2	B85546	hypothetical prote	829	4	44.4	177	2	D82638	hypothetical prote
757	4	44.4	159	2	T48837	hypothetical prote	830	4	44.4	178	1	E69389	hypothetical prote
758	4	44.4	160	2	S78308	plascocquinoi--plas	831	4	44.4	178	2	T09585	high mobility grou
759	4	44.4	160	2	H69015	ribosomal protein	832	4	44.4	178	2	T09584	high mobility grou

833	4	44.4	178	2	S24298	906	4	44.4	191	2	T18828	hypothetical prote
834	4	44.4	178	2	T45019	907	4	44.4	191	2	S28736	hypothetical prote
835	4	44.4	178	2	B75406	908	4	44.4	191	2	J01999	hypothetical 21.5k
836	4	44.4	179	1	A42840	909	4	44.4	191	2	H82047	conserved hypotnet
837	4	44.4	179	2	T04897	910	4	44.4	192	2	S15930	hypothetical 21.5k
838	4	44.4	179	2	T22734	911	4	44.4	192	2	S55252	mushroom-inducing
839	4	44.4	180	1	IGHUC2	912	4	44.4	193	2	A69155	hypothetical prote
840	4	44.4	180	1	HLHUC3	913	4	44.4	193	2	S74058	hypothetical prote
841	4	44.4	180	2	S70836	914	4	44.4	193	2	E96766	hypothetical prote
842	4	44.4	180	2	G29504	915	4	44.4	193	2	S38467	hypothetical prote
843	4	44.4	180	2	T29803	916	4	44.4	194	2	T16382	hypothetical prote
844	4	44.4	181	2	B60738	917	4	44.4	194	2	H72037	conserved hypotnet
845	4	44.4	181	2	D49233	918	4	44.4	194	2	C86586	Cr647 hypothetical
846	4	44.4	181	2	F84934	919	4	44.4	194	2	E75297	hypothetical prote
847	4	44.4	181	2	C81041	920	4	44.4	195	1	S74599	2 amino-4-hydroxy-
848	4	44.4	181	2	D72060	921	4	44.4	195	1	Q06CAA	yaca protein - Esc
849	4	44.4	181	2	A86564	922	4	44.4	195	1	B32048	gliding motility p
850	4	44.4	181	2	T49728	923	4	44.4	195	2	E85492	hypothetical prote
851	4	44.4	181	2	A70673	924	4	44.4	195	2	A83902	hypothetical prote
852	4	44.4	181	2	T04643	925	4	44.4	196	2	PC1148	amlogenin precurs
853	4	44.4	181	2	B84162	926	4	44.4	196	2	JC2391	amlogenin precurs
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855	4	44.4	181	2	A86451	928	4	44.4	196	2	G85435	TINY-like protein
856	4	44.4	181	2	F82750	929	4	44.4	196	2	T13595	hypothetical prote
857	4	44.4	182	2	H70818	930	4	44.4	197	2	S57948	HMG1/Y protein - g
858	4	44.4	182	2	A82684	931	4	44.4	197	2	B49247	merozolite surface
859	4	44.4	182	2	T35142	932	4	44.4	197	2	C49247	merozolite surface
860	4	44.4	182	2	S73046	933	4	44.4	197	2	PQ0327	heparin-binding fi
861	4	44.4	182	2	JC7196	934	4	44.4	198	2	D82253	dedd protein VC100
862	4	44.4	182	2	T16472	935	4	44.4	198	2	E70357	conserved hypotnet
863	4	44.4	183	2	S02423	936	4	44.4	198	2	A96811	unknown protein T1
864	4	44.4	183	2	I67610	937	4	44.4	199	2	P83540	probable alkyl hyd
865	4	44.4	183	2	A32338	938	4	44.4	199	2	H75401	hypothetical prote
866	4	44.4	183	2	I54288	939	4	44.4	199	2	T24595	hypothetical prote
867	4	44.4	183	2	I79496	940	4	44.4	200	2	S55609	hypothetical prote
868	4	44.4	183	2	S72802	941	4	44.4	200	2	T37187	hypothetical prote
869	4	44.4	183	2	T34330	942	4	44.4	200	2	T50442	hypothetical prote
870	4	44.4	183	2	G83379	943	4	44.4	201	2	T06229	probable superoxid
871	4	44.4	183	2	S24960	944	4	44.4	201	2	T06800	superoxide dismuta
872	4	44.4	184	2	A70149	945	4	44.4	201	2	T46670	probable 3,5-epime
873	4	44.4	184	2	E82345	946	4	44.4	201	2	D38625	GTP-binding protei
874	4	44.4	184	2	C96506	947	4	44.4	201	2	S06147	GTP-binding protei
875	4	44.4	184	2	T00431	948	4	44.4	201	2	JC5337	GTP-binding protei
876	4	44.4	184	2	S77928	949	4	44.4	201	2	T09047	hypothetical protei
877	4	44.4	185	2	D75602	950	4	44.4	202	1	HTVWR2	hemorrhagic protei
878	4	44.4	185	2	S76706	951	4	44.4	202	1	JQ1556	coat protein - Ery
879	4	44.4	185	2	A82636	952	4	44.4	202	2	T15874	hypothetical prote
880	4	44.4	186	2	S43174	953	4	44.4	202	2	S26074	hypothetical prote
881	4	44.4	186	2	F83753	954	4	44.4	202	2	A42410	rydocan precursor
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883	4	44.4	186	2	T31951	956	4	44.4	202	2	F84382	hypothetical prote
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885	4	44.4	187	1	B29830	958	4	44.4	203	2	B75300	hypothetical prote
886	4	44.4	187	2	T36331	959	4	44.4	203	2	JC4990	chymotrypsin inh
887	4	44.4	187	2	T34834	960	4	44.4	204	2	G82149	Holliday junction
888	4	44.4	187	2	F65009	961	4	44.4	204	2	T48091	hypothetical prote
889	4	44.4	187	2	S76728	962	4	44.4	204	2	G81876	probable membrane
890	4	44.4	187	2	H84100	963	4	44.4	204	2	D84190	tryptophan synthas
891	4	44.4	188	2	G70892	964	4	44.4	205	1	TVHUYV	GTP-binding protei
892	4	44.4	188	2	A75392	965	4	44.4	205	1	TVDGYV	GTP-binding protei
893	4	44.4	189	2	S52907	966	4	44.4	205	1	TVMSVP	GTP-binding protei
894	4	44.4	189	2	C83134	967	4	44.4	205	1	TVRTVP	GTP-binding protei
895	4	44.4	189	2	C82515	968	4	44.4	205	2	S38339	GTP-binding protei
896	4	44.4	190	2	S25740	969	4	44.4	205	2	T33117	hypothetical prote
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898	4	44.4	190	2	G85542	971	4	44.4	205	2	T34724	probable membrane
899	4	44.4	190	2	T32265	972	4	44.4	206	1	B69128	precocorrin isomer
900	4	44.4	190	2	T00735	973	4	44.4	206	2	I68547	PA33 protein - hu
901	4	44.4	190	2	I40869	974	4	44.4	206	2	JL0058	H-2 class I histoc
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903	4	44.4	191	2	G64684	976	4	44.4	206	2	S44894	zkl236.6 protein -
904	4	44.4	191	2	S76377	977	4	44.4	206	2	T49138	hypothetical prote
905	4	44.4	191	2	C41892	978	4	44.4	206	2	D72323	conserved hypotnet

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979 4 44.4 206 2 T27766 hypothetical prote
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981 4 44.4 207 2 H72550 probable inorganic
982 4 44.4 207 2 S77728 type 4 fibrinai bi
983 4 44.4 207 2 E69459 hypothetical prote
984 4 44.4 207 2 B75327 hypothetical prote
985 4 44.4 207 2 A83540 phospholipase acce
986 4 44.4 207 2 T08109 oleosin-like prote
987 4 44.4 208 2 T09216 interleukin-6 prec
988 4 44.4 208 2 A26496 granulocyte colony
989 4 44.4 208 2 B49444 ig lambda chain (N
990 4 44.4 208 2 C34503 small nuclear ribo
991 4 44.4 208 2 T46927 hypothetical prote
992 4 44.4 208 2 T34763 probable transcrip
993 4 44.4 208 2 E72241 hypothetical prote
994 4 44.4 208 2 S73699 adhesin p1 precurs
995 4 44.4 208 2 T08132 oleosin-like prote
996 4 44.4 208 2 A43696 Spec3 protein - se
997 4 44.4 209 2 S44650 f42hi0.3 protein -
998 4 44.4 210 1 S03583 ribosomal protein
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ALIGNMENTS

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RESULT 1
A:Accession: A41487
protein p60 precursor - listeria monocytogenes
N:Alternate names: Invasion-associated protein
C:Species: Listeria monocytogenes
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1996
C:Accession: A41487; B41487
R:Koehler, S.; Leimister-Maehtler, M.; Chakraborty, T.; Lottspiech, F.; Goebel, W.
Infect. Immun. 59, 1943-1950, 1990
A:Title: The gene coding for protein p60 of Listeria monocytogenes and its use as a spec
A:Reference number: A41487; MUID:90256283
A:Accession: A41487
A:Molecule type: DNA
A:Residues: 1-484 <KOE>
A:Cross-references: GB:X52268
A:Accession: B41487
A:Molecule type: protein
A:Residues: 28-49 <KO2>
C:Genetics:
A:Gene: iap
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-484/Product: protein p60 #status predicted <MAT>

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Query Match          100.0%; Score 9; DB 2; Length 484;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VSTPVAPPTQ 9
    |||||
Db 145 VSTPVAPPTQ 153

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RESULT 2
F83231
hypothetical protein PA3307 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83231
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: F83231

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A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STO>
A:Cross-references: GB:AE004753; GB:AE004091; NID:99949433; PIDN:AA06695.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3307

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Query Match          66.7%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 PVAPPTQ 9
    |||||
Db 27 PVAPPTQ 32

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RESULT 3
S35162
STR-21 protein - potato
C:Species: Solanum tuberosum (potato)
C>Date: 13-Jan-1995 #sequence_revision 09-May-1997 #text_change 20-Aug-1999
C:Accession: S35162; S11869
R:Matton, D.P.; Prescott, G.; Bertrand, C.; Camirand, A.; Brisson, N.
Plant Mol. Biol. 22, 279-291, 1993
A:Title: Identification of cis-acting elements involved in the regulation of the path
A:Reference number: S35161; MUID:93283632
A:Accession: S35162
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-155 <MAT>
A:Cross-references: EMBL:M29042; NID:9169577; PIDN:AA02829.1; PID:9169578
C:Genetics:
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1990
A:Gene: STR-21
A:Introns: 57/1
C:Superfamily: pathogenesis-related protein

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Query Match          66.7%; Score 6; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 TPVAPT 8
    |||||
Db 12 TPVAPT 17

```

```

RESULT 4
JC4806
core protein G - phage phi-K
C:Species: phage phi-K
C>Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 20-Jun-2000
C:Accession: JC4806; B04253; A04253
R:Kodaira, K.; Oki, M.; Kakikawa, M.; Kimoto, H.; Taketo, A.
J. Biochem. 119, 1062-1069, 1996
A:Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant
A:Reference number: JC4804; MUID:96424987
A:Accession: JC4806
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-187 <KOD>
A:Cross-references: EMBL:X60323; NID:91478118; PIDN:CAA42892.1; PID:91478127
R:Stms, J.; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628, 1979
A:Title: dnag (primase)-dependent origins of DNA replication. Nucleotide sequences of
A:Reference number: A92247; MUID:80049550
A:Accession: B04253
A:Molecule type: DNA
A:Residues: 165-187 <SIM>
A:Comment: This protein is one of the structural components of the bacteriophage caps
C:Genetics:

```

A:Gene: G
C:Superfamily: phage phi-X174 gene G protein
C:Keywords: capsid protein

Query Match 66.7%; Score 6; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
DB 25 TPVAPT 30

RESULT 5
C86847
transcription regulator Tena [Imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86847
R:Boletín, A.; Wincker, P.; Manger, S.; Jallón, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. In press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: C86847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <STO>
A:Cross-references: GB:AE005176; NID:q12724803; PIDN:AAK05877.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: tena
C:Superfamily: transcription activator tena

Query Match 66.7%; Score 6; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
DB 103 TPVAPT 108

RESULT 6
F71504
hypothetical protein CT504 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 18-Aug-2000
C:Accession: F71504
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809
A:Accession: F71504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <ARN>
A:Cross-references: GB:AE001323; GB:AE001273; NID:g3328931; PIDN:AAC68105.1; PID:g332894
C:Genetics:
A:Experimental source: serotype D, strain UW-3/Cx
A:Gene: CT504
C:Superfamily: conserved hypothetical protein TC0791

Query Match 66.7%; Score 6; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVAP 7
DB 131 STPVAP 136

RESULT 7

F75466
hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75466
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75466
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-293 <WHI>
A:Cross-references: GB:AE001940; GB:AE000513; NID:g6458577; PIDN:AAF10447.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0864
A:Map position: 1

Query Match 66.7%; Score 6; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVAP 7
DB 227 STPVAP 232

RESULT 8
T34992
probable lipoprotein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34992
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21550
A:Accession: T34992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-447 <OLI>
A:Cross-references: EMBL:AL031182; PIDN:CAA20169.1; GSPDB:GN00070; SCOEDB:SCA42.17C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCA42.17C

Query Match 66.7%; Score 6; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
DB 63 TPVAPT 68

RESULT 9
F64623
amidase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: F64623
R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatal, H.G.; Glodok, A.; McKee,
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467
A:Accession: F64623
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-453 <TOM>
A:Cross-references: GB:AE000594; GB:AE000511; NID:g2313957; PIDN:AAD07880.1; PID:g231396
C:Superfamily: Indoleacetamide hydrolase

Query Match 66.7%; Score 6; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
|||||
Db 373 TPVAPT 378

RESULT 10
A71891
glu-tRNA amidotransferase, chain A - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence-revision 12-Feb-1999 #text-change 22-Jun-1999
C:Accession: A71891
R:Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557
A:Accession: A71891
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-453 <ARN>
A:Cross-references: GB:AE001507; GB:AE001439; NID:g4155326; PIDN:AAD06348.1; PID:g415533
A:Experimental source: strain J99
C:Genetics:
A:Gene: gata
C:Superfamily: Indoleacetamide hydrolase

Query Match 66.7%; Score 6; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
|||||
Db 373 TPVAPT 378

RESULT 11
T23087
hypothetical protein H13N06.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 18-Feb-2000
C:Accession: T23087
R:Lennard, N.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z19673
A:Accession: T23087
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <WIL>
A:Cross-references: EMBL:Z99942; PIDN:CAB17068.1; GSPDB:GN00028; CESP:H13N06.2
C:Genetics:
A:Gene: CESP:H13N06.2
A:Map position: X
A:introns: 17/1; 294/1; 331/3; 364/1; 414/2; 432/2

Query Match 66.7%; Score 6; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 TPVAPT 8
|||||
Db 73 TPVAPT 78

RESULT 12
S66953
hypothetical protein YOR070c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O2931
C:Species: Saccharomyces cerevisiae
C>Date: 12-Jul-1996 #sequence-revision 12-Jul-1996 #text-change 05-Nov-1999
C:Accession: S66953
R:Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66929
A:Accession: S66953
A:Molecule type: DNA
A:Residues: 1-637 <BOH>
A:Cross-references: EMBL:Z74978; NID:g1420220; PID:e251984; PID:g1420221; GSPDB:GN000
C:Genetics:
A:Gene: MIPS:YOR070c
A:Map position: 15R

Query Match 66.7%; Score 6; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
|||||
Db 181 TPVAPT 186

RESULT 13
T49633
glucan 1,4-alpha-glucosidase related protein [imported] - Neurospora crassa
N:Alternate names: protein B5022.150
C:Species: Neurospora crassa
C>Date: 02-Jun-2000 #sequence-revision 02-Jun-2000 #text-change 02-Jun-2000
C:Accession: T49633
R:Schulte, U.; Aign, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49633
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-748 <SCH>
A:Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.150
C:Genetics:
A:Gene: NCSP:B5022.150
A:Map position: 6
A:introns: 701/1

Query Match 66.7%; Score 6; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTRPVA 6
|||||
Db 506 VSTRPVA 511

RESULT 14
H84913
probable ATP-dependent RNA helicase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Feb-2001 #sequence-revision 02-Feb-2001 #text-change 02-Feb-2001
C:Accession: H84913

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487
A:Accession: H84913
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-748 <STO>
A:Cross-references: GB:AE002093; NID:g2275211; PIDN:AAB63833.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g47330
A:Map position: 2

Query Match 66.7%; Score 6; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPTO 9
|||||
DB 725 PVAPTO 730

RESULT 15
A47282
calcium-binding protein calphotin - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A47282
R:Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993
A:Title: Calphotin: a *Drosophila* photoreceptor cell calcium-binding protein.
A:Reference number: A47282; MUID:93165729
A:Accession: A47282
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-865 <MAR>
A:Cross-references: GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032
A:Experimental source: photoreceptor cells
A:Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIF:124956)
C:Genetics:
A:Gene: FlyBase:Cpn
A:Cross-references: FlyBase:FBgn0010218
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: calcium binding

Query Match 66.7%; Score 6; DB 2; Length 865;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTRPA 6
|||||
DB 97 VSTRPA 102

RESULT 16
T50652
AP-3 complex beta3A chain [imported] - human
C:Species: *Homo sapiens* (man)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50652
R:Simpson, F.; Peden, A.A.; Christopoulos, L.; Robinson, M.S.
J. Cell Biol. 137, 835-845, 1997
A:Title: Characterization of the adaptor-related protein complex, AP-3.
A:Reference number: 225159; MUID:97296491
A:Accession: T50652
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1093 <SIM>
A:Cross-references: EMBL:U91931; PIDN:AAD03778.1

Query Match 66.7%; Score 6; DB 2; Length 1093;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTRPA 6
|||||
DB 826 VSTRPA 831

RESULT 17
T50651
AP3-complex beta-3A-adaptin chain [imported] - human
C:Species: *Homo sapiens* (man)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50651
R:Deil/Angelica, E.C.; Ooi, C.E.; Bonifacio, J.S.
J. Biol. Chem. 272, 15078-15084, 1997
A:Title: Beta3A-adaptin, a subunit of the adaptor-like complex AP-3.
A:Reference number: 225158; MUID:97326075
A:Accession: T50651
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1094
A:Cross-references: EMBL:U81504; PIDN:AAB61638.1
C:Function:
A:Description: involved in the regulation of intracellular protein trafficking
C:Keywords: heterotrimer; phosphoprotein

Query Match 66.7%; Score 6; DB 2; Length 1094;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTRPA 6
|||||
DB 827 VSTRPA 832

RESULT 18
T18295
AP-3 adaptor complex beta3A chain - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18295
R:Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; R
Hum. Mol. Genet. 8, 323-330, 1999
A:Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in th
A:Reference number: 218864; MUID:99135912
A:Accession: T18295
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1105 <FEN>
A:Cross-references: EMBL:AF103809; NID:g3885987; PID:g3885988; PIDN:AAC78338.1
C:Experimental source: strain C3H/HeJ
C:Genetics:
A:Gene: Ap3b1
A:Map position: 13

Query Match 66.7%; Score 6; DB 2; Length 1105;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTRPA 6
|||||
DB 838 VSTRPA 843

RESULT 19
E75264
hypothetical protein - *Deinococcus radiodurans* (strain R1)

C:Species: *Delnoccocus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: E75264
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Shen, M.; Vamathevan, J.C.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Delnoccocus radiodurans* R1.
 A:Reference number: A75250; MWID:20036896
 A:Accession: E75264
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-75 <EMO>
 A:Cross-references: GB:AE002081; GB:AE000513; NID:96460337; PIDN:AAFI2064.1; PID:9646034
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2520
 A:Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPRO 9
 |||||
 DB 24 VAPRO 28

RESULT 20
 T29802
 hypothetical protein C06E4.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T29802
 R:Du, Z.; Gattung, S.
 Submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C06E4.
 A:Reference number: Z20688
 A:Accession: T29802
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <DUZ>
 A:Cross-references: EMBL:U41277; PIDN:AAA82477.1; CESP:C06E4.2
 C:Genetics:
 A:Gene: CESP:C06E4.2
 A:Introns: 31/1

Query Match 55.6%; Score 5; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPRO 9
 |||||
 DB 40 VAPRO 44

RESULT 21
 T34429
 hypothetical protein F55C7.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T34429
 R:Du, Z.; Le, T.
 Submitted to the EMBL Data Library, November 1996
 A:Description: The sequence of C. elegans cosmid F55C7.
 A:Reference number: Z21524
 A:Accession: T34429
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-88 <DUZ>
 A:Cross-references: EMBL:U80436; PIDN:AMC71107.1; GSPDB:GN00019; CESP:F55C7.2

A:Experimental source: strain Bristol N2; clone F55C7
 C:Genetics:
 A:Gene: CESP:F55C7.2
 A:Map position: 1
 A:Introns: 18/3

Query Match 55.6%; Score 5; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
 |||||
 DB 31 STPVA 35

RESULT 22
 K4RB
 Ig kappa-B4 chain C region - rabbit
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C:Date: 31-Jan-1981 #sequence_revision 15-Oct-1982 #text_change 16-Aug-1996
 C:Accession: A93971; A93891; A92176; A02122
 R:Emorine, L.; Dreher, K.; Kindt, T.J.; Max, E.E.
 Proc. Natl. Acad. Sci. U.S.A. 80, 5709-5713, 1983
 A:Title: Rabbit immunoglobulin kappa genes: structure of a germline b4 allotype J-C 1
 A:Reference number: A93971; MWID:83300036
 A:Accession: A93971
 A:Molecule type: DNA
 A:Residues: 1-103 <EMO>
 A:Note: The sequence was determined from the germline gene
 R:Heidmann, O.; Auftray, C.; Cazenave, P.A.; Rougeon, F.
 Proc. Natl. Acad. Sci. U.S.A. 78, 5802-5806, 1981
 A:Title: Nucleotide sequence of constant and 3' untranslated regions of a kappa immun
 A:Reference number: A93891; MWID:82060334
 A:Accession: A93891
 A:Molecule type: mRNA
 A:Residues: 1-103 <HEI>
 A:Residues: 1-103 <HEI>
 R:Chen, K.C.S.; Kindt, T.J.; Krause, R.M.
 J. Biol. Chem. 250, 3289-3296, 1975
 A:Title: Primary structure of the L chain from a rabbit homogeneous antibody to strep
 A:Reference number: A92176; MWID:75133568
 A:Accession: A92176
 A:Molecule type: protein
 A:Residues: 1-57, 'D', '59-103 <CHE>
 A:Note: this chain was obtained from antibody to the specific carbohydrate of group C
 A:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (C
 C:Superfamily: Immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotrimer
 F:19-87/Domain: immunoglobulin homology <IMW>

Query Match 55.6%; Score 5; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
 |||||
 DB 2 PVAPT 6

RESULT 23
 F53275
 Ig kappa-1 chain C region b95 allotype - rabbit (fragment)
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: F53275
 R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
 Immunogenetics 34, 201-207, 1991
 A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
 A:Reference number: A53275; MWID:91372868
 A:Accession: F53275
 A>Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-104 <AYA>
 A:Note: sequence inconsistent with nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBI:56170)
 C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:19-87/Domain: Immunoglobulin homology <IMM>

Query Match 55.6%; Score 5; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PVAPT 8
 |||||
 Db 2 PVAPT 6

RESULT 24
 A34567
 beta-microseminoprotein precursor - human
 M:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pro
 C:Species: Homo sapiens (man)
 C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 20-Aug-1999
 C:Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682
 R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
 Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
 A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein g
 A:Reference number: A34567; MUID:90211299
 A:Accession: A34567
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-114 <GRE>
 A:Cross-references: GB:M34376; NID:9514370; PIDN:AAA59671.1; PID:9514372
 R:Mbikay, M.; Nole, S.; Fournier, S.; Benjannet, S.; Chapelaine, P.; Paradis, G.; Dubé
 DNA 6, 23-29, 1987
 A:Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma p
 A:Reference number: A26451; MUID:87161231
 A:Accession: A26451
 A:Molecule type: mRNA
 A:Residues: 1-114 <MBI>
 A:Cross-references: GB:M15885; NID:9338414; PIDN:AAA36635.1; PID:9338415
 R:Akiyama, K.; Yoshida, Y.; Schmidt, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara, M
 Biochim. Biophys. Acta 829, 288-294, 1985
 A:Title: The amino acid sequence of human beta-microseminoprotein.
 A:Reference number: A29777; MUID:85199574
 A:Accession: A29777
 A:Molecule type: protein
 A:Residues: 21-58; 'PT', 61-113 <AKI>
 R:Seidah, N.G.; Arhault, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.
 FEBS Lett. 175, 349-355, 1984
 A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction c
 A:Reference number: A30984; MUID:85004133
 A:Accession: A30984
 A:Molecule type: protein
 A:Residues: 21-112; 'G', 114 <SEI>
 R:Weber, H.; Andersson, C.; Mune, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
 Am. J. Pathol. 137, 593-604, 1990
 A:Title: Beta microseminoprotein is not a prostate-specific protein.
 A:Reference number: A60673; MUID:90379237
 A:Accession: A60673
 A:Molecule type: protein
 A:Residues: 21; 'X', 23-34 <WEI>
 A:Experimental source: gastric juice
 R:Nole, S.; Mbikay, M.; Chretien, M.
 Biochim. Biophys. Acta 1089, 247-249, 1991
 A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
 A:Reference number: S16237; MUID:91274557
 A:Accession: S16238
 A:Molecule type: DNA
 A:Residues: 1-114 <NOI>
 A:Cross-references: EMBL:X57928; NID:935760; PIDN:CAA41002.1; PID:9825707
 A:Note: the authors translated the codon ACT for residue 54 as Trp

R:Liu, A.Y.; Bradner, R.C.; Vessella, R.L.
 Cancer Lett. 74, 91-99, 1993
 A:Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer
 A:Reference number: I52682; MUID:94115955
 A:Accession: I52682
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-114 <RES>
 A:Cross-references: GB:S67815; NID:9460568; PIDN:AA29732.1; PID:9460569
 C:Comment: This protein is a component of seminal plasma as well as secretory fluids
 C:Genetics:
 A:Gene: GDB:MSMB
 A:Cross-references: GDB:128042; OMIM:157145
 A:Map position: 10q11.2-10q11.2
 A:Introns: 1/3; 37/1; 72/2
 C:Superfamily: seminal plasma protein
 C:Keywords: semen
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 55.6%; Score 5; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VSTPV 5
 |||||
 Db 73 VSTPV 77

RESULT 25
 B49094
 methylmalonyl-CoA decarboxylase (EC 4.1.1.41) delta chain - Veillonella parvula
 C:Species: Veillonella parvula
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
 C:Accession: B49094
 R:Huder, J.B.; Dimroth, P.
 J. Biol. Chem. 268, 24564-24571, 1993
 A:Title: Sequence of the sodium ion pump methylmalonyl-CoA decarboxylase from Veillon
 A:Reference number: A49094; MUID:94043308
 A:Accession: B49094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115 <HND>
 A:Cross-references: GB:L22208; NID:9415592; PIDN:AA36621.1; PID:9415594
 C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 55.6%; Score 5; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TPVAP 7
 |||||
 Db 60 TPVAP 64

RESULT 26
 A72293
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: A72293
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: A72293
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <ARN>

A:Cross-references: GB:AE001770; GB:AE000512; NID:94981658; PIDN:AAD36200.1; PID:9498167
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1124

Query Match 55.6%; Score 5; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
|||||
DB 30 STPVA 34

RESULT 27
C71189
hypothetical protein PH1791 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: G71189

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137

A:Accession: G71189
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-123 <KAW>
A:Cross-references: GB:AP000007; NID:93236134; PIDN:BAA30910.1; PID:93258227
A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by Genbank
C:Genetics:
A:Gene: PH1791

Query Match 55.6%; Score 5; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
|||||
DB 39 VSTPV 43

RESULT 28

I54454
Lymphocyte antigen - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54454

R:Hiraiwa, A.; Seyfried, C.E.; Nepom, G.T.; Milner, E.C.
Immunogenetics 29, 186-190, 1989

A>Title: Sequence analysis of HLA class II domains: characterization of the DQ α 3 family
A:Reference number: I54454; MUID:91173071
A:Accession: I54454

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-126 <RES>
A:Cross-references: GB:M25325; NID:9619801; PIDN:AAA59675.1; PID:9619802
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 55.6%; Score 5; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
|||||
DB 26 STPVA 30

RESULT 29
JN0727

hypothetical 13.4K protein - Escherichia coli

C:Species: Escherichia coli

C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 15-May-1998
C:Accession: JN0727

R:Paton, A.W.; Paton, J.C.; Goldwater, P.N.; Heuzenroeder, M.W.; Manning, P.A.
Gene 129, 87-92, 1993

A>Title: Sequence of a variant Shiga-like toxin type-I operon of Escherichia coli O11
A:Reference number: JN0725; MUID:93328129
A:Accession: JN0727

A:Molecule type: DNA
A:Residues: 1-128 <PAT>
A:Cross-references: GB:L04539

A:Experimental source: serotype O11:H(-)
C:Genetics:
A:Gene: SLT-1

Query Match 55.6%; Score 5; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
|||||
DB 56 VSTPV 60

RESULT 30
T03397

hypothetical protein - maize (fragment)

C:Species: Zea mays (maize)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999
C:Accession: T03397

R:Alba, M.M.; Vintil, G.; Messegue, R.; Pages, M.
Submitted to the EMBL Data Library, April 1997

A:Reference number: Z14927
A:Accession: T03397

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-132 <ALB>

A:Cross-references: EMBL:Y12762; NID:e1045993; PIDN:CAA73301.1; PID:e314311
A:Experimental source: strain L.W64-A

Query Match 55.6%; Score 5; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
|||||
DB 101 VSTPV 105

RESULT 31
B60497

MHC class II histocompatibility antigen RT1 D-1 beta chain precursor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 12-Aug-1996
C:Accession: B60497

R:Holowachuk, E.W.; Greer, M.K.
Diabetes 38, 267-271, 1989

A>Title: Unaltered class II histocompatibility antigens and pathogenesis of IDDM in B

A:Reference number: A60497; MUID:9121214
A:Accession: B60497

A:Molecule type: mRNA
A:Residues: 1-134 <HOL>

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplant
F:1-27/Domain: signal sequence #status predicted <SIG>

Query Match 55.6%; Score 5; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
|||||
DB 21 STPVA 25

RESULT 32

E72580
hypothetical protein APE1924 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: E72580

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339

A:Accession: E72580

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-141 <KAW>

A:Cross-references: DDBJ:AP000062; NID:95105244; PIDN:BAA80930.1; PID:Q1044716; PID:9510

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1924

Query Match 55.6%; Score 5; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 VAPRQ 9
|||||
DB 66 VAPRQ 70

RESULT 33

T15056
Photosystem I chain IV - wood tobacco

N:Alternate names: photosystem I chain PSI-E

C:Species: Nicotiana sylvestris (wood tobacco)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C:Accession: T15056

R:Kubota, T.; Yamamoto, Y.; Obokata, J.

Plant Physiol. 108, 1297-1298, 1995

A:Title: Cloning of a nuclear-encoded photosystem I gene, psaEb, in Nicotiana sylvestris

A:Reference number: 218282; MUID:95357419

A:Accession: T15056

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-147 <KUB>

A:Cross-references: EMBL:DA2070; NID:9575606; PIDN:BAA07667.1; PID:Q1217601

C:Genetics:

A:Gene: psaEb

A:Genome: nuclear

A:Introns: 91/3; 113/3

C:Function:

A:Pathway: photosynthesis

C:Superfamily: photosystem I chain IV

C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 55.6%; Score 5; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
|||||
DB 88 VSTPV 92

RESULT 34
C96568
hypothetical protein F6D8.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: C96568

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mailli, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: C96568

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-161 <SMO>

A:Cross-references: GB:AE05173; NID:95903065; PIDN:AAD55624.1; GSPDB:GN00141

C:Genetics:

A:Gene: F6D8.6

A:Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 PVAPT 8
|||||
DB 40 PVAPT 44

RESULT 35

B84018
hypothetical protein BH2946 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000

C:Accession: B84018

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a

A:Reference number: A83650; MUID:20263314

A:Accession: B84018

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-162 <SMO>

A:Cross-references: GB:AP001517; GB:BA000004; NID:910175500; PIDN:BAB06665.1; GSPDB:G

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH2946

Query Match 55.6%; Score 5; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VSTPV 5
|||||
DB 39 VSTPV 43

RESULT 36

S61230
cytochrome-c-biosynthesis heme-carrier protein cyd - Rhizobium leguminosarum

C:Species: Rhizobium leguminosarum

C:Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 29-Sep-1999

C:Accession: S61230

R:Delgado, M.J.; Yeoman, K.H.; Wu, G.; Vargas, C.; Davies, A.; Poole, R.K.; Johnston,

submitted to the EMBL Data Library, July 1995

A:Description: Characterization of the cyhCCKL genes involved in cytochrome c biogenesis
A:Reference number: S61229
A:Accession: S61230
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165
A:Cross-references: EMBL:X89726; NID:9967064; PIDN:CAA61977.1; PID:9967066
C:Superfamily: Escherichia coli cytochrome-c biosynthesis heme-carrier protein come
C:Keywords: carrier protein; chromoprotein; heme; iron; metalloprotein
F:124/Binding site: heme (His) (covalent) #status predicted

Query Match 55.6%; Score 5; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
DB 45 TPVAP 49

RESULT 37
S11770
Iima protein - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 24-Nov-1999
C:Accession: S11770
R:Goehmann, S.; Lehnlester-Maehter, M.; Schlitz, E.; Goebel, W.; Chakraborty, T.
Mol. Microbiol. 4, 1091-1099, 1990
A:Title: Characterization of a Listeria monocytogenes-specific protein capable of inducing
A:Reference number: S11769; MUID:91041717
A:Accession: S11770
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-170 <GOE>
C:Genetics:
A:Gene: Iima
C:Superfamily: Listeria monocytogenes Iima protein

Query Match 55.6%; Score 5; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
DB 164 TPVAP 168

RESULT 38
E83871
hypothetical protein BH1773 [Imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: E83871
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20263314
A:Accession: E83871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <STO>
A:Cross-references: GB:AP001513; GB:BA000004; NID:910174345; PIDN:BA05492.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1773

Query Match 55.6%; Score 5; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSPV 5
|||||
DB 124 VSPV 128

RESULT 39
T50849
hypothetical protein I10K5.14 [Imported] - sorghum (fragment)
C:Species: Sorghum bicolor (sorghum)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50849
R:Titkonov, A.P.; SanMiguel, P.J.; Nakajima, Y.; Gorenstein, N.M.; Bennettzen, J.L.; A
Proc. Natl. Acad. Sci. U.S.A. 96, 7409-7414, 1999
A:Title: Colinearity and its exceptions in orthologous adh regions of maize and sorgh
A:Reference number: Z25261; MUID:99307423
A:Accession: T50849
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-175 <TRK>
A:Cross-references: EMBL:AF124045; PIDN:AD43043.1
A:Experimental source: cultivar BTx623
C:Genetics:
A:Map position: J
A:Note: I10K5.14

Query Match 55.6%; Score 5; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
DB 68 TPVAP 72

RESULT 40
S57789
hypothetical protein (clone ES2A) - barley
C:Species: Hordeum vulgare (barley)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: S57789
R:Speulman, E.; Salamini, F.
Plant Mol. Biol. 28, 915-926, 1995
A:Title: GA(3)-regulated cDNAs from Hordeum vulgare leaves.
A:Reference number: S57787; MUID:95367651
A:Accession: S57789
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-177 <SPE>
A:Cross-references: EMBL:X79466; NID:9929668; PIDN:CAA55976.1; PID:9929669
C:Superfamily: barley hypothetical protein (clone ES2A)

Query Match 55.6%; Score 5; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
DB 140 TPVAP 144

RESULT 41
KKRT
kappa-casein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C:Accession: A03115
R:Nakhasi, H.L.; Grantham, F.H.; Gullino, P.M.
J. Biol. Chem. 259, 14894-14898, 1984
A:Title: Expression of kappa-casein in normal and neoplastic rat mammary gland is und
A:Reference number: A03115; MUID:85054984
A:Accession: A03115

A:Molecule type: mRNA
 A:Residues: 1-178 <NAK>
 C:Cross-references: GB:R02598; NID:g203320; PIDN:AAA40880.1; PID:g203321
 C:Comment: kappa casein stabilizes micelle formation, preventing casein precipitation in
 C:Comment: ProLactin modules the production of kappa casein mRNA.
 C:Superfamily: kappa-casein
 C:Keywords: glycoprotein; mammary gland; phosphoprotein
 F:1-21/Domains: signal sequence #status predicted <SIG>
 F:12-17/Product: kappa-casein #status predicted <KCA>
 F:11/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:15-16/Cleavage site: Phe-Leu (chymosin) #status predicted
 F:120,145,165/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 55.6%; Score 5; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
 |||||
 DB 139 VSTPV 143

RESULT 42
 S56300
 hypothetical protein YFR045w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein R014
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000
 C:Accession: S56300; S62256; S63792
 R:Murakami, Y.; Naitou, M.; Hagihara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sasano
 submitted to the EMBL Data Library, May 1995
 A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce
 A:Reference number: S56186
 A:Accession: S56300
 A:Molecule type: DNA
 A:Residues: 1-178 <MUR>
 A:Cross-references: EMBL:D50617; NID:g836685; PIDN:BA09284.1; PID:g836800; MIPS:YFR045w
 R:Murakami, Y.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: S62256
 A:Accession: S62256
 A:Molecule type: DNA
 A:Residues: 1-178 <MUW>
 A:Cross-references: EMBL:D44597; NID:g871938; PIDN:BA08011.1; PID:g871944
 R:EKI, T.; Naitou, M.; Hagihara, H.; Ozawa, M.; Sasamura, S.I.; Sasamura, M.; Tsuchiya,
 Yeast 12, 149-167, 1996
 A:Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome Y
 A:Reference number: S63787; MUID:96287652
 A:Accession: S63792
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 101-154 <EKI>
 A:Cross-references: EMBL:D44597
 C:Genetics:
 A:Map position: 6R
 A:Note: YFR045w
 C:Superfamily: hypothetical protein YFR045w; ADP-ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein

Query Match 55.6%; Score 5; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
 |||||
 DB 27 STPVA 31

RESULT 43
 S01400
 H+-transporting ATP synthase (EC 3.6.1.34) delta chain - thermophilic bacterium PS-3

C:Species: thermophilic bacterium PS-3
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 22-Jun-1999
 C:Accession: S01400
 R:Ohba, S.; Yoda, M.; Ishizuka, M.; Hirata, H.; Hamamoto, T.; Otawara-Hamamoto, Y.;
 Blochim. Biophys. Acta 933, 141-155, 1988
 A:Title: Sequence and over-expression of subunits of adenosine triphosphate synthase
 A:Reference number: S01397; MUID:88163679
 A:Accession: S01400
 A:Molecule type: DNA
 A:Residues: 1-179 <OHT>
 A:Cross-references: EMBL:X07804; NID:g45808; PIDN:CAA30651.1; PID:g45813
 A:Note: part of this sequence, including the amino end of the mature protein, was con
 C:Superfamily: H+-transporting ATP synthase delta chain
 C:Keywords: ATP biosynthesis; hydrolase
 F:1-179/Product: H+-transporting ATP synthase delta chain #status experimental <MAT>

Query Match 55.6%; Score 5; DB 2; Length 179;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
 |||||
 DB 69 VSTPV 73

RESULT 44
 G84789
 hypothetical protein At2g37200 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84789
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beilto, M.I.; Town, C.D.; Fujii, C.Y
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon,
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84789
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-179 <STO>
 A:Cross-references: GB:AE002093; NID:g4371281; PIDN:AA018139.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g37200
 A:Map position: 2

Query Match 55.6%; Score 5; DB 2; Length 179;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
 |||||
 DB 15 PVAPT 19

RESULT 45
 A05080
 kappa-casein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 23-Feb-1997
 C:Accession: A05080
 R:Thompson, M.D.; Dave, J.R.; Nakhast, H.L.
 DNA 4, 263-271, 1985
 A:Reference number: A05080; MUID:86004062
 A:Accession: A05080
 A:Molecule type: mRNA
 A:Residues: 1-181 <THO>
 A:Note: the authors translated the codon GAU for residue 27 as Asn
 C:Superfamily: kappa-casein
 C:Keywords: phosphoprotein

Query Match 55.6%; Score 5; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

OY 1 VSTPV 5
|||||
Db 142 VSTPV 146

RESULT 46

D96572
Protein F12M16.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96572
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D96572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <STO>
A:Cross-references: GB:AE005173; NID:97769876; PIDN:AAF69554.1; GSPDB:GN00141
C:Genetics:
A:Gene: F12M16.6
A:Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
|||||
Db 12 PVAPT 16

RESULT 47

H86404
Probable lipid transfer protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H86404
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H86404
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <STO>
A:Cross-references: GB:AE005172; NID:911024871; PIDN:AAG26955.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match

55.6%; Score 5; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
Db 139 TPVAP 143

RESULT 48

D85875
Probable minor fibrial subunit Z3598 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: D85875
R:Penna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamotis, K.; Apoda
Nature 409, 523-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:AE005174; NID:912516700; PIDN:AAG57464.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3598

Query Match 55.6%; Score 5; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
|||||
Db 48 VSTPV 52

RESULT 49

F86832
Hypothetical protein yrbB [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: F86832
R:Boletín, A.; Winkler, P.; Mauger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: F86832
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <STO>
A:Cross-references: GB:AE005176; NID:912724674; PIDN:AAK05760.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yrbB

Query Match 55.6%; Score 5; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPRO 9
|||||
Db 96 VAPRO 100

RESULT 50

S69748
Hypothetical protein YDR537c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 04-Mar-2000
C:Accession: S69748

R: Dietrich, F.S.; Mulligan, J.; Allen, E.; Arango, R.; Aviles, E.; Berro, A.; Carpenter, H.; Lin, D.; Mosedale, D.; Nakahara, K.; Namath, A.; Oefner, P.; Oh, C.; Petel, F.X.; R
W. submitted to the EMBL Data Library, December 1995
A: Reference number: S62017
A: Accession: S69748
A: Molecule type: DNA
A: Residues: 1-201 <DIE>
A: Cross-references: EMBL:U43834; NID:G1165292; PID:q2194177; GSPDB:GN00004; MIPS:YDR537C
C: Geneticks:
A: Gene: MIPS:YDR537C
A: Map position: 4R
C: Superfamily: Saccharomyces cerevisiae hypothetical protein YDR537C

Query Match	55.6%	Score 5:	DB 2:	Length 201:
Best Local Similarity	100.0%	Pred. No.	1	5e+02:
Matches	5:	Conservative	0:	Mismatches 0:
				Indels 0:
				Gaps 0:
OY	3	TPVAP	7	
DB	121	TPVAP	125	

Search completed: August 15, 2001, 12:34:31
Job time: 96 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:34:50 ; Search time 20.38 seconds
(without alignments)
15.128 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 9

Sequence: 1 VSTPVAPro 9

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	484	1 P60_LISMO	P21171 listeria mo
2	6	66.7	155	1 PRS1_SOLTU	P17641 solanum tub
3	6	66.7	187	1 VGG_BPPIK	Q38042 bacterioph
4	6	66.7	239	1 SOD3_PLEBO	P50060 plectonema
5	6	66.7	453	1 GATTA_HELPJ	Q92113 helicobacte
6	6	66.7	453	1 GATTA_HELPY	P56114 helicobacte
7	6	66.7	711	1 CADA_LISMO	Q60048 listeria mo
8	6	66.7	865	1 CPN1_DROME	Q02910 drosophila
9	6	66.7	1540	1 RML_DROME	Q9y7h4 drosophila
10	5	55.6	103	1 KAC4_RABIT	P01840 oryctolagus
11	5	55.6	104	1 ST12_MOUSE	Q62401 mus musculu
12	5	55.6	114	1 PSSP_HUMAN	P08118 homo sapien
13	5	55.6	166	1 YELJ_SCHPO	O13883 schizosacch
14	5	55.6	178	1 CASK_RAT	P04468 rattus norv
15	5	55.6	178	1 YFL5_YEAST	P43617 saccharomyc
16	5	55.6	179	1 ARPD_BACD3	P09220 bacillus ps
17	5	55.6	181	1 CASK_MOUSE	P06796 mus musculu
18	5	55.6	217	1 V33P_ADE41	P19416 human adeno
19	5	55.6	218	1 RPE_TREPA	O66107 treponema p
20	5	55.6	225	1 Y574_AERPE	Q9yeka4 aeropyrum p
21	5	55.6	229	1 PRL_BOVIN	P01239 bos taurus
22	5	55.6	229	1 PRL_CAPHI	O28318 capra hircu
23	5	55.6	229	1 PRL_SHEEP	P01240 ovis aries
24	5	55.6	261	1 HB21_HUMAN	P01918 homo sapien
25	5	55.6	261	1 HB24_HUMAN	P01920 homo sapien
26	5	55.6	263	1 GP3D_CHLTR	P10557 chlamydia t
27	5	55.6	264	1 PSBP_FRING	O49080 fritillaria
28	5	55.6	268	1 HB2X_HUMAN	P05538 homo sapien
29	5	55.6	271	1 YSM4_CAEEL	Q10124 caenorhabdi
30	5	55.6	277	1 Y4OR_RHISN	P35603 rhizobium s
31	5	55.6	303	1 PPV_DROME	Q27884 drosophila
32	5	55.6	305	1 PPP6_HUMAN	O00743 homo sapien
33	5	55.6	305	1 PPP6_RAT	Q64620 rattus norv

34	5	55.6	309	1 POLG_HCVH7	P27955 hepatitis c
35	5	55.6	314	1 ACCO_MALDO	O00985 malus domes
36	5	55.6	321	1 SPLR_NPYOP	O65328 oryza pseu
37	5	55.6	323	1 PF27_MOUSE	P52875 mus musculu
38	5	55.6	325	1 HMGL_HUMAN	P35914 homo sapien
39	5	55.6	325	1 MODD_MYCBO	O30620 mycobacteri
40	5	55.6	325	1 MODD_MYCBO	O50906 mycobacteri
41	5	55.6	325	1 MODD_MYCBO	P21574 xenopus lae
42	5	55.6	337	1 R13_METTH	O26110 methanobact
43	5	55.6	354	1 YWA3_MYCBO	Q02279 mycobacteri
44	5	55.6	356	1 HIS8_ECOLI	P06986 escherichia
45	5	55.6	359	1 HIS9_SALTY	P10369 salmonella
46	5	55.6	362	1 SRK2_SPOA	P42688 spongilla l
47	5	55.6	366	1 RRPO_REOVD	P03526 reovirus (t
48	5	55.6	366	1 RRPO_REOVD	P12002 reovirus (t
49	5	55.6	366	1 RRPO_REOVL	P07940 reovirus (t
50	5	55.6	366	1 YH85_YEAST	O04806 saccharomyc
51	5	55.6	367	1 MTG1_CHVT3	P36216 chlorella v
52	5	55.6	367	1 NUIJM_PODAN	P19041 podosporea a
53	5	55.6	377	1 TTL_BOVIN	P38584 bos taurus
54	5	55.6	379	1 TTL_PIG	P38160 sus scrofa
55	5	55.6	380	1 SUC2_ARCFU	O28097 archaeoglob
56	5	55.6	380	1 YMH7_CAEEL	P34474 caenorhabdi
57	5	55.6	386	1 YG5V_YEAST	P53334 saccharomyc
58	5	55.6	390	1 EMRA_ECOLI	P27303 escherichia
59	5	55.6	391	1 THAB_PAROL	O91242 paralichthy
60	5	55.6	394	1 ALR2_BACSU	P94494 bacillus su
61	5	55.6	414	1 HRTD_CROAT	P15167 croctalus at
62	5	55.6	415	1 YLN2_CAEEL	O18964 caenorhabdi
63	5	55.6	423	1 ODB2_PSEPU	P09062 pseudomonas
64	5	55.6	428	1 SCK_HUMAN	P98077 homo sapien
65	5	55.6	432	1 BRAC_XENLA	P24781 xenopus lae
66	5	55.6	435	1 RAS2_KLULA	P41768 kluyveromyc
67	5	55.6	442	1 TTG_CHLYR	O84713 chlamydia t
68	5	55.6	453	1 YOTA_CAEEL	P34656 caenorhabdi
69	5	55.6	458	1 RRA_XENLA	P51126 xenopus lae
70	5	55.6	468	1 PCOL_MOUSE	O61398 mus musculu
71	5	55.6	468	1 PCOL_RAT	O08628 rattus norv
72	5	55.6	470	1 GLNA_FREDI	P33035 fremyella d
73	5	55.6	473	1 GLNA_SYNT3	P77961 synechocyst
74	5	55.6	473	1 YCLC_BACSU	P94405 bacillus su
75	5	55.6	474	1 YDCQ_STRD7	O94697 streptomyce
76	5	55.6	474	1 VP61_NPYOP	O10270 oryza pseu
77	5	55.6	478	1 HRTF_CROAT	P34182 croctalus at
78	5	55.6	480	1 DISA_TRIGA	P15503 trimeresuru
79	5	55.6	488	1 EXON_HSV62	P24447 human herpe
80	5	55.6	488	1 PE24_RABIT	P52448 human herpe
81	5	55.6	488	1 SPL1_CANAL	P87185 candida alb
82	5	55.6	498	1 ACHP_HUMAN	P30926 homo sapien
83	5	55.6	501	1 YH92_CAEEL	O23236 caenorhabdi
84	5	55.6	504	1 ARF5_HUMAN	O13568 homo sapien
85	5	55.6	509	1 CPT7_BOVIN	P05185 bos taurus
86	5	55.6	509	1 CX56_CHICK	P24415 gallus galli
87	5	55.6	509	1 PSBB_GUTHR	O75511 gallinula
88	5	55.6	509	1 VLI_HPV49	P38742 human papil
89	5	55.6	510	1 PUR1_YEAST	P04046 saccharomyc
90	5	55.6	512	1 VLI_HPV24	P05079 human papil
91	5	55.6	514	1 VLI_HPV2	P06417 human papil
92	5	55.6	514	1 VLI_HPV47	P22424 human papil
93	5	55.6	514	1 VLI_HPV4	P50818 human papil
94	5	55.6	515	1 VLI_HPV50	P24424 human papil
95	5	55.6	516	1 VLI_HPV05	P06917 human papil
96	5	55.6	516	1 VLI_HPV20	P50787 human papil
97	5	55.6	516	1 VLI_HPV30	P50812 human papil
98	5	55.6	517	1 VLI_HPV12	P36733 human papil
99	5	55.6	517	1 VLI_HPV25	O02051 human papil
100	5	55.6	518	1 VLI_HPV14	P36734 human papil
101	5	55.6	518	1 VLI_HPV21	P50787 human papil
102	5	55.6	525	1 VLI_HPV58	P25537 human papil
103	5	55.6	546	1 VLI_HPV19	O02050 human papil
104	5	55.6	552	1 COX1_SYNVU	O02676 synechococc
105	5	55.6	556	1 CAG1_DROME	O94350 drosophila
106	5	55.6	562	1 CHS5_CANAL	O74161 candida alb

107	5	55.6	601	1	DNM_MYCGE	P47442	mycoplasma	180	4	44.4	48	1	TXA2_RADPA	P01534	radiantanthus
108	5	55.6	604	1	BAP2_YEAST	P41815	saccharomyc	181	4	44.4	60	1	YTR2_SPIAU	P22042	spirochaeta
109	5	55.6	609	1	BAP3_YEAST	P38084	saccharomyc	182	4	44.4	62	1	UCR3_BOVIN	P00130	bos taurus
110	5	55.6	612	1	SYT_HELPJ	O92m03	helicobacte	183	4	44.4	63	1	ANP2_MACAM	P19609	macrozoarc
111	5	55.6	612	1	SYT_HELPY	P56071	helicobacte	184	4	44.4	64	1	ANP2_MACAM	P19608	macrozoarc
112	5	55.6	614	1	YEO_ECOLI	P33353	eschlerichia	185	4	44.4	65	1	YNOL_RHIFR	P33214	thiobolium f
113	5	55.6	634	1	VEI_HPVS1	P26544	human papil	186	4	44.4	66	1	YGLR_STRCO	O05954	streptomyce
114	5	55.6	634	1	Z147_MOUSE	O61510	mus musculu	187	4	44.4	66	1	YYCD_BACSV	P37480	bacillus su
115	5	55.6	642	1	DP3X_SALTY	P74876	salmonella	188	4	44.4	67	1	HJAI_METJA	O57632	methanococc
116	5	55.6	643	1	DP3X_ECOLI	P66710	eschlerichia	189	4	44.4	67	1	HJAI_METJA	O58342	methanococc
117	5	55.6	644	1	ARNT_DRDME	O15945	drosoophila	190	4	44.4	67	1	HJAI_METJA	O58655	methanococc
118	5	55.6	648	1	YDEE_SCHPO	O10447	schizosacch	191	4	44.4	67	1	HJAI_METJA	O60264	methanococc
119	5	55.6	649	1	DREB_HUMAN	O16643	homo sapien	192	4	44.4	70	1	F261_MOUSE	P70286	mus musculu
120	5	55.6	671	1	ALYS_ENTFA	P37710	enterococcu	193	4	44.4	71	1	RL30_MYCLE	O33001	mycobacteri
121	5	55.6	707	1	BMP1_XENTIA	P98070	xenopus lae	194	4	44.4	72	1	CCAA_ECOLI	O46595	eschlerichia
122	5	55.6	760	1	AHM4_ARATH	O9szw5	arabidopsis	195	4	44.4	72	1	VG35_BPM15	O05235	mycobacteri
123	5	55.6	767	1	YNYT_YEAST	P53852	saccharomyc	196	4	44.4	77	1	RUXG_YEAST	P40204	saccharomyc
124	5	55.6	781	1	YGS5_YEAST	P53316	saccharomyc	197	4	44.4	79	1	PSBH_CHDVU	P56323	chlorella v
125	5	55.6	790	1	SMY2_YEAST	P32909	saccharomyc	198	4	44.4	80	1	GONI_CLAGA	P33459	claris gar
126	5	55.6	794	1	PMS1_SCHPO	P54280	schizosacch	199	4	44.4	87	1	ANP1_MACAM	P07457	macrozoarc
127	5	55.6	806	1	NUOG_MYCTU	P95175	mycobacteri	200	4	44.4	87	1	ANP5_MACAM	P19607	macrozoarc
128	5	55.6	808	1	FTFB_DRDME	O05192	drosoophila	201	4	44.4	87	1	ANPD_MACAM	P19604	macrozoarc
129	5	55.6	811	1	Y104_SYNY3	P54371	synecocyst	202	4	44.4	93	1	IM05_ARATH	O9x9Y9	arabidopsis
130	5	55.6	817	1	VRP1_YEAST	P37370	saccharomyc	203	4	44.4	93	1	YQIC_CABEL	O09283	caenorhabdi
131	5	55.6	834	1	POLG_ENNGO	P12296	mengo encp	204	4	44.4	98	1	P531_MOUSE	P70399	mus musculu
132	5	55.6	835	1	INVA_YEREN	P19196	yersinia en	205	4	44.4	99	1	SY08_BOVIN	O09141	bos taurus
133	5	55.6	836	1	Y167_HUMAN	O99490	homo sapien	206	4	44.4	100	1	POL_SIV33	P12501	simlan immu
134	5	55.6	845	1	RRPO_IPNVJ	P22173	infectious	207	4	44.4	101	1	VNST_BUNYW	P16494	bunyamwera
135	5	55.6	866	1	DYN2_MOUSE	P39054	mus musculu	208	4	44.4	101	1	VNST_MAGV	P16605	maguari vlr
136	5	55.6	870	1	DYN2_HUMAN	P50570	homo sapien	209	4	44.4	102	1	SGP3_CHRVI	O52055	chromatium
137	5	55.6	870	1	DYN2_RAT	P39052	rattus norv	210	4	44.4	102	1	VE7_PAPVE	P01331	deer papill
138	5	55.6	901	1	POLG_ENNG3	P32540	mengo encp	211	4	44.4	102	1	VE7_PAPVE	P13132	europan el
139	5	55.6	909	1	CT1A_FUSO	P52958	fusarium so	212	4	44.4	103	1	LAC_CHICK	P20763	gallus gall
140	5	55.6	930	1	PRGR_RABIT	P06186	oryctolagus	213	4	44.4	104	1	GAST_BOVIN	P01352	bos taurus
141	5	55.6	933	1	PRGR_HUMAN	P06401	homo sapien	214	4	44.4	104	1	GAST_SHEEP	O02686	ovis aries
142	5	55.6	939	1	ST20_YEAST	O03487	saccharomyc	215	4	44.4	104	1	YR7H_ECOLI	P21322	eschlerichia
143	5	55.6	951	1	AHM5_ARATH	O9szw4	arabidopsis	216	4	44.4	105	1	LAC_HUMAN	P01842	homo sapien
144	5	55.6	953	1	Y442_HUMAN	O9upv9	homo sapien	217	4	44.4	105	1	NDQ1_BRAJA	P26024	bradyrhizob
145	5	55.6	954	1	BIR1_YEAST	P47134	saccharomyc	218	4	44.4	105	1	YMO3_CABEL	P34494	caenorhabdi
146	5	55.6	983	1	Y144_HUMAN	O14157	homo sapien	219	4	44.4	106	1	KACB_RABIT	P01839	oryctolagus
147	5	55.6	986	1	BMP1_HUMAN	P13497	homo sapien	220	4	44.4	106	1	TBCA_YEAST	P48606	saccharomyc
148	5	55.6	991	1	BMP1_MOUSE	P98063	mus musculu	221	4	44.4	107	1	U139_ARATH	O9s888	arabidopsis
149	5	55.6	1009	1	DPOL_HSVSA	P24907	herpesvltus	222	4	44.4	108	1	HDEB_ECOLI	P26605	eschlerichia
150	5	55.6	1018	1	HMW1_MYCPN	O50365	mycoplasma	223	4	44.4	109	1	CORT_MOUSE	P56469	mus musculu
151	5	55.6	1027	1	POL_SIVC2	P17283	chimpanzee	224	4	44.4	112	1	CL34_DROMI	O01774	drosoophila
152	5	55.6	1057	1	SEFI_YEAST	P34228	saccharomyc	225	4	44.4	113	1	Y12K_BPPHH	P23788	bacteriopho
153	5	55.6	1141	1	MYPS_HUMAN	O00872	homo sapien	226	4	44.4	114	1	CU05_HOMAM	P81389	homoarv ame
154	5	55.6	1171	1	NIEF_KLEPN	P03833	klebsiella	227	4	44.4	114	1	ET3_RABIT	P19998	oryctolagus
155	5	55.6	1172	1	AHM2_ARATH	O64474	arabidopsis	228	4	44.4	115	1	GUAN_RAT	P28902	rattus norv
156	5	55.6	1178	1	RPOB_MYCTU	P47766	mycobacteri	229	4	44.4	115	1	KV51_MOUSE	P01642	mus musculu
157	5	55.6	1179	1	RPOB_MYCLE	P30760	mycobacteri	230	4	44.4	116	1	B2MG_BRARE	O04475	brachydanto
158	5	55.6	1213	1	T2D2_DRDME	O24325	drosoophila	231	4	44.4	116	1	GUAN_MOUSE	P33680	mus musculu
159	5	55.6	1253	1	POLS_SFV	P03315	semliki for	232	4	44.4	117	1	NLT5_ORYSA	O65091	oryza sativ
160	5	55.6	1293	1	IRR_HUMAN	P14616	homo sapien	233	4	44.4	119	1	MLP3_BOVIN	O4315	bos taurus
161	5	55.6	1300	1	IRR_CAYPO	P14617	cavia porce	234	4	44.4	120	1	CUT1_ARADI	P80515	ataeneus dia
162	5	55.6	1337	1	P152_YEAST	P39685	saccharomyc	235	4	44.4	120	1	YRM7_CABEL	O09416	caenorhabdi
163	5	55.6	1500	1	SSP5_STRGN	P16932	streptococc	236	4	44.4	121	1	RLA2_TAESO	P50879	taenila soil
164	5	55.6	1627	1	ADP1_MYCPN	P11311	mycoplasma	237	4	44.4	121	1	YH1P_AOUAE	O65336	aquifex aeo
165	5	55.6	1670	1	CA34_HUMAN	O01955	homo sapien	238	4	44.4	124	1	SGP2_CHRVI	O52179	chromatium
166	5	55.6	1736	1	ZOL_HUMAN	O07157	homo sapien	239	4	44.4	124	1	VNS4_CVMS	P29075	murine coro
167	5	55.6	1781	1	AKAC_HUMAN	O02952	homo sapien	240	4	44.4	125	1	FLIO_SALTY	P54699	salmonella
168	5	55.6	1794	1	YAVI_SCHPO	O10172	schizosacch	241	4	44.4	126	1	CU24_ARADI	P80516	ataeneus dia
169	5	55.6	1833	1	ZEPI_HUMAN	P31629	homo sapien	242	4	44.4	127	1	CB21_EUGGR	P12327	euglena gra
170	5	55.6	2208	1	POLN_MANCV	O69014	manchester	243	4	44.4	127	1	YCB2_ARADI	P480517	ataeneus dia
171	5	55.6	2290	1	POLG_EMKV	P03304	encephalomyc	244	4	44.4	127	1	YCBK_HAEIN	P44384	haemophilus
172	5	55.6	2292	1	POLG_EMKVB	P17593	encephalomyc	245	4	44.4	127	1	YFID_HAEIN	P44455	haemophilus
173	5	55.6	2292	1	POLG_EMKVD	P17594	encephalomyc	246	4	44.4	129	1	IGF2_MUSVI	P41694	muscicla vis
174	5	55.6	2440	1	NCRI_HUMAN	O75376	homo sapien	247	4	44.4	129	1	RL7_TREPA	O83368	treponema p
175	5	55.6	2476	1	ZAN_PIG	O28983	sus scrofa	248	4	44.4	130	1	RS8_METVA	P14038	methanococc
176	5	55.6	3133	1	HMC7_BOMO	P98092	bombyx mori	249	4	44.4	130	1	YNO5_MYCTU	P71056	mycobacteri
177	5	55.6	3418	1	BRC2_HUMAN	P51587	homo sapien	250	4	44.4	131	1	YNO9_YEAST	P53841	saccharomyc
178	4	44.4	48	1	TXA1_RADMA	P30831	radiantanthus	251	4	44.4	132	1	HEX9_ADE40	P48312	human adeno
179	4	44.4	48	1	TXA2_RADMA	P30783	radiantanthus	252	4	44.4	132	1	IF5A_METJA	O58625	methanococc

253	4	44.4	133	1	HEX9_ADE41	P32539	human	adeno	326	4	44.4	164	1	YOJ3_CAEEL	P34626	caenorhabd1
254	4	44.4	133	1	PROF_HELAN	094982	helianthus		327	4	44.4	167	1	VNS3_BMDNV	P05841	hombry dens
255	4	44.4	133	1	RS8_LEPIN	081282	leptosira		328	4	44.4	168	1	HEM2_SALTY	P37408	salmonella
256	4	44.4	133	1	RS8_METTH	026126	methanobact		329	4	44.4	168	1	YNP7_YEAST	P53897	saccharomyc
257	4	44.4	135	1	PIL6_PSEAE	P46384	pseudomonas		330	4	44.4	171	1	IF3_LISMO	053084	listeria mo
258	4	44.4	136	1	EXB2_XANCP	034258	xanthomonas		331	4	44.4	171	1	YSYM_RHIET	008815	rhizobium e
259	4	44.4	137	1	NIFB_KLEOX	P56265	klebsiella		332	4	44.4	172	1	RUB2_PSEOL	P00227	pseudomonas
260	4	44.4	138	1	CXA4_PIG	029559	sus scrofa		333	4	44.4	174	1	NEUJ_RAT	P12760	rattus norv
261	4	44.4	138	1	NEDR_MICVI	002835	micromonos		334	4	44.4	175	1	LPFE_SALTY	P33664	salmonella
262	4	44.4	140	1	MRP_CLOPE	P53381	clostridium		335	4	44.4	175	1	RBS_AEGSO	Q38793	aegilops sq
263	4	44.4	140	1	Y14K_CSMY	P18920	chlortis str		336	4	44.4	176	1	CON8_NEUCO	P01669	neurospora
264	4	44.4	140	1	YB60_HELPY	025775	helicobacte		337	4	44.4	176	1	IPYR_AERPE	Q9YBA5	aeropyrum p
265	4	44.4	141	1	AT92_HUMAN	006055	homo sapien		338	4	44.4	178	1	ATPD_BACCA	P41011	baetillus ca
266	4	44.4	141	1	MPL3_RAT	062625	rattus norv		339	4	44.4	179	1	IGF2_HORSE	PK275	TOBAC
267	4	44.4	142	1	IL3_CALJA	Q28334	callithrix		340	4	44.4	180	1	IGF2_HUMAN	IF22	HUMAN
268	4	44.4	142	1	IL3_SAGOE	P51445	saguius oe		341	4	44.4	180	1	YMER_STYAU	YMER	STYAU
269	4	44.4	142	1	RECX_PSEPU	P37862	pseudomonas		342	4	44.4	180	1	YPKW_THRCU	YPKW	THRCU
270	4	44.4	142	1	Y83A_METJA	P81322	methanococc		343	4	44.4	181	1	IGF2_HORSE	IGF2	HORSE
271	4	44.4	142	1	YJ87_MYCTU	010870	mycobacteri		344	4	44.4	181	1	IGF2_PIG	IGF2	PIG
272	4	44.4	143	1	AT92_BOVIN	P07926	bos taurus		345	4	44.4	181	1	NUSG_BUCAI	NUSG	BUCAI
273	4	44.4	143	1	AT92_SHEEP	006056	ovis aries		346	4	44.4	182	1	RBS_MANES	RBS	MANES
274	4	44.4	143	1	IL4_MERUN	P47966	meriones un		347	4	44.4	183	1	OLEC_BRANA	OLEC	BRANA
275	4	44.4	143	1	PER_DROPI	Q25206	drosophila		348	4	44.4	184	1	NUSG_BORBU	NUSG	BORBU
276	4	44.4	143	1	SGCA_ECOLI	P39363	escherichia		349	4	44.4	185	1	SC6_SCHCO	SC6	SCHCO
277	4	44.4	144	1	HEX9_ADE12	P03284	human adeno		350	4	44.4	186	1	ARDH_LEIDO	ARDH	LEIDO
278	4	44.4	144	1	RISB_PHOLE	001994	photobacter		351	4	44.4	187	1	BNZB_PSEPU	BNZB	PSEPU
279	4	44.4	145	1	YNR9_YEAST	P53880	saccharomyc		352	4	44.4	187	1	MAVE_METEX	MAVE	METEX
280	4	44.4	146	1	H2B_TOBAC	P93354	nicotiana t		353	4	44.4	187	1	TOD2_PSEPU	TOD2	PSEPU
281	4	44.4	146	1	HBB1_ONCMY	P02142	oncorhynchu		354	4	44.4	190	1	WS3_HUMAN	WS3	HUMAN
282	4	44.4	147	1	YACA_ECOLI	P10409	escherichia		355	4	44.4	190	1	YBAY_ECOLI	YBAY	ECOLI
283	4	44.4	151	1	SOD1_LYCES	P14830	lycopersico		356	4	44.4	190	1	YELM_SALTY	YELM	SALTY
284	4	44.4	152	1	CORA_RAT	Q65332	rattus norv		357	4	44.4	191	1	HQPE_RHILV	HQPE	RHILV
285	4	44.4	152	1	PSAL_SYNP2	Q54755	synechococc		358	4	44.4	191	1	PGHD_CANPA	PGHD	CANPA
286	4	44.4	152	1	PYR1_PYRHO	058452	pyrococcus		359	4	44.4	191	1	RL3_HELPY	RL3	HELPY
287	4	44.4	153	1	PSAL_PORPU	P51222	porphyra pu		360	4	44.4	191	1	KADA_METVO	KADA	METVO
288	4	44.4	153	1	RECX_PSEAE	P37860	pseudomonas		361	4	44.4	192	1	PM1_HUMAN	PM1	HUMAN
289	4	44.4	153	1	YPH4_CHRYI	P45373	chromatium		362	4	44.4	192	1	ASH2_HUMAN	ASH2	HUMAN
290	4	44.4	154	1	PUTR_RHOCA	052710	rhodobacter		363	4	44.4	193	1	HIS7_SUSO	HIS7	SUSO
291	4	44.4	155	1	BCCP_HAETN	P43874	haemophilus		364	4	44.4	193	1	PGHD_HORSE	PGHD	HORSE
292	4	44.4	155	1	PRL_PHAUV	P25985	phaseolus v		365	4	44.4	194	1	HPPK_SYNT3	HPPK	SYNT3
293	4	44.4	155	1	PR2_PHAUV	P25986	phaseolus v		366	4	44.4	195	1	YI33_AGRU	YI33	AGRU
294	4	44.4	156	1	CU55_ARADI	P80518	araneus dia		367	4	44.4	195	1	AMEL_MOUSE	AMEL	MOUSE
295	4	44.4	156	1	MAFK_HUMAN	060675	homo sapien		368	4	44.4	200	1	SSUE_PSEPU	SSUE	PSEPU
296	4	44.4	157	1	FLIN_PSEAE	051466	pseudomonas		369	4	44.4	201	1	COAT_LVX	COAT	LVX
297	4	44.4	157	1	HS2C_CHURE	P12811	chlamydomon		370	4	44.4	201	1	RB1B_RAT	RB1B	RAT
298	4	44.4	157	1	PRTG_CANPA	Q28278	canis famli		371	4	44.4	201	1	YPT1_PHYTN	YPT1	PHYTN
299	4	44.4	157	1	YI17_YEAST	P40502	saccharomyc		372	4	44.4	202	1	AMEL_MONDO	AMEL	MONDO
300	4	44.4	158	1	YI02_BP12	P42547	bacteriopho		373	4	44.4	202	1	COAT_ELV	COAT	ELV
301	4	44.4	158	1	ILVH_BUCAP	085294	buchnera ap		374	4	44.4	202	1	HR2A_TRIFL	HR2A	TRIFL
302	4	44.4	158	1	SAM2_SOYBN	P26987	glycine max		375	4	44.4	202	1	RAB1_DISOM	RAB1	DISOM
303	4	44.4	158	1	Y524_METJA	057944	methanococc		376	4	44.4	202	1	SDC4_RAT	SDC4	RAT
304	4	44.4	159	1	CU57_ARADI	P80519	araneus dia		377	4	44.4	202	1	TZM2_METTF	TZM2	METTF
305	4	44.4	159	1	YBAK_ECOLI	P31175	escherichia		378	4	44.4	204	1	BFY3_MOUSE	BFY3	MOUSE
306	4	44.4	159	1	PETD_ODOSI	P31174	salmonella		379	4	44.4	205	1	HYFA_ECOLI	HYFA	ECOLI
307	4	44.4	160	1	PHAA_CVAPA	P49489	odonotelia s		380	4	44.4	205	1	RAB1_LYMET	RAB1	LYMET
308	4	44.4	160	1	RI10_METTH	027191	methanobact		381	4	44.4	205	1	RB1A_HUMAN	RB1A	HUMAN
309	4	44.4	160	1	RI21_CAEEL	P34334	caenorhabd1		382	4	44.4	205	1	COBH_METTH	COBH	METTH
310	4	44.4	161	1	ID4_MOUSE	P41139	mus musculu		383	4	44.4	206	1	Y086_CAEEL	Y086	CAEEL
311	4	44.4	161	1	VG41_HSVSA	001027	herpesvirus		384	4	44.4	206	1	PICR_PSEAE	PICR	PSEAE
312	4	44.4	162	1	MAFG_HUMAN	015525	homo sapien		385	4	44.4	207	1	CSF3_MOUSE	CSF3	MOUSE
313	4	44.4	162	1	MAFG_MOUSE	054790	mus musculu		386	4	44.4	208	1	IL16_HORSE	IL16	HORSE
314	4	44.4	163	1	HMCS_DICDI	P54872	dicyosteli		387	4	44.4	208	1	NOLV_RHISN	NOLV	RHISN
315	4	44.4	163	1	ILVH_ECOLI	P00894	escherichia		388	4	44.4	208	1	SPC3_STRPU	SPC3	STRPU
316	4	44.4	163	1	ILVH_HAETN	P45260	haemophilus		389	4	44.4	208	1	YC02_KLEPN	YC02	KLEPN
317	4	44.4	163	1	ILVH_SALTY	P21622	salmonella		390	4	44.4	209	1	YLZ3_CAEEL	YLZ3	CAEEL
318	4	44.4	164	1	FLAV_HELPJ	Q94K53	helicobacte		391	4	44.4	209	1	COBH_METJA	COBH	METJA
319	4	44.4	164	1	FLAV_HELPJ	Q25776	helicobacte		392	4	44.4	210	1	RS7_HAUA	RS7	HAUA
320	4	44.4	164	1	IM17_SCHPO	P87130	schizosacch		393	4	44.4	210	1	T1P1_YEAST	T1P1	YEAST
321	4	44.4	164	1	NOLB_RHTR	P33208	rhizobium f		394	4	44.4	210	1	DEDD_ECOLI	DEDD	ECOLI
322	4	44.4	164	1	NOLB_RHTR	P55713	rhizobium s		395	4	44.4	211	1	TX10_HUMAN	TX10	HUMAN
323	4	44.4	164	1	T2DA_XENLA	091858	xenopus lae		396	4	44.4	211	1			
324	4	44.4	164	1	TSTP_HSVSA	P18347	herpesvirus		397	4	44.4	211	1			
325	4	44.4	164	1					398	4	44.4	211	1			

399	4	44.4	212	1	YTFB_ECOLI	P39310	eschlerichia	472	4	44.4	244	1	YR01_CAEEL	Q10014
400	4	44.4	213	1	CHRR_RHOSH	P40655	rhodobacter	473	4	44.4	245	1	KAD_CHLTR	084130
401	4	44.4	213	1	HISS_LESPN	O91623	legionella	474	4	44.4	246	1	SIX6_HUMAN	095475
402	4	44.4	213	1	KITH_RHOSI	O91623	rhodothermu	475	4	44.4	246	1	Y984_CAMJE	045191
403	4	44.4	214	1	RSMB_RAT	P17136	rattus norv	476	4	44.4	247	1	CUP3_MYCTU	P63318
404	4	44.4	214	1	SC14_SCACO	P35755	schizophylli	477	4	44.4	247	1	PMX2_MOUSE	006348
405	4	44.4	215	1	Y034_NPVAC	P21287	autographa	478	4	44.4	247	1	RS3_CAEEL	P48152
406	4	44.4	217	1	YD67_SCHPO	O10319	schizosacch	479	4	44.4	247	1	SUMT_PSEFL	P34752
407	4	44.4	219	1	H1B_XENLA	P06863	xenopus lae	480	4	44.4	248	1	TRYP_CLOAB	052693
408	4	44.4	219	1	ISPD_CHLTR	O84468	chlamydia t	481	4	44.4	248	1	TRYP_FUSOX	P35049
409	4	44.4	220	1	TRKA_MYCTU	O07194	mycobacteri	482	4	44.4	249	1	1431_LYCES	P93206
410	4	44.4	222	1	AMVB_SECCO	P30271	seccate cere	483	4	44.4	249	1	HMX1_CHICK	P28361
411	4	44.4	223	1	I12A_MARMO	O61728	marmola mon	484	4	44.4	249	1	REP2_ZYGBA	P13780
412	4	44.4	224	1	DEOC_MERTH	O26909	methanobact	485	4	44.4	249	1	RU2A_ARATH	P43323
413	4	44.4	224	1	HXB6_HUMAN	P17509	homo sapien	486	4	44.4	249	1	YBFT_BACSU	O31458
414	4	44.4	224	1	HXB6_MOUSE	P09023	mus musculu	487	4	44.4	250	1	FCG3_BOVIN	P79107
415	4	44.4	224	1	VV_MUMPE	P30927	mumps virus	488	4	44.4	250	1	PSD8_CAEEL	O23449
416	4	44.4	224	1	VV_MUMPK	P30928	mumps virus	489	4	44.4	250	1	TAD2_YEAST	P47058
417	4	44.4	224	1	VV_MUMPS	P33483	mumps virus	490	4	44.4	250	1	YNCW_BACSU	O31803
418	4	44.4	224	1	YPJG_BACSU	P34981	bacillus su	491	4	44.4	251	1	CB24_ARATH	P27521
419	4	44.4	225	1	XYNA_THELA	O43097	theriomycos	492	4	44.4	251	1	COBM_MYCTU	O10672
420	4	44.4	226	1	ATP6_HELPJ	O92115	helicobacte	493	4	44.4	251	1	TPIS_LETME	P14849
421	4	44.4	226	1	ATP6_HELPY	P56085	helicobacte	494	4	44.4	251	1	TPIS_TRXCR	P52270
422	4	44.4	226	1	CXB2_MOUSE	O00977	mus musculu	495	4	44.4	251	1	TRPA_PYRKO	P52270
423	4	44.4	226	1	CXB2_RAT	P21994	rattus norv	496	4	44.4	252	1	TRPA_PYRKO	P52270
424	4	44.4	226	1	CXB2_SHEEP	P46691	ovis aries	497	4	44.4	252	1	EBSD_ENTFA	O95949
425	4	44.4	226	1	HMMB_BRARE	O01704	brachydanio	498	4	44.4	253	1	HEMD_MERTH	P36923
426	4	44.4	226	1	LPOT_MYCTU	P96384	mycobacteri	499	4	44.4	253	1	KAD_CHLMU	O26268
427	4	44.4	227	1	SVT_PSESY	P52833	pseudomonas	500	4	44.4	253	1	KDSE_HAEIN	O94970
428	4	44.4	228	1	RPE_RHOCA	P51012	rhodobacter	501	4	44.4	253	1	PMX2_HUMAN	O99811
429	4	44.4	229	1	IRLR_BURPS	O51355	burkholderi	502	4	44.4	254	1	GLTF_ECOLI	P28721
430	4	44.4	229	1	Y4MB_RH1SN	P55561	rhizobium s	503	4	44.4	254	1	KDSB_CHLPN	O92829
431	4	44.4	231	1	YD74_MYCPN	P75407	rhizobium s	504	4	44.4	254	1	YN08_YEAST	P53304
432	4	44.4	231	1	FLGH_PSEPU	O52081	pseudomonas	505	4	44.4	255	1	GRPS_MYXXA	P95333
433	4	44.4	231	1	RSMB_MOUSE	P27048	mus musculu	506	4	44.4	256	1	GI02_RHOCA	P96981
434	4	44.4	232	1	CASB_PIG	P39037	sus scrofa	507	4	44.4	256	1	GSC_MOUSE	O02591
435	4	44.4	232	1	FLGH_ECOLI	P75940	eschlerichia	508	4	44.4	257	1	CHIF_SALTY	O05630
436	4	44.4	234	1	YG1B_ECOLI	P24195	eschlerichia	509	4	44.4	257	1	CG1C_ORYSA	P93411
437	4	44.4	235	1	AURB_CHLAU	P27197	chloroflexu	510	4	44.4	257	1	COAT_TYLCM	P27257
438	4	44.4	235	1	MSRA_HUMAN	O9u168	homo sapien	511	4	44.4	257	1	COAT_TYLCM	P38608
439	4	44.4	235	1	VP26_VZVD	P09279	varicella-z	512	4	44.4	257	1	YZG1_CAEEL	P55326
440	4	44.4	235	1	YVHO_HAEIN	P44908	haemophilus	513	4	44.4	258	1	HB21_SPAEH	P15464
441	4	44.4	236	1	GAMT_HUMAN	O14353	homo sapien	514	4	44.4	258	1	HB2D_PIG	P15983
442	4	44.4	236	1	GAMT_MOUSE	O35969	mus musculu	515	4	44.4	259	1	MOTR_TREPA	O07886
443	4	44.4	236	1	YMI3_CAEEL	O21018	caenorhabdi	516	4	44.4	259	1	MSP8_EIMAC	P09125
444	4	44.4	237	1	COX2_TIRIU	O01556	trichophyto	517	4	44.4	259	1	RNS2_ARATH	P42814
445	4	44.4	237	1	DRNF_AERHY	O44064	aeromonas h	518	4	44.4	260	1	1433_LYCES	P93309
446	4	44.4	237	1	GUN_ASPAC	P22669	aspergillus	519	4	44.4	260	1	143C_TOBAC	P93343
447	4	44.4	237	1	MTRA_METTH	O27227	methanobact	520	4	44.4	260	1	COAT_TYLCV	P27256
448	4	44.4	237	1	MTRA_METTM	P80184	methanobact	521	4	44.4	260	1	SHP_MOUSE	O62227
449	4	44.4	237	1	PSA5_SOYBN	O9m418	glycine max	522	4	44.4	260	1	VG38_BPK3	P07876
450	4	44.4	237	1	YGHS_ECOLI	P46843	eschlerichia	523	4	44.4	261	1	CXBB_HUMAN	O95452
451	4	44.4	238	1	ET3_HUMAN	P14138	homo sapien	524	4	44.4	261	1	CXBB_MOUSE	P70669
452	4	44.4	238	1	YT23_AGRVI	P70793	agrobacteri	525	4	44.4	261	1	HB22_HUMAN	P01919
453	4	44.4	239	1	RIMY_YEAST	O04724	saccharomyc	526	4	44.4	261	1	HB23_HUMAN	P05357
454	4	44.4	239	1	TRBH_ECOLI	P19381	eschlerichia	527	4	44.4	261	1	HB23_HUMAN	P03927
455	4	44.4	239	1	WT1_SMIMA	P49953	smithopsis	528	4	44.4	261	1	HB2C_PIG	P15982
456	4	44.4	240	1	8512_TRCCR	P18270	trypanosoma	529	4	44.4	261	1	RNGC_MOUSE	P28078
457	4	44.4	240	1	COAT_NMY	P15100	narcissus m	530	4	44.4	261	1	TFEP_MORBO	P20666
458	4	44.4	240	1	FX24_RHITY	P24290	rhizobium l	531	4	44.4	261	1	Y497_MYCLE	P54880
459	4	44.4	240	1	RSMB_CHICK	O9pV94	gallus galli	532	4	44.4	261	1	YF25_MYCTU	O50582
460	4	44.4	240	1	RSMB_ERIEU	O9tU67	erlinaceus e	533	4	44.4	261	1	YFUB_HAEIN	O44497
461	4	44.4	240	1	RSMB_HUMAN	P14678	homo sapien	534	4	44.4	261	1	YQBA_CAEEL	O99257
462	4	44.4	240	1	RSMB_MONDO	O9tU66	monodelphis	535	4	44.4	262	1	APAI_BRARE	O42363
463	4	44.4	240	1	RSMB_HUMAN	P14648	homo sapien	536	4	44.4	263	1	T2TR_THETH	P29748
464	4	44.4	241	1	RASH_MSYHA	P01115	harvey muri	537	4	44.4	263	1	TRPA_ANTSP	P31204
465	4	44.4	242	1	CCWC_RHOCA	P29961	rhodobacter	538	4	44.4	264	1	APAI_ANAPL	O42296
466	4	44.4	243	1	GSCA_XENLA	P29454	xenopus lae	539	4	44.4	264	1	APAI_CHICK	P08250
467	4	44.4	243	1	GSCB_XENLA	P53546	xenopus lae	540	4	44.4	264	1	APAI_COTJA	P32918
468	4	44.4	243	1	TRUA_MYCPN	O50291	mycoplasma	541	4	44.4	264	1	CXB1_XENLA	P08983
469	4	44.4	244	1	VLPE_MYCHR	O49537	mycoplasma	542	4	44.4	264	1	DMPH_PSESP	P49156
470	4	44.4	244	1	CAH_ERMCA	O52558	erythria car	543	4	44.4	264	1	GP3D_CHLMU	O46771
471	4	44.4	244	1	H1O_CHLTH	O07134	chiltonomus	544	4	44.4	264	1	RSF4_STRPU	P46771

545	4	44.4	264	1	T2FB_XENLA	003123 xenopus lae	618	4	44.4	288	1	Y940_MYCTU	P71569 mycobacteri
546	4	44.4	264	1	TRPA_SYNY3	P77960 synechocyst	619	4	44.4	289	1	FAHO_SYNASP	P64017 anabena sp
547	4	44.4	264	1	VAL1_MDV	P06847 wheat dwarf	620	4	44.4	290	1	AROE_SYNY3	P74591 synechocyst
548	4	44.4	264	1	YMS3_CAEEL	Q10939 caenorhabdi	621	4	44.4	290	1	ITVE_RICPR	O05970 rickettsia
549	4	44.4	265	1	LECNC_PEA	P16270 pisum sativ	622	4	44.4	290	1	TRX2_MOUSE	O08550 mus musculu
550	4	44.4	265	1	PSBP_NARPS	Q40407 narctissus p	623	4	44.4	291	1	CC21_MEDSA	P24923 medicago sa
551	4	44.4	265	1	TRPA_MERTM	P26920 methanobact	624	4	44.4	291	1	CLTB_HAEIN	P44460 haemophilus
552	4	44.4	265	1	YMI2_PARRE	P15613 paramecium	625	4	44.4	291	1	SP13_YEAST	P33522 buchnera ap
553	4	44.4	266	1	ETH2_ACICA	P00632 acinetobact	626	4	44.4	291	1	72EB_HUMAN	P23068 homo sapien
554	4	44.4	266	1	ETFB_MYCLE	O33095 mycobacteri	627	4	44.4	291	1	YXUO_BACSU	P29181 bacillus su
555	4	44.4	266	1	HMUV_YERPE	O56993 yerstinla pe	628	4	44.4	292	1	CC22_ORYSA	P29619 oryza sativ
556	4	44.4	266	1	SURE_METYA	O57979 methanococ	629	4	44.4	292	1	Y185_BUCAL	P51282 buchnera ap
557	4	44.4	267	1	PSBP_SPIOL	P12302 spinnacia ol	630	4	44.4	293	1	HMX1_MOUSE	P313297 mus musculu
558	4	44.4	267	1	TRPA_BACSU	O07601 bacillus su	631	4	44.4	293	1	SYK3_AOUAE	O66965 aquifex aeo
559	4	44.4	268	1	INHA_MYCAV	O07400 mycobacteri	632	4	44.4	293	1	Y311_BORBU	O51291 borrellia bu
560	4	44.4	268	1	KSGA_RICPR	O05952 r dimethyla	633	4	44.4	294	1	CC21_ORYSA	P29618 oryza sativ
561	4	44.4	268	1	YHC6_YEAST	P38740 saccharomyc	634	4	44.4	294	1	CC22_MEDSA	O05006 medicago sa
562	4	44.4	269	1	INHA_MYCSM	P42829 mycobacteri	635	4	44.4	294	1	CC2A_ANTMA	O38772 antirrhinum
563	4	44.4	269	1	INHA_MYCTU	P46533 mycobacteri	636	4	44.4	294	1	CC2A_ARATH	P24100 arabidopsis
564	4	44.4	269	1	NIDC_VIRCH	O9v27 vibrio chol	637	4	44.4	294	1	CC2_MAIZE	P23111 zea mays (m
565	4	44.4	269	1	TRPA_BACST	P19867 bacillus st	638	4	44.4	294	1	CC2_VIGUN	P52389 vigna ungui
566	4	44.4	270	1	HCE1_ORYLA	P31580 oryzias lat	639	4	44.4	295	1	CAC3_HAECO	P16253 haemochus
567	4	44.4	270	1	TRPA_MERTM	O27697 methanobact	640	4	44.4	295	1	YK05_MYCTU	O10851 mycobacteri
568	4	44.4	271	1	Y228_TREBA	O83256 treponema p	641	4	44.4	296	1	CC01_CAEEL	P08124 caenorhabdi
569	4	44.4	272	1	RSR1_YEAST	P13856 saccharomyc	642	4	44.4	296	1	MY88_MOUSE	P22366 mus musculu
570	4	44.4	272	1	VG67_HSEVB	P28984 equine hepr	643	4	44.4	297	1	CC2_BOVIN	P06493 bos taurus
571	4	44.4	272	1	YIS2_SHISO	P16940 shigella so	644	4	44.4	297	1	CC2_HUMAN	P06493 homo sapien
572	4	44.4	273	1	BAS1_MOUSE	P18572 mus musculu	645	4	44.4	297	1	CC2_MOUSE	P11440 mus musculu
573	4	44.4	274	1	BPAL_STRAU	P33912 streptomyc	646	4	44.4	297	1	CC2_RAT	P33951 rattus norv
574	4	44.4	274	1	PRCE_ARATH	O23717 arabidopsis	647	4	44.4	297	1	HMX1_BOVIN	P02786 bos taurus
575	4	44.4	274	1	SAC7_YEAST	P13121 saccharomyc	648	4	44.4	297	1	HMX1_HUMAN	O28360 homo sapien
576	4	44.4	274	1	VGLE_HSV2	P31289 herpes slimp	649	4	44.4	297	1	VDX2_SCHPO	O13719 schistosach
577	4	44.4	274	1	YBIC_SCHPO	O9vrv0 schizosach	650	4	44.4	298	1	Y33K_HUMAN	O04323 homo sapien
578	4	44.4	274	1	YDDG_ECOLI	P46136 escherichia	651	4	44.4	299	1	PLTA_MYCPO	Q12635 mycosphaere
579	4	44.4	275	1	RK2_CYAPA	P15764 cyanophora	652	4	44.4	299	1	YC59_MYCTU	Q11059 mycobacteri
580	4	44.4	275	1	VE39_NPVAC	P11042 autographa	653	4	44.4	299	1	Y7H9_YEAST	P47032 saccharomyc
581	4	44.4	276	1	VGIM_PUUMB	P22959 tobacco nec	654	4	44.4	300	1	CCPM_BACHD	O92977 bacillus ha
582	4	44.4	276	1	COAT_TNVA	P46769 caenorhabdi	655	4	44.4	301	1	ERA_BACSU	P10087 escherichia
583	4	44.4	276	1	RSPA_CAEEL	P18284 halobacteri	656	4	44.4	301	1	NHAR_ECOLI	P31243 rhododact
584	4	44.4	277	1	TRPA_HALVO	O58801 pyrococcus	657	4	44.4	301	1	PORI_RHOCA	P12402 bacillus su
585	4	44.4	277	1	YAF4_PYRHO	O58801 pyrococcus	658	4	44.4	301	1	YXAC_BACSU	P28550 macropus eu
586	4	44.4	278	1	VGIL_HCMV1	O68667 human cytom	659	4	44.4	302	1	CASB_MACSU	P07862 escherichia
587	4	44.4	278	1	VGIL_HCMW2	O68668 human cytom	660	4	44.4	302	1	CC21_XENLA	P33567 xenopus lae
588	4	44.4	278	1	VGIL_HCMW3	O68669 human cytom	661	4	44.4	302	1	CC22_XENLA	P24033 xenopus lae
589	4	44.4	278	1	VGIL_HCMW4	O68670 human cytom	662	4	44.4	302	1	CC2_CARAU	P51958 carassius a
590	4	44.4	278	1	VGIL_HCMW5	O68671 human cytom	663	4	44.4	302	1	CLTB_ECOLI	P77770 escherichia
591	4	44.4	278	1	VGIL_HCMW6	O68672 human cytom	664	4	44.4	302	1	YE86_MYCTU	P71766 mycobacteri
592	4	44.4	278	1	VGIL_HCMW7	O68673 human cytom	665	4	44.4	303	1	CC2_CHICK	P13863 gallus gall
593	4	44.4	278	1	VGIL_HCMW8	O68674 human cytom	666	4	44.4	303	1	NIJM_CABUN	O78700 cabassous u
594	4	44.4	278	1	VGIL_HCMW9	O68675 human cytom	667	4	44.4	304	1	HEV1_CANFA	O95522 canis famli
595	4	44.4	278	1	VGIL_HCMW9	O68676 human cytom	668	4	44.4	304	1	HEV1_HUMAN	O95522 canis famli
596	4	44.4	279	1	HCE2_ORYLA	P31581 oryzias lat	669	4	44.4	304	1	PFEB_BACAM	P41029 bacillus am
597	4	44.4	279	1	YA21_MERTM	O27101 methanobact	670	4	44.4	305	1	DDLB_ECOLI	P07862 escherichia
598	4	44.4	280	1	CC2B_ANTMA	Q38773 antirrhinum	671	4	44.4	305	1	HEM3_AERPE	O99910 aeropyrum p
599	4	44.4	280	1	Y747_RICPR	O92c13 rickettsia	672	4	44.4	305	1	HM23_CAEEL	P34663 caenorhabdi
600	4	44.4	281	1	TRPA_MERTM	O60180 methanococ	673	4	44.4	305	1	MAIM_SALTY	P26478 salmonella
601	4	44.4	281	1	YD3B_SCHPO	Q10275 schizosacch	674	4	44.4	305	1	Y40A_SYNY3	P74430 synechocyst
602	4	44.4	281	1	YD3B_SCHPO	O14175 schizosacch	675	4	44.4	306	1	ARG1_BRUAB	O54174 bruceella ab
603	4	44.4	282	1	CHER_THEMA	O94y15 thermotoga	676	4	44.4	306	1	METF_STRLI	O54235 streptomyc
604	4	44.4	283	1	CXBI_HUMAN	P08034 homo sapien	677	4	44.4	307	1	RB33_CAEEL	O20365 caenorhabdi
605	4	44.4	283	1	CXBI_MOUSE	P28230 mus musculu	678	4	44.4	307	1	VP53_BPAPS	O91195 bacterioph
606	4	44.4	283	1	CXBI_RAT	P08033 rattus norv	679	4	44.4	307	1	Y995_MYCTU	O33196 mycobacteri
607	4	44.4	284	1	CRCV_CAPAE	O29478 capra aegag	680	4	44.4	307	1	KDGD_BACSU	P42235 bacillus su
608	4	44.4	284	1	CX32_MITCN	P51915 micropogoni	681	4	44.4	308	1	PPIB_MYCTU	O50639 mycobacteri
609	4	44.4	284	1	CXBI_BOVIN	O18968 bos taurus	682	4	44.4	308	1	TF2B_SULSH	O67619 sulfobolus
610	4	44.4	284	1	RP32_PROMI	P50509 pectus mir	683	4	44.4	309	1	APBA_AOUAE	O67619 aquifex aeo
611	4	44.4	284	1	UL06_HCMVA	P16720 human cytom	684	4	44.4	310	1	ABE_MOUSE	P08226 mus musculu
612	4	44.4	284	1	Y556_CAEEL	O09378 caenorhabdi	685	4	44.4	311	1	PROQ_NEUCR	Q12641 neurospora
613	4	44.4	288	1	FXE3_MOUSE	O99y14 mus musculu	686	4	44.4	311	1	YBBU_BORBR	O06702 bordetella
614	4	44.4	288	1	HMXX_CHICK	P50223 gallus gall	687	4	44.4	311	1	YG95_MYCLE	O49897 mycobacteri
615	4	44.4	288	1	H01_PTG	O08143 podospora a	688	4	44.4	313	1	FMT_THEMA	O94y28 thermotoga
616	4	44.4	288	1	SMR2_PODAN	P50902 alligator m	689	4	44.4	313	1	LYTB_BURPS	O94y28 thermotoga
617	4	44.4	288	1	WT1_A1LMT		690	4	44.4	313	1		

691	4	44.4	313	1	PEPM_STRHY	P29247	streptomyc	764	4	44.4	332	1	LDHH_CHICK	P00337	gallus gall
692	4	44.4	313	1	VU47_HSVJ7	P25255	human herpe	765	4	44.4	332	1	LDH_DROME	095028	drosophila
693	4	44.4	314	1	ACCD_ANGLY	P28252	angliopteris	766	4	44.4	332	1	LYTB_MYCLE	09x071	mycobacteri
694	4	44.4	314	1	FMT_PSEAE	085732	pseudomonas	767	4	44.4	332	1	SIX3_HUMAN	095333	homo sapien
695	4	44.4	314	1	SIX3_CHICK	042406	gallus gall	768	4	44.4	332	1	SR4_PHYTO	P11113	physarum po
696	4	44.4	314	1	YM78_YEAST	004013	saccharomyc	769	4	44.4	332	1	THCR_RHOER	P43422	rhodococcus
697	4	44.4	315	1	GBF71_ARATH	P42774	arabidopsis	770	4	44.4	333	1	SIX3_MOUSE	062223	mus musculu
698	4	44.4	315	1	HYFC_ECOLI	P72653	escherichia	771	4	44.4	333	1	VINT_BPMD2	038381	mycobacteri
699	4	44.4	315	1	ISPE_SYNY3	P29654	synecocyst	772	4	44.4	334	1	VINT_BPMFR	P25462	mycobacteri
700	4	44.4	315	1	MCH_METKA	P49693	methanopyru	773	4	44.4	334	1	CXAX_XENLA	P16864	xenopus lae
701	4	44.4	315	1	RPOA_CLOPE	091bw9	clostridium	774	4	44.4	334	1	MRPL_CAEEL	093449	caenorhabdi
702	4	44.4	316	1	MCH_ARCEU	028344	archaeoglob	775	4	44.4	334	1	YI11_HALNT	P23464	halobacteri
703	4	44.4	316	1	VAM7_YEAST	P22912	saccharomyc	776	4	44.4	335	1	FIMH_SALTY	P37925	salmonella
704	4	44.4	317	1	APE_HUMAN	P02649	homo sapien	777	4	44.4	335	1	G3P_HALVA	048365	halocaula
705	4	44.4	317	1	FLGL_ECOLI	P29744	escherichia	778	4	44.4	335	1	LYBI_MYCTU	P38200	saccharomyc
706	4	44.4	317	1	LDH_BACCA	P10655	bacillus ca	779	4	44.4	335	1	SLAM_HUMAN	013291	homo sapien
707	4	44.4	317	1	RSP4_URECA	P38981	urechis cau	780	4	44.4	335	1	T2G1_HERAU	P25261	herpetosiph
708	4	44.4	318	1	ATPS_YEAST	P24243	saccharomyc	781	4	44.4	337	1	FABH_PSEAE	P20382	pseudomonas
709	4	44.4	318	1	CH11_HORVU	P11955	hordium vul	782	4	44.4	337	1	G3PC_MESCR	P17878	mesembryant
710	4	44.4	318	1	NUIM_TAMTE	078699	lamandua te	783	4	44.4	337	1	G3P_LACIA	P52987	lactococcus
711	4	44.4	318	1	ONCA_TAETA	P22080	taenia taen	784	4	44.4	337	1	KCIA_CHICK	P70065	gallus gall
712	4	44.4	319	1	FMT_TREPA	083737	treponema p	785	4	44.4	337	1	KCIA_HUMAN	P48729	homo sapien
713	4	44.4	319	1	HA11_RAT	P15978	rattus norv	786	4	44.4	337	1	YFGA_ECOLI	P27424	escherichia
714	4	44.4	319	1	MCH_METTM	P51616	methanobact	787	4	44.4	338	1	MBR3_YEAST	P32488	saccharomyc
715	4	44.4	319	1	MOCB_STYP7	Q56208	synecococc	788	4	44.4	338	1	TR19_HUMAN	015653	homo sapien
716	4	44.4	320	1	GSHB_SYNY3	Q01578	zymomonas m	789	4	44.4	338	1	YBD1_YEAST	P19304	saccharomyc
717	4	44.4	320	1	HXA4_HUMAN	P73493	synecocyst	790	4	44.4	338	1	YORT_TTV1	P15701	erynia chr
718	4	44.4	320	1	MCH_METTH	000056	homo sapien	791	4	44.4	339	1	KDGT_ERMCH	P57721	homo sapien
719	4	44.4	320	1	THTR_STYP7	Q26867	methanobact	792	4	44.4	339	1	PCB3_HUMAN	P45477	haemophilus
720	4	44.4	320	1	THTR_STYP7	P27477	synecococc	793	4	44.4	339	1	PYRD_HAEIN	P45477	haemophilus
721	4	44.4	321	1	LIPA_ECOLI	P25845	escherichia	794	4	44.4	339	1	RL28_SPLIC	031163	spiroplasma
722	4	44.4	321	1	MCH_METBA	P94919	methanosarc	795	4	44.4	339	1	YJGB_ECOLI	P27220	escherichia
723	4	44.4	321	1	SAPB_ECOLI	Q47623	escherichia	796	4	44.4	339	1	YN28_CAEEL	P45968	caenorhabdi
724	4	44.4	321	1	SAPB_SALTY	P36668	salmonella	797	4	44.4	340	1	DAF_PONPY	P49457	pono pygma
725	4	44.4	321	1	Y541_PYROH	058276	pyrococcus	798	4	44.4	340	1	YMD2_YEAST	003703	saccharomyc
726	4	44.4	322	1	ADT_SCHRO	Q09188	schizosacch	799	4	44.4	341	1	COA2_POVMK	P24506	mouse polyo
727	4	44.4	322	1	HA10_MOUSE	P18189	mus musculu	800	4	44.4	341	1	MDHW_CAEEL	002640	caenorhabdi
728	4	44.4	322	1	HCR_ECOLI	P75824	escherichia	801	4	44.4	342	1	HEAD_BP21	P03620	bacterioph
729	4	44.4	323	1	FLK_RAT	P09760	rattus norv	802	4	44.4	343	1	GALR_ECOLI	P30204	escherichia
730	4	44.4	323	1	MCH_METEX	085014	methylobact	803	4	44.4	343	1	VMAT_SSPVB	P16628	subcutis sc
731	4	44.4	323	1	MCH_METJA	059030	methanococc	804	4	44.4	344	1	RECA_MAGMG	P16054	magnetospi
732	4	44.4	323	1	OTX1_BRARE	Q91994	brachydanio	805	4	44.4	345	1	AOX_TRYBB	Q26710	trypnosoma
733	4	44.4	323	1	THIG_RHET	Q04293	thizobactum e	806	4	44.4	345	1	ODPA_ACHLA	P34545	acholepiasm
734	4	44.4	323	1	YM98_MYCTU	Q50668	mycobacteri	807	4	44.4	345	1	VE2_HP34	P36792	human papil
735	4	44.4	324	1	ARG1_AGRU	P14001	agrobacteri	808	4	44.4	346	1	HRP_PSESY	005393	pseudomonas
736	4	44.4	324	1	BM11_MOUSE	P25916	mus musculu	809	4	44.4	346	1	KORA_ARCFU	029781	archaeoglob
737	4	44.4	324	1	CAHC_HORVU	P40880	hordium vul	810	4	44.4	346	1	NU2M_CONJA	P24971	coltrinx co
738	4	44.4	325	1	KCIA_BOVIN	P35506	bos taurus	811	4	44.4	346	1	YI61_XANCA	P25478	xanthomonas
739	4	44.4	325	1	KCIA_RAT	P97633	rattus norv	812	4	44.4	347	1	GABC_HUMAN	006345	homo sapien
740	4	44.4	326	1	BM11_HUMAN	P35226	homo sapien	813	4	44.4	347	1	GABC_MOUSE	000421	mus musculu
741	4	44.4	326	1	TH14_YEAST	P32318	saccharomyc	814	4	44.4	347	1	VIT3_CHICK	091025	gallus gall
742	4	44.4	326	1	VP40_EBOZM	005158	ebola virus	815	4	44.4	348	1	EXOB_AZOBR	059083	azospirillum
743	4	44.4	326	1	VS09_RORZM	P10501	human rotav	816	4	44.4	349	1	NU2M_ONCMY	P48175	oncorhynch
744	4	44.4	326	1	VS09_RORHV	P11865	human rotav	817	4	44.4	349	1	NU2M_SALSA	035924	salmo salar
745	4	44.4	326	1	VS09_RORPV	P09365	porcine rot	818	4	44.4	349	1	STY1_SCHPO	009882	schizosacch
746	4	44.4	327	1	CP27_PIG	P79402	sus scrofa	819	4	44.4	349	1	VAL1_PHOV	006923	pepper huas
747	4	44.4	327	1	ENT2_MOUSE	O61672	m equilibra	820	4	44.4	351	1	CX41_XENLA	P51914	xenopus lae
748	4	44.4	327	1	GLSA_SYNY3	P73903	synecocyst	821	4	44.4	351	1	MSS2_YEAST	P40990	saccharomyc
749	4	44.4	328	1	HMDL_DROME	P20009	drosophila	822	4	44.4	351	1	MURR_BORPE	09x628	bordeletia
750	4	44.4	328	1	COPB_PRESM	P12375	pseudomonas	823	4	44.4	351	1	PSBD_GUTTH	078427	guillartidia
751	4	44.4	328	1	GNDS_HUMAN	Q12967	homo sapien	824	4	44.4	351	1	PSBD_ODOST	P49478	odontotelia s
752	4	44.4	329	1	IBP2_HUMAN	O86779	homo sapien	825	4	44.4	351	1	PSBD_PORPU	P24090	rattus norv
753	4	44.4	329	1	COAA_STRCO	O67799	streptomyce	826	4	44.4	352	1	AZHS_RAT	P50863	baacillus su
754	4	44.4	331	1	Y493_MYCTU	O1158	mycobacteri	827	4	44.4	352	1	MRP_BACSU	P06007	chlamydomon
755	4	44.4	331	1	AR73_HUMAN	095154	homo sapien	828	4	44.4	352	1	PSBD_CHIRE	P56319	chlorella v
756	4	44.4	331	1	MAZ_MESNU	P56670	mesocricetu	829	4	44.4	352	1	PSBD_CHIVU	P48079	cyanophora
757	4	44.4	331	1	PELB_COLGL	O59599	colletotric	830	4	44.4	352	1	PSBD_CYAPA	P31557	euglena gira
758	4	44.4	332	1	AXHA_ASPNG	P79019	aspergillus	831	4	44.4	352	1	PSBD_EUGGR	P06006	pisum sativ
759	4	44.4	332	1	AXHA_ASPETU	P79021	aspergillus	832	4	44.4	352	1	PSBD_PEA	P06005	spinacia ol
760	4	44.4	332	1	CXAX_HUMAN	P35212	homo sapien	833	4	44.4	352	1	PSBD_SPTOL	P11005	synecococc
761	4	44.4	332	1	CXAX_MOUSE	P28235	mus musculu	834	4	44.4	352	1	PSBD_SYNP7	P42705	canis famli
762	4	44.4	332	1	CXAX_RAT	003190	rattus norv	835	4	44.4	352	1	TPO_CANFA	P49469	odontotelia s
763	4	44.4	332	1	LDHH_ANAPL	P13743	anas platytr	836	4	44.4	353	1	CHL1_ODOST		

837	4	44.4	353	1	LEU3_BACFR	P54354 bacteroides	910	4	44.4	370	1	KCC1_HUMAN	Q14012 homo sapien
838	4	44.4	353	1	PSBD_ARATH	P56167 arabidopsis	911	4	44.4	370	1	KDPR_SYNY3	P73870 synechocyst
839	4	44.4	353	1	PSBD_HORVU	P11849 hordeum vul	912	4	44.4	370	1	ODPA_BACSU	P21881 bacillus su
840	4	44.4	353	1	PSBD_MAIZE	P48184 zea mays (m	913	4	44.4	370	1	VP40_BDV	Q01552 botra disea
841	4	44.4	353	1	PSBD_MARPO	P06404 marchantia	914	4	44.4	371	1	HA12_RAT	P16391 rattus norv
842	4	44.4	353	1	PSBD_ORYSA	P12095 oryza sativ	915	4	44.4	371	1	MURG_SYNY3	P74657 synechocyst
843	4	44.4	353	1	PSBD_PINTH	P41644 pinus thunb	916	4	44.4	371	1	VZRH_HUMAN	P30518 homo sapien
844	4	44.4	353	1	PSBD_SECE	P10803 secale cere	917	4	44.4	371	1	YOJE_BACSU	P54542 bacillus su
845	4	44.4	353	1	PSBD_TOBAC	P06403 nicotiana t	918	4	44.4	372	1	HMEN_BOMMO	P27605 bombyx mori
846	4	44.4	354	1	CVE2_AGRVU	P54082 agrobacteri	919	4	44.4	372	1	NOIC_SYNY3	P26522 synechocyst
847	4	44.4	354	1	MTD2_HERAV	P25265 herpetosiph	920	4	44.4	373	1	MLE_TRICU	P46057 trichosporo
848	4	44.4	354	1	V415_SYNY3	P22040 synechocyst	921	4	44.4	373	1	YN28_YEAST	P53829 saccharomyc
849	4	44.4	355	1	CXA5_RAT	P28234 rattus norv	922	4	44.4	374	1	ADH3_KLUOA	P49384 kluyveromyc
850	4	44.4	356	1	CXA5_CANFA	P33725 canis famli	923	4	44.4	374	1	FUT5_HUMAN	O11128 homo sapien
851	4	44.4	356	1	NMRB_RHOCA	P09431 rhodobacter	924	4	44.4	374	1	FUT5_PANTR	P56433 pan troglod
852	4	44.4	356	1	TPO_MOUSE	P40226 mus musculu	925	4	44.4	374	1	OY1A_DROME	Q9VUK5 drosophila
853	4	44.4	357	1	CXA5_HUMAN	P36382 homo sapien	926	4	44.4	374	1	RLIG_BPT4	P00971 bacterioph
854	4	44.4	357	1	PYRD_MOUSE	O01231 mus musculu	927	4	44.4	375	1	FTS2_HALN1	Q48290 halobacteri
855	4	44.4	357	1	PYRD_MYCTU	O06236 mycobacteri	928	4	44.4	375	1	YKUS_CAEEL	O17778 caenorhabdi
856	4	44.4	358	1	AZHS_CAVPO	O70159 cavia porce	929	4	44.4	376	1	BCA2_YEAST	P41399 botdetella
857	4	44.4	358	1	LEU3_HAETN	P43860 haemophilus	930	4	44.4	376	1	DHAS_BOREP	O84198 thermus aqu
858	4	44.4	358	1	TTCC3_AGRVI	O34296 agrobacteri	931	4	44.4	376	1	HOSC_THERH	P38779 saccharomyc
859	4	44.4	358	1	TTCC3_AGRVI	P70792 agrobacteri	932	4	44.4	376	1	YHL2_YEAST	P16863 xenopus lae
860	4	44.4	358	1	TTCC5_AGRVI	O34295 agrobacteri	933	4	44.4	378	1	CXAL_XENLA	P29303 drosophila
861	4	44.4	358	1	VCOM_ADE40	P48753 human adeno	934	4	44.4	378	1	HAIR_DROYI	P36790 human papil
862	4	44.4	359	1	GUN_CELUD	P18336 cellulomona	935	4	44.4	378	1	VE2_HPV30	P4867 bacillus su
863	4	44.4	359	1	MANR_PSEPU	P14444 pseudomonas	936	4	44.4	379	1	ACDA_BACSU	P28004 saccharomyc
864	4	44.4	359	1	T2D1_HERAV	P24599 herpetosiph	937	4	44.4	379	1	YAD2_YEAST	P28004 saccharomyc
865	4	44.4	359	1	MDH_PYRHO	P34258 caenorhabdi	938	4	44.4	380	1	COSC_YEAST	P53053 saccharomyc
866	4	44.4	360	1	PSB1_AGRVU	O59028 pyrococuss	939	4	44.4	380	1	CXAL_BRARE	O5474 brachydanto
867	4	44.4	360	1	PSB1_SYNP7	P04996 synechococc	940	4	44.4	381	1	DAF_HUMAN	P08174 homo sapien
868	4	44.4	360	1	PSB2_SYNP7	P04997 synechococc	941	4	44.4	381	1	Y926_HELPY	P55985 helicobacte
869	4	44.4	360	1	UPP_TREPA	O83462 leptonema p	942	4	44.4	381	1	YBD2_YEAST	P38199 saccharomyc
870	4	44.4	360	1	VC47_BPMO	O911v2 bacterioph	943	4	44.4	382	1	COAL_POVNA	P00420 mus musculu
871	4	44.4	361	1	COBT_MYCTU	O10396 mycobacteri	944	4	44.4	382	1	GABB_MOUSE	P01104 avian myelo
872	4	44.4	361	1	VCOM_ADEB2	O96625 bovine aden	945	4	44.4	382	1	MYB_AV1MB	P27019 human parai
873	4	44.4	362	1	HA11_MOUSE	P01899 mus musculu	946	4	44.4	382	1	YVAT_P14HA	P27020 human parai
874	4	44.4	362	1	HA11_MOUSE	P01897 mus musculu	947	4	44.4	382	1	VNAT_P14HB	P36790 human papil
875	4	44.4	363	1	MURG_BORBU	O51708 botrellia bu	948	4	44.4	383	1	COAL_POVNA3	P03091 mouse polyo
876	4	44.4	364	1	MURG_STRCO	O92bas streptomyc	949	4	44.4	383	1	COAL_POVNC	P12907 mouse polyo
877	4	44.4	364	1	RECFC_AZOV1	P49997 azotobacter	950	4	44.4	383	1	COAL_POVMP	P49302 mouse polyo
878	4	44.4	364	1	TTCC1_AGRVI	O44471 agrobacteri	951	4	44.4	383	1	VE2_HPV03	P36778 human papil
879	4	44.4	364	1	TTCC2_AGRVI	P70787 agrobacteri	952	4	44.4	384	1	VE2_HPV53	P26997 human papil
880	4	44.4	365	1	COAL_POVHO	P24848 bovine poly	953	4	44.4	385	1	CD34_HUMAN	P36907 homo sapien
881	4	44.4	365	1	COMT_MEDSA	P28002 medicago sa	954	4	44.4	385	1	YD16_SCHPO	O92344 schizosach
882	4	44.4	365	1	COMT_POPTM	Q00763 populus tre	955	4	44.4	385	1	YH1U_ECOCI	P71636 escherichia
883	4	44.4	365	1	COMT_PPRDU	O43609 prunus dulc	956	4	44.4	386	1	PSD4_ARATH	P55034 arabidopsis
884	4	44.4	365	1	ECT11_SCHPO	O9ut16 schizosach	957	4	44.4	387	1	NMT_DROME	O61613 drosophila
885	4	44.4	365	1	GLDA_PSEPU	P50173 pseudomonas	958	4	44.4	387	1	UJ33_RCMVW	O12000 rat cytomeg
886	4	44.4	365	1	NEMA_ECOCI	P77258 escherichia	959	4	44.4	387	1	VE2_HPV41	P27552 human papil
887	4	44.4	366	1	RECFC_PSEPU	P13456 pseudomonas	960	4	44.4	390	1	ACKA_MYCPN	P75245 mycoplasma
888	4	44.4	366	1	CYCR_RHOGE	P51758 rhodocyclus	961	4	44.4	390	1	IDA4_ECOCI	P33377 escherichia
889	4	44.4	366	1	OM3A_RHILV	Q05811 rhizobium 1	962	4	44.4	390	1	PS3_MOUSE	P03340 mus musculu
890	4	44.4	367	1	A2HS_HUMAN	P02765 homo sapien	963	4	44.4	390	1	RRPP_MUMP1	P19717 mumps virus
891	4	44.4	367	1	CPTT_CRIGR	P49584 cricetulus	964	4	44.4	391	1	DP3B_SYNY3	P72856 synechocyst
892	4	44.4	367	1	CPTT_HUMAN	P49585 homo sapien	965	4	44.4	391	1	HERP_MOUSE	O91jks mus musculu
893	4	44.4	367	1	CPTT_MOUSE	P49586 mus musculu	966	4	44.4	391	1	KC21_CHICK	P21868 gallus galli
894	4	44.4	367	1	CPTT_RAT	P19836 rattus norv	967	4	44.4	391	1	KC21_HUMAN	P19138 homo sapien
895	4	44.4	367	1	GOX1_ARATH	Q91rso arabidopsis	968	4	44.4	391	1	KC21_MOUSE	P33674 oryctolagus
896	4	44.4	367	1	GOX2_ARATH	Q91rtr arabidopsis	969	4	44.4	391	1	KC21_RABIT	P19139 rattus norv
897	4	44.4	367	1	MREC_ECOCI	P16926 escherichia	970	4	44.4	391	1	KC21_RAT	P10361 rattus norv
898	4	44.4	367	1	TISD_MOUSE	P23949 mus musculu	971	4	44.4	391	1	PS3_RAT	P10361 rattus norv
899	4	44.4	368	1	CXA5_CHICK	P18860 gallus galli	972	4	44.4	391	1	RRPP_MUMPE	P16072 mumps virus
900	4	44.4	368	1	HA14_MOUSE	P14427 mus musculu	973	4	44.4	391	1	RRPP_MUMPM	P16595 mumps virus
901	4	44.4	368	1	HA1D_MOUSE	P01902 mus musculu	974	4	44.4	391	1	VIE2_RAT	P24909 murine cyto
902	4	44.4	368	1	HA1W_MOUSE	P03991 mus musculu	975	4	44.4	392	1	SYD1_RAT	O55145 rattus norv
903	4	44.4	368	1	LIVE_MYCTU	O10399 mycobacteri	976	4	44.4	393	1	C143_MYCTU	O59936 mycobacteri
904	4	44.4	368	1	ODPA_BACST	P21873 bacillus st	977	4	44.4	393	1	DSOR_DROME	O24324 drosophila
905	4	44.4	368	1	VE2_HPV6A	O84294 human papil	978	4	44.4	393	1	LA2M_MYCSM	P21795 mycobacteri
906	4	44.4	368	1	YC08_SULSO	P59997 sulfolobus	979	4	44.4	393	1	PS3_HUMAN	P04637 homo sapien
907	4	44.4	369	1	HA1B_MOUSE	P01901 mus musculu	980	4	44.4	393	1	PS3_TUPGB	O9tcal tupala glis
908	4	44.4	369	1	HA1K_MOUSE	P04223 mus musculu	981	4	44.4	393	1	YIP3_YEAST	P40454 saccharomyc
909	4	44.4	369	1	HA1K_MOUSE	P04223 mus musculu	982	4	44.4	394	1	A2AB_RABIT	O77830 oryctolagus

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983 4 44.4 394 1 CC91_YEAST P41733 saccharomyc
984 4 44.4 394 1 NUCC_SYNY3 P27724 synechocyst
985 4 44.4 394 1 PGK_BACSU P40924 bacillus su
986 4 44.4 394 1 Y332_SCHPO 009709 schizosacch
987 4 44.4 394 1 YFDE_ECOLI P76518 escherichia
988 4 44.4 395 1 HMPA_ERWCH Q47286 erwilia chr
989 4 44.4 395 1 LEUK_MOUSE P15702 mus musculi
990 4 44.4 395 1 LHX3_XENLA P36200 xenopus lae
991 4 44.4 396 1 AGS_AGRH P28748 agrobacteri
992 4 44.4 396 1 DCOP_SORMA P78748 sordaria ma
993 4 44.4 396 1 EPTU_STRAU P42479 stigmateila
994 4 44.4 396 1 GLPC_ECOLI P13034 escherichia
995 4 44.4 396 1 YJTB_BACSU 034374 bacillus su
996 4 44.4 396 1 YL65_MYCTU 006212 mycobacteri
997 4 44.4 397 1 DCOP_NEUCR P05035 neurospora
998 4 44.4 397 1 STAD_GOSHI Q42770 gossypium h
999 4 44.4 398 1 TAP_DROME O16867 drosophila
1000 4 44.4 399 1 CXAB_CHICK P36381 gallus gall

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ALIGNMENTS

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RESULT 1
P60_LISMO STANDARD; PRT; 484 AA.
ID P60_LISMO
AC P21171;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-49.
RC STRAIN-SVL/2A BGD(KAUFMANN);
RX MEDLINE=90256283; Pubmed=2111287;
RA Koehler S., Leimelster-Maehter M., Chakraborty T., Lottspeich F.,
RA Geibel W.;
RT "The gene coding for protein p60 of Listeria monocytogenes and its
RT use as a specific probe for Listeria monocytogenes.";
RL Infect. Immun. 58:1943-1950(1990).
RN [2]
RP MEDLINE=93094153; Pubmed=1459966;
RX Buber A., Kuhn W., Geibel W., Koehler S.;
RT "Structural and functional properties of the p60 proteins from
RT different Listeria species.";
RL J. Bacteriol. 174:8166-8171(1992).
CC -1- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE
CC INVASION OF NONPROFESSIONAL PHAGOCYTIC CELLS BY LISTERIA.
CC -1- SIMILARITY: BELONGS TO THE E. COLI NLPC / LISTERIA P60 FAMILY.
CC -----
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CC -----
CC EMBL: X52268; CAA36509.1; -
CC PIR: A41487; A41487.
CC InterPro: IPR000064; -
CC InterPro: IPR002482; -
CC Pfam: PF00877; NLPC_P60; 1.
CC Pfam: PF01476; PG_binding_2; 2.
CC Signal: Repeat.
FT CHAIN 1 27 PROTEIN P60.
FT 28 484

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FT DOMAIN 311 355 19 X 2 AA TANDEM REPEATS OF T-N.
SQ SEQUENCE 484 AA; 50587 MW; 3C0DF0591E14E0F CRC64;

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Query Match 100.0%; Score 9; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VSTPVAPPTQ 9
Db 145 VSTPVAPPTQ 153

```

RESULT 2

```

PRSL_SOLITU STANDARD; PRT; 155 AA.
ID PRSL_SOLITU
AC P17641;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE PATHOGENESIS-RELATED PROTEIN STH-21.
GN STH-21.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91346678; Pubmed=2102864;
RA Matton D.P., Brisson N.;
RT "Nucleotide sequence of a pathogenesis-related gene of potato.";
RL Plant Mol. Biol. 14:863-865(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92190624; Pubmed=2520162;
RA Matton D.P., Brisson N.;
RT "Cloning, expression, and sequence conservation of
RT pathogenesis-related gene transcripts of potato.";
RL Mol. Plant Microbe Interact. 2:325-331(1989).
CC -1- INDUCTION: BY WOUNDING AND ELICITOR TREATMENTS.
CC -1- SIMILARITY: BELONGS TO THE BETV1 FAMILY OF PATHOGENESIS-RELATED
CC PROTEIN.
CC -----
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CC -----
CC EMBL: M25156; AAA03020.1; -
CC PIR: M28042; AAA02829.1; -
CC DR HSP; S11869; S11869.
CC DR HSP; P15494; IRTV.
CC InterPro: IPR000916; -
CC Pfam: PF00407; Bet.v.I.1.
CC PRINTS: PR00634; BETALLERGEN.
CC PROSITE: PS00451; PATHOGENESIS-BETV1; 1.
CC KEGG: PATHOGENESIS-RELATED PROTEIN; MultiGene family.
SQ SEQUENCE 155 AA; 17200 MW; 02A78EE6D26A7CD9 CRC64;

```

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Query Match 66.7%; Score 6; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 TPVAPPT 8
Db 12 TPVAPPT 17

```

RESULT 3
VCG_BPPHK STANDARD: PRT: 187 AA.
AC 038042:
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE MAJOR SPIKE PROTEIN (G PROTEIN) (GPG).
GN G.
OS Bacteriophage phi-K.
OC Viruses: ssDNA viruses; Microviridae; Microvirus.
ON NCBI_TaxID=10848;
RX [1]
RP SEQUENCE FROM N.A.
RA Kodaira K., Tadokoro H., Suzuki K., Oki M., Mantou S., Taketo A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAJOR SPIKE COMPONENT. INVOLVED IN THE ATTACHMENT TO
CC THE BACTERIAL HOST.
CC -1- SUBUNIT: THE VIRION IS COMPOSED OF 60 COPIES EACH OF THE F, G, AND
CC J PROTEINS, AND 12 COPIES OF THE H PROTEIN. THERE ARE 12 SPIKES
CC WHICH ARE EACH COMPOSED OF 5 G AND ONE H PROTEINS.
CC -----
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CC or send an email to license@sdb.ch).
CC -----
CC EMBL: X60323; CAA42892.1; -.
CC DR HSSP: P03643; IALU.
CC KW Coat protein
SQ SEQUENCE 187 AA: 19569 MW: C5C5CEC891241701 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 187;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
Db 25 TPVAPT 30

RESULT 4
SOD3_PLEBO STANDARD: PRT: 239 AA.
AC P50060:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE SUPEROXIDE DISMUTASE [MN] 3 PRECURSOR (EC 1.15.1.1) (FRAGMENT).
GN SOD3.
OS Plectonema boryanum.
OC Bacteria: Cyanobacteria; Oscillatoriales; Plectonema.
ON NCBI_TaxID=1184;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN-UTEX 485;
RX MEDLINE-95164530; PubMed-7860607;
RA Campbell W.S., Landenbach D.E.;
RT "Characterization of four superoxide dismutase genes from a
RT filamentous cyanobacterium."
RL J. Bacteriol. 177:964-972(1995).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC -----
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CC -----
CC EMBL: U17611; AAA69953.1; -.
CC DR HSSP: P09214; LMNG.
CC DR InterPro: IPR001189; -.
CC DR Pfam: PF00081; sodfe; 1.
CC DR PROSITE: PS00088; SOD_MN; 1.
CC KW Oxidoreductase; Manganese; Multigene family; Signal.
FT NON TER 1 1
FT SIGNAL <1 30 POTENTIAL.
FT CHAIN 31 239 SUPEROXIDE DISMUTASE [MN] 3.
FT METAL 57 57 MANGANESE(BY SIMILARITY).
FT METAL 112 112 MANGANESE(BY SIMILARITY).
FT METAL 195 195 MANGANESE(BY SIMILARITY).
FT METAL 199 199 MANGANESE(BY SIMILARITY).
SQ SEQUENCE 239 AA: 26854 MW: 242CBD3C9C61D100 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVA 6
Db 17 VSTPVA 22

RESULT 5
GATA_HELPD STANDARD: PRT: 453 AA.
ID GATA_HELPD
AC Q9ZL13:
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 01-OCT-2000 (rel. 40, Last annotation update)
DE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADT
DE SUBUNIT A).
GN GATA OR JHP0769.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria: Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCBI_TaxID=85963;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99120557; PubMed-9923682;
RA Alm R.A., Ling L.S.L., Molt D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Voyis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC GLN-TRNA(GLN) THROUGH THE TRANSAMINATION OF MISACYLATED GLU-
CC TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
CC REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
CC AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE -> ADP
CC + PHOSPHATE + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMATE.
CC -1- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
CC -----
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CC -----
CC EMBL: AEO01507; AAD06348.1; -
CC InterPro: IPR000120; -
CC Pfam: PF01425; AMIDase; 1.
CC PROSITE: PS00571; AMIDASES; 1.
CC Protein biosynthesis; Ligase.
CC KW SEQUENCE 453 AA; 49749 MW; FD97731532E77397 CRC64;
CC
CC Query Match 66.7%; Score 6; DB 1; Length 453;
CC Best Local Similarity 100.0%; Pred. No. 13;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 TPVAPT 8
CC |||||
CC Db 373 TPVAPT 378
CC
CC RESULT 6
CC GATA_HELPY
CC ID GATA_HELPY STANDARD; PRT; 453 AA.
CC AC P56114:
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADT
CC SUBUNIT A).
CC GN GATA OR HP0830.
CC OS Helicobacter pylori (Campylobacter pylori).
CC OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
CC CC Helicobacter.
CC OX NCBI_TaxID=210;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=26695 / ATCC 700392;
CC RX MEDLINE=9739467; PubMed=9252185;
CC RA Tomb J.-F., White O., Kervavage A.R., Clayton R.A., Sutton G.G.,
CC RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
CC RA Loftus K., Quackenbush J., Zhou L., Kirness E.F., Peterson S.,
CC RA Nelson B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
CC RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
CC RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
CC RA Colton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
CC RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
CC RA Venter J.C.;
CC RT "The complete genome sequence of the gastric pathogen Helicobacter
CC pylori".
CC RL Nature 388:539-547(1997).
CC CC
CC CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC GIN-TRNA(GLN) THROUGH THE TRANSMUTATION OF MISACETYLATED GLU-
CC TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
CC REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
CC AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
CC CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) = ADP
CC + PHOSPHATE + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE.
CC CC -1- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
CC CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
CC CC
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CC -----
CC EMBL: AEO00594; AAD07880.1; -
CC DR TIGR: HP0830; -
CC DR InterPro: IPR000120; -
CC DR Pfam: PF01425; AMIDase; 1.
CC DR PROSITE: PS00571; AMIDASES; 1.
CC KW Protein biosynthesis; Ligase.

CC
CC SO SEQUENCE 453 AA; 49652 MW; A35814B32F1AE13A CRC64;
CC
CC Query Match 66.7%; Score 6; DB 1; Length 453;
CC Best Local Similarity 100.0%; Pred. No. 13;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 TPVAPT 8
CC |||||
CC Db 373 TPVAPT 378
CC
CC RESULT 7
CC CADA_LISMO
CC ID CADA_LISMO STANDARD; PRT; 711 AA.
CC AC 060048:
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC DE PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1.-) (CADMIUM EFFLUX
CC ATPASE).
CC GN CADA.
CC OS Listeria monocytogenes.
CC OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC OC Bacillus/staphylococcus group; Listeria.
CC OX NCBI_TaxID=1639;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=LM74;
CC RX MEDLINE=94245633; PubMed=8188605;
CC RA Lebrun M., Audurier A., Cossart P.;
CC RT "Plasmid-borne cadmium resistance genes in Listeria monocytogenes are
CC similar to cda and cadC of Staphylococcus aureus and are induced by
CC cadmium".
CC RL J. Bacteriol. 176:3040-3048(1994).
CC [2]
CC RN
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=LM74; TRANSPOSON-Tn5422;
CC RX MEDLINE=94245634; PubMed=8188606;
CC RA Lebrun M., Audurier A., Cossart P.;
CC RT "Plasmid-borne cadmium resistance genes in Listeria monocytogenes are
CC present on tn5422, a novel transposon closely related to tn917".
CC RL J. Bacteriol. 176:3049-3061(1994).
CC CC -1- FUNCTION: THIS ELECTRONEUTRAL ANTI-PORTER EFFECTS ONE CD(2+) WHILE
CC ACCUMULATING TWO PROTONS BY AN ENERGY-DEPENDENT EFFLUX MECHANISM.
CC CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
CC CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (F1-E2 ATPASES).
CC CC
CC CC -1- SIMILARITY: CONTAINS 1 HEAVY-METAL-ASSOCIATED (HMA) DOMAIN.
CC CC
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CC -----
CC EMBL: L28104; AAA25275.1; -
CC DR InterPro: IPR001366; -
CC DR InterPro: IPR001366; -
CC DR InterPro: IPR001366; -
CC DR Pfam: PF00122; E1-E2 ATPase; 1.
CC DR Pfam: PF00403; HMA; 1.
CC DR PRINTS: PR00941; CDATPASE.
CC DR PROSITE: PS00154; ATPASE_E1_E2; 1.
CC DR PROSITE: PS01047; HMA; 1.
CC KW Hydrolyase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
CC Cadmium; Plasmid; Cadmium resistance; Transposable element.
CC FT DOMAIN 9 38 HMA.
CC METAL 14 14 CADMIUM (POTENTIAL).

FT METAL 17 17 CADMIUM (POTENTIAL).
 FT MOD_RES 398 398 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 711 AA: 77089 MM: C23BFEB7E20CEE9A CRC64;

Query Match 66.7%; Score 6; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVA 6
 |||||
 DB 360 VSTPVA 365

RESULT 8
 CPN_DROME STANDARD; PRT: 865 AA.
 ID CPN_DROME 002910;
 AC 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE CALPHOTIN.
 GN CPN OR CAP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RX MEDLINE=93165729; PubMed=8094559;
 RA Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
 RL "Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RX MEDLINE=93165730; PubMed=8434015;
 RA Ballinger D.G., Xue N., Harshman K.D.;
 RT "Calcium and contains a leucine zipper.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
 CC -1- FUNCTION: MIGHT FUNCTION AS A CALCIUM-SENSITIZING "SPONGE" TO
 CC REGULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BINDS 0.3 MOL
 CC OF CA+2 PER MOL OF PROTEIN.
 CC -1- SUBUNIT: HOMODIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODERMIS COMPARTMENT.
 CC -1- TISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CELLS OF
 CC COMPOUND EYES AND OCELLI.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELL
 CC DEVELOPMENT.
 CC -----
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 CC -----
 CC EMBL: L02111; AAA28405.1; -;
 CC EMBL: L05080; AAA28420.1; -;
 DR PIR: A47282; A47282.
 DR PIR: A47282; FBgn010218; Cpn.
 KM Calcium-binding.
 FT CONFLICT 36 36 A -> AVAPAVA (IN REF. 2).
 FT CONFLICT 43 43 I -> T (IN REF. 2).
 FT CONFLICT 64 64 I -> V (IN REF. 2).
 FT CONFLICT 76 76 T -> A (IN REF. 2).
 FT CONFLICT 100 100 P -> PP (IN REF. 2).
 FT CONFLICT 126 127 VO -> AP (IN REF. 2).
 FT CONFLICT 154 154 I -> V (IN REF. 2).

FT CONFLICT 160 160 S -> T (IN REF. 2).
 FT CONFLICT 534 534 A -> E (IN REF. 2).
 FT CONFLICT 699 699 I -> T (IN REF. 2).
 FT CONFLICT 703 703 V -> L (IN REF. 2).
 FT CONFLICT 721 721 D -> E (IN REF. 2).
 SQ SEQUENCE 865 AA: 84781 MM: 2110417E0B0E7CFE CRC64;

Query Match 66.7%; Score 6; DB 1; Length 865;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVA 6
 |||||
 DB 97 VSTPVA 102

RESULT 9
 RW1_DROME STANDARD; PRT: 1540 AA.
 ID RW1_DROME 09V7H4;
 AC 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RW1 PROTEIN HOMOLOG.
 GN CG8370.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jajala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimball B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclel J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AEO03808; AAF58081.1; -
DR FlyBase: FBgn0034060; CG8370.
SQ SEQUENCE 1540 AA; 170274 MW; 5AB097531D425846 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 1540;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVA 6
| | | | |
DB 1207 VSTPVA 1212

RESULT 10
KAC4_RABIT STANDARD; PRT; 103 AA.
ID KAC4_RABIT
AC P01840;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA-B4 CHAIN C REGION.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83300036; PubMed=6412231;
RA Emorine L., Dreher K.L., Kind T.J., Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
RT allotype J-C locus and evidence for several b4-related sequences in
RT the rabbit genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a
RT kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.C.S., Kind T.J., Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody
RT to streptococcal carbohydrate. II. Sequence determination of peptides
RT from tryptic and peptic digests.";
RL J. Biol. Chem. 250:3289-3296(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE
CC SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI & WAS ISOLATED FROM
CC THE SERUM OF A SINGLE RABBIT.
CC
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CC
CC EMBL: X00231; CAA25051.1; -
DR PIR: A02122; KARB.
DR InterPro: IPR000495; -

DR InterPro: IPR003006; -
DR Pfam: PF00047; 1g; 1.
DR PROSITE: PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 85
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT CONFLICT 58 58 N -> D (IN REF. 3).
SQ SEQUENCE 103 AA; 11043 MW; 5FC5ACB860E68DB CRC64;

Query Match 55.68%; Score 5; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
| | | | |
DB 2 PVAPT 6

RESULT 11
SY12_MOUSE STANDARD; PRT; 104 AA.
ID SY12_MOUSE
AC Q62401;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SMALL INDUCIBLE CYTOKINE A12 PRECURSOR (MONOCYTE CHEMOTACTIC PROTEIN
DE 5) (MCP-5) (MCP-1 RELATED CHEMOKINE).
GN SCYA12 OR MCP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079149; PubMed=8920881;
RA Jia G.-Q., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C.,
RA Wershl B.K., Gutierrez-Ramos J.C.;
RT "Distinct expression and function of the novel mouse chemokine
RT monocyte chemoattractant protein-5 in lung allergic inflammation.";
RL J. Exp. Med. 184:1939-1951(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97149438; PubMed=8996246;
RA Sarraf M.N., Garcia-Zepeda E.A., McLean J.A., Charo I.F., Luster A.D.;
RT "Murine monocyte chemoattractant protein (MCP)-5: a novel CC
RT chemokine that is a structural and functional homologue of human
RT MCP-1.";
RL J. Exp. Med. 185:99-109(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX SPRAT-B10.S/J, BALB/C, DBA/2J, AND NOD/LTJ; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Tauscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blanehorn E.P.;
RT "Sequence polymorphisms in the chemokines Sycal (TCA-3), Sycal2
RT (monocyte chemoattractant protein (MCP)-1), and Sycal2 (MCP-5) are
RT candidates for eae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
RN [4]
RP FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS EOSINOPHILS, MONOCYTES,
CC AND LYMPHOCYTES BUT NOT NEUTROPHILS. POTENT MONOCYTE ACTIVE
CC CHEMOKINE THAT SIGNALS THROUGH CCR2. INVOLVED IN ALLERGIC
CC INFLAMMATION AND THE HOST RESPONSE TO PATHOGENS AND MAY PLAY A
CC PIVOTAL ROLE DURING EARLY STAGES OF ALLERGIC LUNG INFLAMMATION.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE LYMPH NODES AND
CC THYMUS. ALSO FOUND IN THE SALIVARY GLANDS CONTAINING LYMPH NODES,
CC BREAST, HEART, LUNG, BRAIN, SMALL INTESTINE, KIDNEY AND COLON.
CC -1- INDUCTION: BY IFN-GAMMA AND LIPOPOLYSACCHARIDE (LPS).
CC -1- SIMILARITY: BELONGS TO THE INTERCINE BETA FAMILY (SMALL CYTOKINE

CC (C-C) (CHEMOKINE CC).

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 DR EMBL: U50712; AAB50053.1; -;
 DR EMBL: U66670; AAB49424.1; -;
 DR EMBL: AF065934; AAF15384.1; -;
 DR EMBL: AF065935; AAF15385.1; -;
 DR EMBL: AF065936; AAF15386.1; -;
 DR EMBL: AF065937; AAF15387.1; -;
 DR HSSP: P13500; IDOL.
 DR MGD: MGI:108224; Scya12.
 DR InterPro: IPR000827; -;
 DR InterPro: IPR001811; -;
 DR Pfam: PF00048; IL8; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 DR Cytokine; Chemotaxis; Signal; Inflammatory response.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 104 SMALL INDUCIBLE CYTOKINE A12.
 FT DISULFID 33 58 BY SIMILARITY.
 FT DISULFID 34 74 BY SIMILARITY.
 FT SEQUENCE 104 AA: 11659 MW: 80102P4FF4CC3DBF CRC64:

 Query Match 55.6%; Score 5; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy 1 VSTPV 5
 11111
 Db 27 VSTPV 31

 RESULT 12
 PSSP_HUMAN STANDARD; PRT; 114 AA.
 ID PSSP_HUMAN P08118; P11999;
 AC 01-AUG-1988 (Rel. 08. Created)
 DT 01-AUG-1988 (Rel. 08. Last sequence update)
 DT 01-OCT-2000 (Rel. 40. Last annotation update)
 DE PROSTATE SECRETED SEMINAL PLASMA PROTEIN PRECURSOR (PSP-94) (BETA-
 DE MICROSEMINOPROTEIN) (SEMINAL PLASMA BETA-INHIBIN) (IMMUNOGLOBULIN
 DE BINDING FACTOR) (IGBF) (PROSTATE SECRETORY PROTEIN PSP94) (PM44).
 GN MSMB OR PSP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87161231; PubMed=3829888;
 RA Mdkay M., Nolet S., Fournier S., Benjannet S., Chapdelaine P.,
 RA Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidah N.G.,
 RA Chretien M.;
 RA "Molecular cloning and sequence of the cDNA for a 94-amino-acid
 RT seminal plasma protein secreted by the human prostate.";
 RL DNA 6:23-29(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91274357; PubMed=2054385;
 RA Nolet S., Mdkay M., Chretien M.;
 RT "Prostatic secretory protein PSP94: gene organization and promoter
 RT sequence in rhesus monkey and human.";
 RL Biochim. Biophys. Acta 1089:247-249(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90211299; PubMed=232265;

RA Green C.B., Liu W.Y., Kwok S.C.M.;
 RT "Cloning and nucleotide sequence analysis of the human beta-
 RT microseminoprotein gene.";
 RL Biochem. Biophys. Res. Commun. 167:1184-1190(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90073664; PubMed=2590204;
 RA Ulysback M., Lindstroem C., Welber H., Abrahamsson P.-A., Lilja H.,
 RA Lundwall A.;
 RT "Molecular cloning of a small prostate protein, known as beta-
 RT microseminoprotein, PSP94 or beta-inhibin, and demonstration of
 RT transcripts in non-genital tissues.";
 RL Biochem. Biophys. Res. Commun. 164:1310-1315(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=94115955; PubMed=7506990;
 RA Liu A.Y., Bradner R.C., Vessella R.L.;
 RT "Decreased expression of prostatic secretory protein PSP94 in
 RT prostate cancer.";
 RL Cancer Lett. 74:91-99(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Bajjal-Gupta M., Clarke M.W.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 21-113.
 RX MEDLINE=8519974; PubMed=3995056;
 RA Akiyama K., Yoshioke Y., Schmid K., Offner G.D., Troxler R.F.,
 RA Tsuda R., Hara M.;
 RT "The amino acid sequence of human beta-microseminoprotein.";
 RL Biochim. Biophys. Acta 829:288-294(1985).
 RN [8]
 RP SEQUENCE OF 21-114.
 RX MEDLINE=85004133; PubMed=6434350;
 RA Seidah N.G., Arbatli N.J., Rochemont J., Sheth A.R., Chretien M.;
 RT "Complete amino acid sequence of human seminal plasma beta-inhibin.
 RT Prediction of post Glu-Arg cleavage as a maturation site.";
 RL FEBS Lett. 175:349-355(1984).
 RN [9]
 RP SEQUENCE OF 21-50 AND 113-114.
 RX MEDLINE=92028964; PubMed=1930232;
 RA Liang Z.G., Kamada M., Koide S.S.;
 RT "Structural identity of immunoglobulin binding factor and prostatic
 RT secretory protein of human seminal plasma.";
 RL Biochem. Biophys. Res. Commun. 180:356-359(1991).
 CC -1- FUNCTION: INHIBITS THE SECRETION OF FSH BY PITUITARY CELLS.
 CC -1- SUBCELLULAR LOCATION: SPERM SURFACE.
 CC -1- PTM: RICH IN DISULFIDE BONDS (POTENTIAL).
 CC -1- MISCELLANEOUS: SPECIFIC RECEPTORS FOR THIS PROTEIN ARE FOUND ON
 CC SPERMATOZOA AND IN THE PROSTATE.

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 DR EMBL: M34376; AAB59871.1; -;
 DR EMBL: M34373; AAB59871.1; JOINED.
 DR EMBL: M34374; AAB59871.1; JOINED.
 DR EMBL: M34375; AAB59871.1; JOINED.
 DR EMBL: M15885; AAB59871.1; -;
 DR EMBL: M57928; AAB59871.1; -;
 DR EMBL: M57929; AAB59871.1; JOINED.
 DR EMBL: X57930; AAB59871.1; JOINED.
 DR EMBL: X57931; AAB59871.1; JOINED.
 DR EMBL: S67815; AAB59871.1; JOINED.
 DR EMBL: U78976; AAB59871.1; -;
 DR PIR: A26451; A26451.
 DR PIR: A29777; A29777.

```

RT "Analysis of the nucleotide sequence of chromosome VI from
RL Saccharomyces cerevisiae."
RN Nat. Genet. 10:261-268(1995).
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE-96287652; PubMed-8686379;
RA Ekl T., Naitou M., Hagihara H., Ozawa M., Sasamura S.-I.,
RA Sasamura M., Tsuchiya Y., Shibata T., Hanaka F., Murakami Y.;
RT "Analysis of a 36.2 kb DNA sequence including the right telomere of
RL chromosome VI from Saccharomyces cerevisiae."
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: D50617; BAA09284.1; -
DR EMBL: D44597; BAA08011.1; -
DR SGD: S0001941; YFR045W.
DR InterPro: IPR001993; -
DR Pfam: PF00133; mltocarr; 1.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
KW Transmembrane; Transport.
SQ SEQUENCE 178 AA; 19901 MW; D57433A7D1AA4FE5 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
| | | | |
DB 27 STPVA 31

RESULT 16
ATPD_BACP3 STANDARD; PRT; 179 AA.
AC P09220;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34);
GN ATPH.
OS Bacillus PS3 (Thermophilic bacterium PS-3).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=70306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-88163679; PubMed-2894854;
RA Ohba S., Yohda M., Ishizuka M., Hirata H., Hamamoto T.,
RA Ohtawa-Hamamoto Y., Matsuda K., Kagawa Y.;
RT "Sequence and over-expression of subunits of adenosine triphosphate
RT synthase in thermophilic bacterium PS3."
RL Biochim. Biophys. Acta 933:141-155(1988).
CC -1- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS
CC CF(0) TO CF(1). IT EITHER TRANSMITS CONFORMATIONAL CHANGES FROM
CC CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.

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CC -----
DR EMBL: X07804; CAA30651.1; -
DR PIR: S01400; S01400.
DR InterPro: IPR000711; -
DR Pfam: PF00213; OSCP; 1.
DR PROSITE: PS00389; ATPASE_DELTA; 1.
KW Hydrolyase; ATP synthesis; CF(1); Hydrogen ion transport.
SQ SEQUENCE 179 AA; 19657 MW; 8168E151121380E5 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
| | | | |
DB 69 VSTPV 73

RESULT 17
CASK_MOUSE STANDARD; PRT; 181 AA.
AC P06796;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE KAPPA CASEIN PRECURSOR.
GN CSN10 OR CSN3 OR CSNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-66004062; PubMed-4042811;
RA Thompson M.D., Dave J.R., Nakhasi H.L.;
RT "Molecular cloning of mouse mammary gland kappa-casein: comparison
RT with rat kappa-casein and rat and human gamma-fibrinogen."
RL DNA 4:263-271(1985).
CC -1- FUNCTION: KAPPA CASEIN STABILIZES MICELLE FORMATION, PREVENTING
CC CASEIN PRECIPITATION IN MILK.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
CC -1- SIMILARITY: BELONGS TO THE KAPPA-CASEIN FAMILY.
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CC -----
DR EMBL: M10114; AAA37370.1; -
DR PIR: A05080; A05080.
DR MGD: MGI:107461; CSNK.
DR InterPro: IPR000117; -
DR Pfam: PF00997; casein_kappa; 1.
KW Milk; Glycoprotein; Phosphorylation; Signal.
FT SIGNAL 1 21
FT CHAIN 22 181 KAPPA CASEIN.
FT SITE 119 CLEAVAGE (BY CHYMOSIN (=RENNIN)).
FT MOD_RES 123 123 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 181 AA; 20062 MW; E5AEBF016679C5DC CRC64;

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Query Match 55.6%; Score 5; DB 1; Length 181;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 11111
 Db 142 VSTPV 146

RESULT 18
 V33P_ADE41 STANDARD; PRT; 217 AA.
 AC P19416; Q64818;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE 33 KDa PHOSPHOPROTEIN.
 OS Human adenovirus type 41.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 NCBI_TaxID=10524;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-TAK;
 RC MEDLINE=90272433; PubMed=2349115;
 RA Stemenda S.B., Pieniazek N.J., Velarde J. Jr., Pieniazek D.,
 Luftig R.B.;
 RT "Nucleotide sequence of the region coding for 100K and 33K proteins
 of human enteric adenovirus type 41 (Tak).";
 RL Nucleic Acids Res. 18:3069-3069(1990).
 RN [2]
 RP SEQUENCE OF 203-217 FROM N.A.
 RC STRAIN-TAK;
 RX MEDLINE=89345113; PubMed=2762136;
 RA Pieniazek N.J., Velarde J. Jr., Pieniazek D., Luftig R.B.;
 RT "Nucleotide sequence of human enteric adenovirus type 41 hexon-
 associated protein VIII precursor (pVIII) including the early region
 E3 promoter.";
 RL Nucleic Acids Res. 17:5398-5398(1989).
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 CC -----
 CC EMBL: X52532; CAB38632.1; -;
 DR EMBL: X15137; CAA33236.1; -;
 DR PIR: S04851; S04851.
 DR PIR: S10212; S10212.
 KW Late protein; Phosphorylation.
 SQ SEQUENCE 217 AA; 24740 MW; B6ECDAB3C24EC3E CRC64;

Query Match 55.6%; Score 5; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
 11111
 Db 118 PVAPT 122

RESULT 19
 RPE_TREPA STANDARD; PRT; 218 AA.
 ID RPE_TREPA
 AC 066107;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1) (PENTOSE-5-PHOSPHATE 3-

DE EPIMERASE) (PPE) (R5P3E).
 GN RPE OR TP0945.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shevchenko D.V., Akins D.R., Radolf J.D.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-NICHOLS;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Karger H., Richardson D., Howell J.K., Chidambaram M., Uitterlinden J.,
 RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 agent."
 RL Science 281:375-388(1998).
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 5-PHOSPHATE - D-XYLULOSE 5-PHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE RIBULOSE-PHOSPHATE 3-EPIMERASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: U97573; AAC08057.1; -;
 DR EMBL: AE001263; AAC65902.1; -;
 DR TIGR: TP0945;
 DR InterPro: IPR000056; -;
 DR Pfam: PF00834; Ribul_P_3_epim: 1.
 DR PROSITE: PS01085; RIBUL_P_3_EPIMER_1; 1.
 DR PROSITE: PS01086; RIBUL_P_3_EPIMER_2; 1.
 KW Isomerase; Carbohydrate metabolism.
 SQ SEQUENCE 218 AA; 23514 MW; 0066263301FA2PCA CRC64;

Query Match 55.6%; Score 5; DB 1; Length 218;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
 11111
 Db 120 STPVA 124

RESULT 20
 Y574_AERPE STANDARD; PRT; 225 AA.
 ID Y574_AERPE
 AC Q9YEK4;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PUTATIVE SHIKIMATE 5-DEHYDROGENASE-LIKE PROTEIN APE0574.
 GN APE0574.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;
 OC Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,

RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kusuda N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 CC -1- SIMILARITY: BELONGS TO THE SHIKIMATE DEHYDROGENASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AP000060; BAA79542.1; -
 DR Hypothetical protein: Oxidoreductase.
 SO SEQUENCE 225 AA; 23273 MW; 13110B4615003F6C CRC64;

Query Match 55.6%; Score 5; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 |||||
 Db 147 VSTPV 151

RESULT 21
 PRL_BOVIN STANDARD: PRT: 229 AA.
 ID P01239; Q95112; Q29417;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PROLACTIN PRECURSOR (PRL).
 GN PRL.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RX MEDLINE=82098114; PubMed=6274859;
 RA Sasavaga N.L., Nilsson J.H., Horowitz S., Rottman F.M.;
 RT "Nucleotide sequence of bovine prolactin messenger RNA. Evidence for
 RT sequence polymorphism.";
 RL J. Biol. Chem. 257:678-681(1982).
 RN [2]
 RP SEQUENCE OF 21-229 FROM N.A.
 RX MEDLINE=83157107; PubMed=6299665;
 RA Miller W.L., Colt D., Baxter J.D., Martial J.A.;
 RT "Cloning of bovine prolactin cDNA and evolutionary implications of
 RT its sequence.";
 RL DNA 1:37-50(1981).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=83182016; PubMed=6897772;
 RA Miller W.L., Colt D., Baxter J.D., Martial J.A.;
 RT "Bovine prolactin: corrected cDNA sequence and genetic
 RT polymorphisms.";
 RL DNA 1:313-314(1982).
 RN [4]
 RP SEQUENCE OF 96-229 FROM N.A.
 RA Rubtsov P.M., Oganesyan R.G., Gorbulev V.G., Skryabin K.G., Baev A.A.;
 RT "Genetic engineering of peptide hormones. II. Possible polymorphism of
 RT preprolactin in cattle. Data of molecular cloning.";
 RL Mol. Biol. (Mosk) 22:117-127(1988).

RN [5]
 RP PRELIMINARY SEQUENCE OF 31-229.
 RX MEDLINE=75031394; PubMed=4608931;
 RA Wallis M.;
 RT "The primary structure of bovine prolactin.";
 RL FEBS Lett. 44:205-208(1974).
 RN [6]
 RP SEQUENCE OF 31-46.
 RX MEDLINE=71150631; PubMed=5507606;
 RA Graf L., Cseh G., Nagy I., Kurcz M.;
 RT "An evidence for deamidation of prolactin monomer.";
 RL Acta Biochim. Biophys. Acad. Sci. Hung. 5:299-303(1970).
 RN [7]
 RP PHOSPHORYLATION SITES.
 RC TISSUE-Pituitary;
 RX MEDLINE=94071839; PubMed=8250856;
 RA Kim B.G., Brooks C.L.;
 RT "Isolation and characterization of phosphorylated bovine prolactin.";
 RL Biochem. J. 296:41-47(1993).
 CC -1- FUNCTION: PROLACTIN ACTS PRIMARILY ON THE MAMMARY GLAND BY
 CC PROMOTING LACTATION.
 CC -----
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -----
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 CC -----

DR EMBL: V00112; CAA23446.1; -
 DR EMBL: X01452; -; NOT_ANNOTATED_CDS.
 DR EMBL: X01744; CAA25880.1; -
 DR EMBL: M36873; AAA30737.1; -
 DR EMBL: M36874; AAA30738.1; -
 DR EMBL: X14320; CAA32500.1; -
 DR EMBL: X14321; CAA32501.1; -
 DR PIR: A01508; LCBO.
 DR HSSP: Q28632; IAN3.
 DR InterPro: IPR001400; -
 DR Pfam: PF00103; hormone.1.
 DR PRINTS: PR00836; SOMATOTROPIN.
 DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
 KW Hormone; Parturition; Lactation; Pituitary; Signal; Phosphorylation.
 FT SIGNAL 1 30
 FT CHAIN 1 229 PROLACTIN.
 FT DISULFID 34 41
 FT DISULFID 88 204
 FT DISULFID 221 229
 FT MOD_RES 56 56 PHOSPHORYLATION.
 FT MOD_RES 64 64 PHOSPHORYLATION.
 FT MOD_RES 120 120 PHOSPHORYLATION.
 FT CONFLICT 61 61 D->N (IN REF. 5).
 SO SEQUENCE 229 AA; 25792 MW; E7E9BB655A26F3D CRC64;

Query Match 55.6%; Score 5; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 |||||
 Db 29 VSTPV 33

RESULT 22
 PRL_CAPHI STANDARD: PRT: 229 AA.
 ID Q28318; Q28329;
 AC 01-NOV-1997 (Rel. 35, Created)

```

DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 01-NOV-1997 (Rel. 35, last annotation update)
DE PROLACTIN PRECURSOR (PRL).
GN PRL.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95059806; PubMed=7969789;
RA Le Provost F., Leroux C., Martin P., Gaye P., Djiane J.;
RA Prolactin gene expression in ovine and caprine mammary gland.;
RL Neuroendocrinology 60:305-313(1994).
CC -1- FUNCTION: PROLACTIN ACTS PRIMARILY ON THE MAMMARY GLAND BY
CC PROMOTING LACTATION.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
CC -----
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CC -----
CC EMBL: X76049; CAA53634.1; -.
CC EMBL: X76048; CAA53633.1; -.
CC HSSP: Q28632; IAN3.
CC InterPro: IPR001400; -.
CC DR Pfam: PF00103; hormone.1.
CC DR PRINTS: PR00836; SOMATOTROPIN.
CC DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
CC DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
CC KW hormone; Parturition; Lactation; Pituitary; Signal.
CC FT CHAIN 1 30 BY SIMILARITY.
CC FT CHAIN 31 229 BY SIMILARITY.
CC FT DISULFID 34 41 BY SIMILARITY.
CC FT DISULFID 88 204 BY SIMILARITY.
CC FT DISULFID 221 229 BY SIMILARITY.
CC FT VARIANT 164 164 L->F.
CC SQ SEQUENCE 229 AA; 25773 MW; 331C640C66134DDA CRC64;

Query Match 55.6%; Score 5; DB 1; Length 229;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
Db 29 VSTPV 33

RESULT 23
PRL_SHEEP STANDARD; PRT; 229 AA.
AC P01240; Q28587;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROLACTIN PRECURSOR (PRL).
GN PRL.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pituitary;
RX MEDLINE=89098399; PubMed=2911473;

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RA Adams T.E., Baker L., Brandon M.R.;
RA "Cloning and nucleotide sequence of an ovine prolactin cDNA.";
RT Nucleic Acids Res. 17:440-440(1989).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=89326152; PubMed=2666265;
RA Varma S., Kwok S., Ebner K.E.;
RT "Cloning and nucleotide sequence of ovine prolactin cDNA.";
RL Gene 77:349-359(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95059806; PubMed=7969789;
RA Le Provost F., Leroux C., Martin P., Gaye P., Djiane J.;
RA "Prolactin gene expression in ovine and caprine mammary gland.";
RL Neuroendocrinology 60:305-313(1994).
RN [4]
RP SEQUENCE OF 31-229.
RX MEDLINE=71091978; PubMed=5497153;
RA Li C.H., Dixon J.S., Lo T.-B., Schmidt K.D., Pankov Y.A.;
RA "Studies on pituitary lactogenic hormone. XXX. The primary structure
RA of the sheep hormone.";
RL Arch. Biochem. Biophys. 141:705-737(1970).
RN [5]
RP REVISIONS.
RX MEDLINE=76189476; PubMed=1270193;
RA Li C.H.;
RA "Studies on pituitary lactogenic hormone. The primary structure of
RA the porcine hormone. Res. 8:205-224(1976).
RL Int. J. Pept. Protein Res. 8:205-224(1976).
CC -1- FUNCTION: PROLACTIN ACTS PRIMARILY ON THE MAMMARY GLAND BY
CC PROMOTING LACTATION, MAMMOGENESIS, MITOGENESIS AND OSMOREGULATION.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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CC -----
CC EMBL: X13483; CAA31839.1; -.
CC DR EMBL: M27057; AAA31578.1; ALT_INIT.
CC DR EMBL: X76050; CAA53635.1; -.
CC DR PIR: A01509; ICSH.
CC DR PIR: S02104; S02104.
CC DR PIR: J50200; J50200.
CC HSSP: Q28632; IAN3.
CC InterPro: IPR001400; -.
CC DR Pfam: PF00103; hormone.1.
CC DR PRINTS: PR00836; SOMATOTROPIN.
CC DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
CC DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
CC KW hormone; Parturition; Lactation; Pituitary; Signal; Glycoprotein.
CC FT CHAIN 1 30 BY SIMILARITY.
CC FT CHAIN 31 229 BY SIMILARITY.
CC FT DISULFID 34 41 BY SIMILARITY.
CC FT DISULFID 88 204 BY SIMILARITY.
CC FT DISULFID 221 229 BY SIMILARITY.
CC FT CARBOHYD 61 61 N-LINKED (GLCNAC. .) (PARTIAL).
CC FT CONFLICT 40 40 N->D (IN REF. 2).
CC SQ SEQUENCE 229 AA; 25777 MW; 97FD8AF2991B9B39 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 229;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
Db 29 VSTPV 33

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PFam: PF00047; 19; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 32
 FT CHAIN 33 261
 FT DOMAIN 33 261
 FT DOMAIN 127 226
 FT DOMAIN 221 230
 FT TRANSMEM 231 251
 FT DOMAIN 252 261
 FT DISULFID 47 111
 FT DISULFID 149 205
 FT CARBOHYD 51 51
 SQ SEQUENCE 261 AA; 29870 MW; 8C2CFE6C080D4AF1 CRC64; N-LINKED (GLCNAC. . .) (POTENTIAL).
 Query Match 55.6%; Score 5; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 STPYA 6
 Db 26 STPYA 30
 RESULT 26
 GP3D_CHLTR STANDARD; PRT; 263 AA.
 ID AC P10557; P08783; P08784; Q46431;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VIRULENCE PLASMID PROTEIN PGP3-D (PROTEINS P-6/P-7).
 OS Chlamydia trachomatis.
 OC Plasmid pLGV440, Plasmid pCHL1, and Plasmid pCTT1.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_Taxid=813;
 RX STRAIN-L2/434/BU; PLASMID-pLGV440;
 RX MEDLINE-89013895; PubMed-2845228;
 RA Commanducci M., Ricci S., Ratti G.;
 RT "The structure of a plasmid of Chlamydia trachomatis believed to be required for growth within mammalian cells."
 RL Mol. Microbiol. 2:531-538(1988).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L1/440/LN; PLASMID-pLGV440;
 RX MEDLINE-8823398; PubMed-2836808;
 RA Halt C., Ward M.E., Clarke I.N.;
 RT "Analysis of the entire nucleotide sequence of the cryptic plasmid of Chlamydia trachomatis serovar L1. Evidence for involvement in DNA replication."
 RL Nucleic Acids Res. 16:4053-4067(1988).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-G0/86 / SEROTYPE D; PLASMID-pCHL1;
 RX MEDLINE-90301796; PubMed-2194229;
 RA Commanducci M., Ricci S., Cevenini R., Ratti G.;
 RT "Diversity of the Chlamydia trachomatis common plasmid in biovars with different pathogenicity."
 RL Plasmid 23:149-154(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROTYPE B; PLASMID-pCTT1;
 RX MEDLINE-88177106; PubMed-3444855;
 RA Sriprakash K.S., Macavoy E.S.;
 RT "Characterization and sequence of a plasmid from the trachoma biovar of Chlamydia trachomatis."
 RL Plasmid 18:205-214(1987).
 RN [5]
 RP SEQUENCE OF 1-10.

RC STRAIN-L2/434/BU;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
 RA Commanducci M., Christian G., Birkelund S., Viret E., Ratti G.,
 RA Pallini V.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: PGP3-D IS REQUIRED FOR GROWTH WITHIN MAMMALIAN CELLS.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF PLASMID pLGV440.
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 126.
 CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 38.
 CC -----
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 CC -----
 DR EMBL; X07547; CAA30423.1; -;
 DR EMBL; X06707; CAA28984.1; -;
 DR EMBL; J03321; AAA91571.1; -;
 DR EMBL; M19487; AAB02589.1; ALT_FRAME.
 DR PIR; S01922; S01922.
 DR PIR; S00790; S00790.
 DR PIR; S00791; S00791.
 KW Plasmid.
 FT INITMET 0 0
 FT VARIANT 11 11 Q -> E (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 60 60 P -> S (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 85 85 D -> N (IN PLASMID PCTT1).
 FT VARIANT 89 89 G -> D (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 108 108 T -> K (IN PLASMID PCHL1).
 FT VARIANT 137 137 R -> S (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 188 188 K -> N (IN PLASMID PCTT1).
 FT VARIANT 190 190 Y -> C (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 200 200 V -> I (IN PLASMID PCHL1).
 FT VARIANT 209 209 R -> S (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 211 211 I -> T (IN PLASMIDS PCHL1 AND PCTT1).
 SQ SEQUENCE 263 AA; 27791 MW; A3FF2469B1C89703 CRC64;
 Query Match 55.6%; Score 5; DB 1; Length 263;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 STPYA 6
 Db 39 STPYA 43
 RESULT 27
 PSBP_FRIAG STANDARD; PRT; 264 AA.
 ID AC Q49080;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OXYGEN-EVOLVING ENHANCER PROTEIN 2, CHLOROPLAST PRECURSOR (OEE2) (23 KDA SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (OEC 23 KDA DE SUBUNIT) (23 KDA THYLAKOID MEMBRANE PROTEIN).
 GN PSBP.
 OS Eritillaria agrestis.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Liliales; Liliaceae; Eritillaria.
 ON NCBI_Taxid=64177;
 RN [1].
 RP SEQUENCE FROM N.A.
 RA Panico E., Baysdorfer C.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF PHOTOSYSTEM II.

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
CC WITH THE PHOTOSYSTEM II COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE PSBO FAMILY.
CC -----
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CC -----
DR EMBL: AF037458; AAC04809.1; -
DR Mende: 28047; F1ag:PsbP;28047.
DR InterPro: IPR002683; -
DR Pfam: PF01789; PsbP; 1.
KW Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
KW Thylakoid membrane.
FT TRANSIT 1 78 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 79 264 OXYGEN-EVOLVING ENHANCER PROTEIN 2.
SQ SEQUENCE 264 AA: 28111 MW: 1E214D433C95809B CRC64;

Query Match 55.6%; Score 5; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
DB 194 VSTPV 198
|||||
DB 194 VSTPV 198

RESULT 28
HB2X_HUMAN STANDARD: PRT; 268 AA.
ID HB2X_HUMAN
AC P05538;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DX BETA CHAIN PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87250501; PubMed-3036828;
RA Jonsson A.K., Hyldig-Nielsen J.J., Serenius B., Larhammar D.,
RA Andersson G., Joergensen F., Peterson P.A., Rask L.;
RT "Class II genes of the human major histocompatibility complex.
RT Comparisons of the DQ and DX alpha and beta genes.";
RL J. Biol. Chem. 262:8767-8777(1987).
RN [2]
RP SEQUENCE OF 38-125 FROM N.A.
RX MEDLINE-85216510; PubMed-3858830;
RA Okada K., Boss J.M., Prentice H., Spies T., Mengler R., Auffray C.,
RA Lillie J.W., Grossberger D., Strominger J.L.;
RT "Gene organization of DC and DX subregions of the human major
RT histocompatibility complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3410-3414(1985).
CC -----
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CC -----
DR EMBL: M29614; -; NOT_ANNOTATED_CDS.
DR EMBL: M29615; -; NOT_ANNOTATED_CDS.
DR EMBL: M11136; -; NOT_ANNOTATED_CDS.
DR PIR: D29312; D29312.

DR HSSP: P13760; 2SEB.
DR InterPro: IPR000353; -
DR InterPro: IPR000495; -
DR InterPro: IPR003006; -
DR Pfam: PF00969; MHC_II_beta; 1.
DR Pfam: PF00047; Ig; 1.
DR PROSITE: PS00290; IG-MHC; 1.
KW MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 32
FT CHAIN 33 268 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 33 126 DX BETA CHAIN.
FT DOMAIN 127 229 EXTRACELLULAR BETA-1.
FT TRANSMEM 230 250 EXTRACELLULAR BETA-2.
FT DOMAIN 251 268 CYTOPLASMIC TAIL.
FT DISULFD 47 110 BY SIMILARITY.
FT DISULFD 148 204 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 268 AA: 30386 MW: 2746ED6CC5D44AF2 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SNPVA 6
DB 26 SNPVA 30
|||||
DB 26 SNPVA 30

RESULT 29
YSM4_CAEEL STANDARD: PRT; 271 AA.
ID YSM4_CAEEL
AC Q10124;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 30.6 KDA PROTEIN F52C9.4 IN CHROMOSOME III.
GN F52C9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Faveilo T.;
RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO CHIMPANZEE PROTEIN GOR, YEAST YGR276C AND X.LAEVIS
CC XPMC2.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U39850; AAA81059.1; -
DR WormPep: F52C9.4; CE01962.
DR InterPro: IPR000520; -
DR Pfam: PF00929; Exonuclease; 1.
KW Hypothetical protein.
SQ SEQUENCE 271 AA: 30613 MW: 4BA6FC40603D583 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
DB 1 VSTPV 5
|||||
DB 1 VSTPV 5

Db 87 VSTPV 91

RESULT 30
Y4OR_RHISN
ID Y4OR_RHISN STANDARD; PRT; 277 AA.
AC p55603;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE PROBABLE ABC TRANSPORTER PERMEASE PROTEIN Y4OR.
GN Y4OR.
OS Rhizobium sp. (strain NGR234).
OC Bacterioides; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes."
RL Nucleu 387:394-401(1997).
CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM Y4OPQRS. THIS SYSTEM PROBABLY TRANSPORTS A SUGAR-LIKE
CC MOLECULE. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE MALFG
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL: AEO00089; AAB91804.1; -
DR InterPro: IPR000515; -
DR Pfam: PF00528; BPD_transp. 1.
DR PROSITE: PS00402; BPD_TRANSF.INN_MEMBR. 1.
KM Hypothetical protein; Inner membrane; Transmembrane; Transport;
KW plasmid.
FT TRANSMEM 15 35 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 110 130 POTENTIAL.
FT TRANSMEM 140 160 POTENTIAL.
FT TRANSMEM 189 209 POTENTIAL.
FT TRANSMEM 214 234 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
SQ SEQUENCE 277 AA; 30576 MW; 48B863DD615B1D3D CRC64;

Query Match 55.6%; Score 5; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
Db 252 VSTPV 256

RESULT 31
PPV_DROME
ID PPV_DROME STANDARD; PRT; 303 AA.
AC Q27884; Q9M328;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SERINE/THREONINE PROTEIN PHOSPHATASE pp-v (EC 3.1.3.16).
GN PPV OR PPV6A OR CG12217.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=OREGON-R; TISSUE=Head, and Eye Imaginal disk;
RX MEDLINE=94038968; PubMed=8223492;
RA Mann D.J., Dombadi V., Cohen P.T.W.;
RT "Drosophila protein phosphatase V functionally complements a SIT4
RT mutant in Saccharomyces cerevisiae and its amino-terminal region can
RT confer this complementation to a heterologous phosphatase catalytic
RT domain."
RL EMO J. 12:4833-4842(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang X., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Godler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideyang C.,
RA Jallat M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Welnstock G.M., Welschensch J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000)
CC -1- FUNCTION: MAY BE INVOLVED IN CONTROLLING CELLULARIZATION OR IN
CC REGULATING TRANSCRIPTION OF THE GENES INVOLVED IN THIS PROCESS.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O =
CC A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE
CC SPECIFIC).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGHEST LEVELS IN 2-4 H
CC EMBRYOS.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V
CC SUBFAMILY.
CC -----
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CC EMBL: X75980; CAA53588.1; -
 DR EMBL: AE003437; AAF46163.1; -
 DR HSSP: P08129; 1FJM; PPV.
 DR Flybase: FBgn003139; PPV.
 DR InterPro: IPR000934; -
 DR Pfam: PF00149; STPHSPHATase; 1.
 DR PRINTS: PR00114; STPHSPHASE.
 DR PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.
 KW Hydrolase; Iron; Manganese.
 FT METAL 51 51 IRON (BY SIMILARITY).
 FT METAL 53 53 IRON (BY SIMILARITY).
 FT METAL 79 79 IRON AND MANGANESE (BY SIMILARITY).
 FT METAL 111 111 MANGANESE (BY SIMILARITY).
 FT ACT_SITE 112 112 GENERAL ACID (BY SIMILARITY).
 FT METAL 161 161 MANGANESE (BY SIMILARITY).
 FT METAL 235 235 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 303 AA; 34759 MW; 5269F971416E55EC CRC64;

Query Match 55.6%; Score 5; DB 1; Length 303;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

OY 1 VSTPV 5
 |||||
 DB 42 VSTPV 46

RESULT 32
 PPP6_HUMAN STANDARD; PRT; 305 AA.
 ID PP6_HUMAN
 AC 000743;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE SERINE/THREONINE PROTEIN PHOSPHATASE 6 (EC 3.1.3.16) (PP6).
 GN PPEC OR PP6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97165573; PubMed=9013334;
 RA Bastians H., Ponstingl H.;
 RT The novel human protein serine/threonine phosphatase 6 is a
 RT functional homologue of budding yeast Slp4 and fission yeast pel,
 RT which are involved in cell cycle regulation.";
 RL J. Cell Sci. 109:2865-2874(1996).
 CC - FUNCTION: MAY FUNCTION IN CELL CYCLE REGULATION.
 CC - CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O =
 CC A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE
 CC SPECIFIC).
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC - TISSUE SPECIFICITY: HIGHEST EXPRESSION LEVELS IN TESTIS, HEART,
 CC AND SKELETAL MUSCLE AND LOWEST IN PLACENTA, LUNG, AND KIDNEY.
 CC - SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V
 CC SUBFAMILY.
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DR EMBL: X92972; CAA63549.1; -
 DR HSSP: P08129; 1FJM.
 DR MIM: 300141; -
 DR InterPro: IPR000934; -
 DR Pfam: PF00149; STPHSPHATase; 1.
 DR PRINTS: PR00114; STPHSPHASE.
 DR PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.
 KW Hydrolase; Iron; Manganese.
 FT METAL 53 53 IRON (BY SIMILARITY).
 FT METAL 55 55 IRON (BY SIMILARITY).
 FT METAL 81 81 IRON AND MANGANESE (BY SIMILARITY).
 FT METAL 113 113 MANGANESE (BY SIMILARITY).
 FT ACT_SITE 114 114 GENERAL ACID (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 FT METAL 237 237 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 305 AA; 35144 MW; 53E95DB6C9A7CF4 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

OY 1 VSTPV 5
 |||||
 DB 44 VSTPV 48

RESULT 33
 PPP6_RAT STANDARD; PRT; 305 AA.
 ID PP6_RAT
 AC 064620;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE SERINE/THREONINE PROTEIN PHOSPHATASE 6 (EC 3.1.3.16) (PP6) (PROTEIN
 DE PHOSPHATASE V) (PP-V).
 GN PPEC OR PPV.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis, and Brain;
 RX MEDLINE=94357899; PubMed=8077208;
 RA Becker W., Kentrup H., Klump S., Schultz J.E., Joost H.G.;
 RT Molecular cloning of a protein serine/threonine phosphatase
 RT containing a putative regulatory tetrapeptide repeat domain.";
 RL J. Biol. Chem. 269:22586-22592(1994).
 CC - FUNCTION: MAY FUNCTION IN CELL CYCLE REGULATION.
 CC - CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O =
 CC A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE
 CC SPECIFIC).
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC - TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SPLEEN, BRAIN AND
 CC LUNG.
 CC - SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V
 CC SUBFAMILY.
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DR EMBL: X77236; CAA54453.1; -
 DR HSSP: P08129; 1FJM.
 DR InterPro: IPR000934; -
 DR Pfam: PF00149; STPHSPHATase; 1.
 DR PRINTS: PR00114; STPHSPHASE.
 DR PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.

KM Hydroxylase: Iron; Manganese.
 FT METAL 53 53 IRON (BY SIMILARITY).
 FT METAL 55 55 IRON (BY SIMILARITY).
 FT METAL 81 81 IRON AND MANGANESE (BY SIMILARITY).
 FT METAL 113 113 MANGANESE (BY SIMILARITY).
 FT ACT_SITE 114 114 GENERAL ACID (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 FT METAL 237 237 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 305 AA; 35106 MW; A91F993FBD8F110 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 |||||
 DB 44 VSTPV 48

RESULT 34
 POLG_HCVH7 STANDARD; PRT; 309 AA.
 AC P27955;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: MATRIX PROTEIN (ENVELOPE PROTEIN M);
 MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN NS1 (FRAGMENT).
 OS Hepatitis C virus (isolate HCT27) (HCV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
 OC Hepacivirus.
 ON NCBI_Taxid=11109;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91112009; PubMed=1846505;
 RA Weiner A.J., Brauer M.J., Rosenblatt J., Richman K.H., Tung J.,
 RA Crawford K., Bonino F., Saracco G., Choo Q.-L., Houghton M.,
 RA Han J.H.;
 RT "Variable and hypervariable domains are found in the regions of HCV
 RT corresponding to the flavivirus envelope and NS1 proteins and the
 RT pestivirus envelope glycoproteins.";
 RL Virology 180:842-848(1991).
 CC -----
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 CC -----
 CC EMBL: X51133; CAA37293.1; -.
 DR InterPro: IPR002519; -.
 DR InterPro: IPR002521; -.
 DR InterPro: IPR002531; -.
 DR Pfam: PF01560; HCV_NS1; 1.
 DR Pfam: PF01542; HCV_core; 1.
 DR Pfam: PF01539; HCV_env; 1.
 KM Polypeptide. Glycoprotein. Coat protein. Envelope protein;
 KM Transmembrane; Nonstructural protein.
 FT NON_TER 1 1
 FT CHAIN <1 63 MATRIX PROTEIN (POTENTIAL).
 FT CHAIN 64 255 MAJOR ENVELOPE PROTEIN E (POTENTIAL).
 FT CHAIN 256 >309 NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).
 FT CARBOHYD 68 68
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 309 309

SQ SEQUENCE 309 AA; 32922 MW; 6E858E9C3D0B9EA9 CRC64;
 Query Match 55.6%; Score 5; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
 |||||
 DB 113 PVAPT 117

RESULT 35
 ACCO_MALDO STANDARD; PRT; 314 AA.
 ID ACCO_MALDO
 AC 000985; 024063;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (EC 1.-.-.-) (ACC OXIDASE)
 DE (ETHYLENE-FORMING ENZYME) (EFE) (PROTEIN AP4 OR PAE12).
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I;
 OC Rosales; Rosaceae; Malus.
 ON NCBI_Taxid=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GOLDEN DELICIOUS; TISSUE=fruit;
 RX MEDLINE=92322950; PubMed=1377961;
 RA Ross G.S., Knighton M.L., Lay-Yee M.;
 RT "An ethylene-related cDNA from ripening apples.";
 RL Plant Mol. Biol. 19:231-238(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dong J.G., Olsen D.B., Silverstone A., Yang S.F.;
 RT "Sequence of a cDNA coding for a 1-aminocyclopropane-1-carboxylate
 RT oxidase homolog from apple fruit.";
 RL Plant Physiol. 98:1530-1531(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GOLDEN DELICIOUS;
 RA Castiglione S., Malerba M., Pirola B., Bianchetti R., Sala F.,
 RA Ventura M., Pancaldi M., Sansavini S.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CHARACTERIZATION, AND SEQUENCE OF 115-134.
 RX MEDLINE=93028348; PubMed=1409700;
 RA Dong J.G., Fernandez-Maculet J.C., Yang S.F.;
 RT "Purification and characterization of
 RT 1-aminocyclopropane-1-carboxylate oxidase from apple fruit.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9789-9793(1992).
 RN [5]
 RP CHARACTERIZATION, AND PARTIAL SEQUENCE.
 RX MEDLINE=93250487; PubMed=7763615;
 RA Dupille E., Rombaldi C., Lelievre J.M., Cleyet-Marel J.C., Pech J.C.,
 RA Lathe A.;
 RT "Purification, properties and partial amino-acid sequence of 1-
 RT aminocyclopropane-1-carboxylic acid oxidase from apple fruits.";
 RL Planta 190:65-70(1993).
 CC -1- CATALYTIC ACTIVITY: 1-AMINOCYCLOPROPANE-1-CARBOXYLATE + O2 -
 CC ETHYLENE + HCN + CO(2) + 2 H(2)O.
 CC -1- COFACTOR: IRON AND ASCORBATE.
 CC -1- PATHWAY: LAST STEP IN THE BIOSYNTHESIS OF ETHYLENE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING FRUIT RIPENING.
 CC -1- INDUCTION: BY ETHYLENE AND BY WOUNDING.
 CC -1- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
 CC OXIDOREDUCTASES.
 CC -----
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DR EMBL; X61390; CAA43662.1; -
 DR EMBL; M81794; AAA33412.1; -
 DR EMBL; Y14005; CAA74328.1; -
 DR PIR; S22513; S22513.
 DR InterPro: IPR002419; -
 DR Pfam: PF00671; Fe_Asc_oxidored; 1.
 DR Fruit ripening: Ethylene biosynthesis; Oxidoreductase; Iron;
 KM Vitamin C; Multigene family.
 SQ SEQUENCE 314 AA; 35410 MW; BEADA64C7AD10E1E CRC64;

Query Match 55.6%; Score 5; DB 1; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
 |||||
 Db 308 STPVA 312

RESULT 36
 SPLR_NPVOP STANDARD: PRT; 321 AA.
 ID SPLR_NPVOP 065328; 012842; 012553;
 AC 065328; 012842; 012553;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 01-NOV-1997 (Rel. 35; Last annotation update)
 DE SPHEROIDIN-LIKE PROTEIN PRECURSOR (SPINDOLIN-LIKE PROTEIN) (37 KDA
 DE GLYCOPROTEIN).
 GN SLP OR GP37.
 OS Orygia pseudotsugata multicausid polyhedrosis virus (OPMPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_Taxid=10450;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93100831; PubMed=8380088;
 RA Gross C.H., Molgnot G.M., Russell R.L., Pearson M.N., Rohmann G.F.;
 RT "A 37-kilodalton glycoprotein from a baculovirus of Orygia
 RT pseudotsugata is localized to cytoplasmic inclusion bodies.";
 RT J. Virol. 67:469-475(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97271300; PubMed=9126251;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohmann G.F.;
 RT "The sequence of the Orygia pseudotsugata multicausid nuclea
 RT polyhedrosis virus genome.";
 RT Virology 229:381-399(1997).
 CC -1- FUNCTION: COMPONENT OF THE VIRUS OCCUSION BODIES, WHICH ARE LARGE
 CC PROTEINACOUS STRUCTURES (POLYHEDRA). THAT PROTECT THE VIRUS FROM
 CC THE OUTSIDE ENVIRONMENT FOR EXTENDED PERIODS UNTIL THEY ARE
 CC INGESTED BY INSECT LARVAE (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE PERIPHERY OF OCCUSION
 CC BODIES AND WITH THE INTERNAL MEMBRANES OF INFECTED CELLS.
 CC -1- DEVELOPMENTAL STAGE: VERY LATE PHASE OF INFECTION.
 CC -1- SIMILARITY: TO CBEPV AND HAEPV SPINDOLINS.
 CC
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EMBL; D13306; BAA02566.1; -

DR EMBL; U75930; AAC59068.1; -
 KM Viral occlusion body; Signal; Glycoprotein; Late protein.
 FT SIGNAL 1 18
 FT CHAIN 19 321
 FT CAROXYD 192 192
 SQ SEQUENCE 321 AA; 36136 MW; B935809F06B56CA9 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
 |||||
 Db 23 STPVA 27

RESULT 37
 PF27_MOUSE STANDARD: PRT; 323 AA.
 ID PF27_MOUSE P52875;
 AC P52875;
 DT 01-OCT-1996 (Rel. 34; Created)
 DT 01-OCT-1996 (Rel. 34; Last sequence update)
 DT 01-OCT-2000 (Rel. 40; Last annotation update)
 DE TRANSMEMBRANE PROTEIN PFT27 (TPA REGULATED LOCUS PROTEIN).
 GN TPRL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Teratocarcinoma;
 RX MEDLINE=89076283; PubMed=3202867;
 RA Akagi J., Nomiyama H., Setoyama C., Shinada K., Akagi M.;
 RT "Messenger RNA expressed in mouse teratocarcinoma stem cells and
 RT down-regulated by a tumor-promoting phorbol ester codes for a novel
 RT transmembrane protein.";
 RL Biochem. Biophys. Res. Commun. 157:548-557(1988).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN UNDIFFERENTIATED MOUSE F9
 CC TERATOCARCINOMA STEM CELLS BUT DISAPPEARING RAPIDLY AFTER
 CC TREATMENT WITH A TUMOR-PROMOTING PHORBOL ESTER.
 CC -1- SIMILARITY: BELONGS TO THE UPF0016 FAMILY.
 CC
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EMBL; M23568; AAA40456.1; -
 DR MGD; MGI:894407; Tprl.
 DR InterPro: IPR001727; -
 DR Pfam; PF01169; UPF0016; 1.
 DR PROSITE; PS01214; UPF0016; 1.
 KW Transmembrane.
 FT TRANSMEM 16 36
 FT TRANSMEM 90 110
 FT TRANSMEM 127 147
 FT TRANSMEM 152 172
 FT TRANSMEM 228 248
 FT TRANSMEM 267 287
 FT TRANSMEM 299 319
 SQ SEQUENCE 323 AA; 34683 MW; 4C1D1201ADEFI333 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
 |||||
 DB 73 TPVAP 77

RESULT 38
 HMGCL_HUMAN STANDARD; PRT; 325 AA.
 ID HMGCL_HUMAN
 AC P35914;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYDROXYMETHYLGUTARYL-COA LYASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.4)
 DE (HMG-COA LYASE) (HL) (3-HYDROXY-3-METHYLGUTARATE-COA LYASE).
 DE HMGCL.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93179448; PubMed=8440722;
 RA Mitchell G.A., Robert M.-F., Hruz P.W., Wang S., Fontaine G.,
 RA Benhke C.E., Mende-Mueller L.M., Schappert K., Lee C., Gibson K.M.,
 RA Mizioro H.M.;
 RT "3-hydroxy-3-methylglutaryl coenzyme A lyase (HL). Cloning of human
 RT and chicken liver HL cDNAs and characterization of a mutation causing
 RT human HL deficiency.";
 RL J. Biol. Chem. 268:4376-4381(1993).
 RN [2]
 RP SEQUENCE OF 21-325 FROM N.A.
 RX MEDLINE=96207305; PubMed=8617516;
 RA Wang S.P., Robert M.-F., Gibson K.M., Wanders R.J.A., Mitchell G.A.;
 RT "3-Hydroxy-3-methylglutaryl CoA lyase (HL): mouse and human HL gene
 RT (HMGCL) cloning and detection of large gene deletions in two
 RT unrelated HL-deficient patients.";
 RL Genomics 33:99-104(1996).
 RN [3]
 RP VARIANT HMG ARG-233.
 RX MEDLINE=96394619; PubMed=8798725;
 RA Roberts J., Mitchell G.A., Mizioro H.M.;
 RT "Modeling of mutational responsible for human 3-hydroxy-3-
 RT methylglutaryl-CoA lyase deficiency implicates histidine-233 as an
 RT active site residue.";
 RL J. Biol. Chem. 271:24604-24609(1996).
 RN [4]
 RP VARIANTS HMG GLN-41; GLU-42; GLY-42 AND HIS-42.
 RX MEDLINE=98130531; PubMed=9463337;
 RA Mitchell G.A., Ozand P.T., Robert M.-F., Ashmarina L., Roberts J.,
 RA Gibson K.M., Wanders R.J., Wang S., Chevallier I., Ploechl E.,
 RA Mizioro H.;
 RT "HMG CoA lyase deficiency: identification of five causal point
 RT mutations in codons 41 and 42, including a frequent Saudi Arabian
 RT mutation, R14Q.";
 RL Am. J. Hum. Genet. 62:295-300(1998).
 RN [5]
 RP CATALYTIC ACTIVITY: (S)-3-HYDROXY-3-METHYLGUTARYL-COA -
 CC ACETYL-COA + ACETOACETATE.
 CC [6]
 RP PATHWAY: FINAL STEP OF KETOGENESIS AND LEUCINE CATABOLISM.
 CC [7]
 RP SUBUNIT: HOMODIMER.
 CC [8]
 RP SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC [9]
 RP TISSUE SPECIFICITY: FIBROBLASTS, LIVER AND LYMPHOBLASTS.
 CC [10]
 RP DISEASE: DEFECTS IN HMGCL ARE THE CAUSE OF AN AUTOSOMAL RECESSIVE
 CC LEAD TO HYPOGLYCEMIA AND COMA.
 CC [11]
 RP LEAD TO HYPOGLYCEMIA AND COMA.
 CC [12]
 RP SIMILARITY: BELONGS TO THE HMG-COA LYASE FAMILY.
 CC [13]
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 CC -----
 DR EMBL: U49719; AAB19099.1; JOINED.
 DR EMBL: U49712; AAB19099.1; JOINED.
 DR EMBL: U49713; AAB19099.1; JOINED.
 DR EMBL: U49714; AAB19099.1; JOINED.
 DR EMBL: U49715; AAB19099.1; JOINED.
 DR EMBL: U49716; AAB19099.1; JOINED.
 DR EMBL: U49717; AAB19099.1; JOINED.
 DR EMBL: U49718; AAB19099.1; JOINED.
 DR MIR: A45470; A45470.
 DR MIR: A45450; A45450.
 DR InterPro: IPR000138; -.
 DR InterPro: IPR000891; -.
 DR Pfam: PF00682; HMGCL-like; 1.
 DR ProSite: PS01062; HMG-COA LYASE; 1.
 KW Lyase; Mitochondrion; Transit peptide; Disease mutation.
 FT TRANSIT 1 27 MITOCHONDRION (BY SIMILARITY).
 FT CHAIN 28 325 HYDROXYMETHYLGUTARYL-COA LYASE.
 FT ACT_SITE 266 266 BY SIMILARITY.
 FT VARIANT 41 41 R -> Q (IN HMG).
 FT VARIANT 42 42 D -> E (IN HMG).
 FT VARIANT 42 42 /FTID=VAR.003745.
 FT VARIANT 42 42 D -> G (IN HMG).
 FT VARIANT 42 42 /FTID=VAR.003746.
 FT VARIANT 42 42 D -> H (IN HMG).
 FT VARIANT 70 70 /FTID=VAR.003747.
 FT VARIANT 70 70 V -> L (IN HMG).
 FT VARIANT 233 233 /FTID=VAR.003748.
 FT VARIANT 233 233 /FTID=VAR.003749.
 FT CONFLICT 243 243 H -> R (IN HMG).
 FT CONFLICT 243 243 T -> A (IN REF. 2).
 SQ SEQUENCE 325 AA; 34390 MW; 4D2B3F9210A67331 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1; le+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 |||||
 DB 51 VSTPV 55

RESULT 39
 MODD_MYCBO STANDARD; PRT; 325 AA.
 ID MODD_MYCBO
 AC O30620;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MOLYBDATE UPTAKE SECRETED PROTEIN PRECURSOR (ALA-PRO RICH 45/47 KDA
 DE SECRETED PROTEIN) (IMMUNOGENIC PROTEIN MP32) (ANTIGEN MP1-32) (45-KDA
 DE GLYCOPROTEIN) (FIBRONECTIN ATTACHMENT PROTEIN) (FAP-B).
 DE GN MODD OR APA.
 OS Mycobacterium bovis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=BCG;
 RA Zhao W., Schorey J.S., Bong-Wastek M., Brown E.J., Ratliff T.L.;
 RT "Identification, sequence and characterization of the M. bovis BCG
 RT fibronectin attachment protein.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC [2]
 RP MODACD FOR MOLYBDENUM (BY SIMILARITY).
 CC [3]
 RP SUBCELLULAR LOCATION: SECRETED.
 CC [4]
 RP SIMILARITY: BELONGS TO THE MODD FAMILY.
 CC [5]
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CC -----
 CC EMBL: AF013569: AAB71842.1: -
 CC Molybdenum; Transport; Glycoprotein; Antigen; Signal.

DR SIGNAL 1 39 BY SIMILARITY.
 FT CHAIN 40 325 MOLYBDATE UPTAKE SECRETED PROTEIN.
 FT CARBOHYD 49 49 O-LINKED (MAN. . .) (BY SIMILARITY).
 FT CARBOHYD 57 57 O-LINKED (MAN. . .) (BY SIMILARITY).
 FT CARBOHYD 66 66 O-LINKED (MAN. . .) (BY SIMILARITY).
 FT CARBOHYD 316 316 O-LINKED (MAN. . .) (BY SIMILARITY).
 FT SEQUENCE 325 AA: 32686 MW: D3419CA5547D91E9 CRC64:

Query Match 55.6%; Score 5; DB 1; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1,1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
 DB 66 TPVAP 70

RESULT 40

MODD_MYCTU STANDARD: PRT: 325 AA.

AC 050906; 008062;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE MOLYBDATE UPTAKE SECRETED PROTEIN PRECURSOR (ALA-PRO RICH 45/47 KDA
 DE SECRETED PROTEIN) (IMMUNOGENIC PROTEIN MPT32) (ANTIGEN MPT-32) (45-KDA
 DE GLYCOPROTEIN) (FIBRONECTIN ATTACHMENT PROTEIN) (FAP-B).
 GN MODD OR APA OR RV1860 OR MTCY359.13.

OS Mycobacterium tuberculosis

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;
 RA MEDLINE=96009758; PubMed=7558311;
 RA Laqueyrie A., Miltzer P., Romain F., Elgmeler K., Cole S.,
 RA Marchel G.;

RT "Cloning, sequencing, and expression of the apa gene coding for the
 RT Mycobacterium tuberculosis 45/47-kilodalton secreted antigen
 RT complex.";

RL Infect. Immun. 63:4003-4010(1995).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;
 RA Laqueyrie A.;

RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;
 RA MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F.,
 RA Badcock K., Besham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Horsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Ruter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrett B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";

RL Nature 393:537-544(1998).
 RN [4]

RP PARTIAL SEQUENCE, AND CHARACTERIZATION.

RX MEDLINE=9109989; PubMed=1898899;
 RA Nagai S., Wiker H.G., Harboe M., Kinomoto M.;

RT "Isolation and partial characterization of major protein antigens in
 RT the culture fluid of Mycobacterium tuberculosis.";

RL Infect. Immun. 59:372-382(1991).
 RN [5]

RP PARTIAL SEQUENCE, AND GLYCOSYLATION.

RX MEDLINE=95347792; PubMed=7622204;
 RA Dobos K.M., Swiderik K., Khoo K.-H., Brennan P.J., Belisle J.T.;

RT "Evidence for glycosylation sites on the 45-kilodalton glycoprotein of
 RT Mycobacterium tuberculosis.";

RL Infect. Immun. 63:2846-2853(1995).
 RN [6]

RP PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.

RX MEDLINE=96196153; PubMed=8626314;
 RA Dobos K.M., Khoo K.-H., Swiderik K.M., Brennan P.J., Belisle J.T.;

RT "Definition of the full extent of glycosylation of the 45-kilodalton
 RT glycoprotein of Mycobacterium tuberculosis.";

RL J. Bacteriol. 178:2498-2506(1996).
 RN [7]

RP FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

MODABC FOR MOLYBDENUM.

CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE MODD FAMILY.

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CC EMBL: X80268; CAA56555.1; -
 DR EMBL: X99258; CAA67645.1; -
 DR EMBL: Z83859; CAB06127.1; -
 DR Tuberculist; RV1860; -
 KW Molybdenum; Transport; Glycoprotein; Antigen; Signal.

FT SIGNAL 1 39
 FT CHAIN 40 325 MOLYBDATE UPTAKE SECRETED PROTEIN.
 FT CARBOHYD 49 49 O-LINKED (MAN. . .).
 FT CARBOHYD 57 57 O-LINKED (MAN. . .).
 FT CARBOHYD 66 66 O-LINKED (MAN. . .).
 FT CARBOHYD 316 316 O-LINKED (MAN. . .).
 FT SEQUENCE 325 AA: 32720 MW: 595D0455A97BED CRC64:

Query Match 55.6%; Score 5; DB 1; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1,1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
 DB 66 TPVAP 70

RESULT 41

YB56_XENLA STANDARD: PRT: 336 AA.

AC P21574;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE CYTOPLASMIC RNA-BINDING PROTEIN P56 (Y BOX BINDING PROTEIN-2) (Y-BOX
 DE TRANSCRIPTION FACTOR) (MRNP4).
 GN FRG2.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae.

CC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-91062413; PubMed-2247479;
 RA Tafuri S.R., Wolfe A.P.;
 RT "Xenopus Y-box transcription factors: molecular cloning, functional
 RT analysis and developmental regulation";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9028-9032(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-92107999; PubMed-1729676;
 RA Murray M.T., Schiller D.L., Franke W.M.;
 RT "Sequence analysis of cytoplasmic RNA-binding proteins of Xenopus
 RT oocytes identifies a family of RNA-binding proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11-15(1992).
 RN [3]
 RP PARTIAL SEQUENCE.
 RX MEDLINE-9232467; PubMed-1629179;
 RA Deschamps S., Viel A., Garrigos M., Denis H., Le Maire M.;
 RT "MRNP4, a major mRNA-binding protein from Xenopus oocytes, is
 RT identical to transcription factor FPG Y2";
 RL J. Biol. Chem. 267:13799-13802(1992).
 RN [4]
 RP PARTIAL SEQUENCE.
 RX MEDLINE-91224309; PubMed-1902800;
 RA Deschamps S., Viel A., Denis H., Le Maire M.;
 RT "Purification of two thermostable components of messenger
 RT ribonucleoprotein particles (mrnp) from Xenopus laevis oocytes,
 RT belonging to a novel class of RNA-binding proteins";
 RL FEBS Lett. 282:110-114(1991).
 CC -1- FUNCTION: BINDS TO CCAAT-CONTAINING Y BOX OF THE HSP70 GENES.
 CC SEEMS TO BE A NEGATIVE REGULATORY FACTOR. ALSO BINDS TO MRNA.
 CC -1- SUBUNIT: POSSIBLY FORMS A HETERODIMER WITH P54 IN THE 6S AND 15S
 CC MNNA-BINDING PARTICLES.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC, EITHER FREE OR ASSOCIATED WITH
 CC RIBONUCLEOPROTEIN PARTICLES.
 CC -1- TISSUE SPECIFICITY: TESTIS AND IMMATURE OOCYTES.
 CC -1- PTM: PHOSPHORYLATION ACTIVATES IN VITRO RNA-BINDING.
 CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
 CC -----
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 CC -----
 DR EMBL: M59454; AAA49716.1; -;
 DR F1R: B38274; B38274;
 DR HSSP: P32081; INMG;
 DR TRANSFAC: T00294; -;
 DR InterPro: IPR002059; -;
 DR Pfam: PF00313; CSD; 1;
 DR PRINTS: PR00050; COLDSHOCK;
 DR PROSITE: PS00352; COLD_SHOCK; 1;
 KW Transcription regulation; DNA-binding; Nuclear protein;
 KM RNA-binding; Phosphorylation.
 FT DOMAIN 44 108 CSD.
 FT CONFLICT 254 254 A -> T (IN REF. 1).
 SQ SEQUENCE 336 AA; 37202 MW; 4AD5038769C6B84D CRC64;

Query Match 55.6%; Score 5; DB 1; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
 DB 207 PVAPT 211

RESULT 42
 RL3_METHH

ID RL3_METHH STANDARD; PRT; 337 AA.
 AC 026110;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L3P.
 GN RPL3P OR MTH2.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacter.
 OX NCBI_TaxID=145262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE-98037514; PubMed-9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AE000795; AB84521.1; -;
 DR InterPro: IPR000597; -;
 DR Pfam: PF00297; RIBOSOMAL_L3; 1;
 DR PROSITE: PS00474; RIBOSOMAL_L3; 1;
 KM Ribosomal protein.
 SQ SEQUENCE 337 AA; 37252 MW; 9BB3B8E0FD744A0B CRC64;

Query Match 55.6%; Score 5; DB 1; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
 DB 67 VSTPV 71

RESULT 43
 ID YMA3_MYCBO STANDARD; PRT; 354 AA.
 AC 002279;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 38.1 KDA PROTEIN IN MAS 3' REGION.
 OS Mycobacterium bovis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BG;
 RX MEDLINE-92406887; PubMed-1527058;
 RA Mathur M., Kolatukudy P.E.;
 RT "Molecular cloning and sequencing of the gene for mycocerosic acid
 RT synthase, a novel fatty acid elongating multifunctional enzyme, from
 RT Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guerin";
 RL J. Biol. Chem. 267:19388-19395(1992).

CC -1- SIMILARITY: SOME, TO M.TUBERCULOSIS RV2285.
 CC -----
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 CC -----
 DR EMBL; M95808; AAA25370.1; -
 DR Hypothetical protein.
 SQ SEQUENCE 354 AA; 37956 MW; 2C77C1259BD3686A CRC64;
 OY 4 PVAPT 8
 DB 284 PVAPT 288
 Query Match 55.6%; Score 5; DB 1; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 44
 HIS8_ECOLI
 ID HIS8_ECOLI STANDARD: PRT; 356 AA.
 AC P06986; 11111
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-
 DE PHOSPHATE TRANSAMINASE).
 OS HISC.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=89094829; Pubmed=3062174;
 RA Carliomagn M.S., Chiarloti L., Alfano P., Nappo A.G., Bruni C.B.;
 RT "Structure and function of the Salmonella typhimurium and Escherichia
 RT coli K-12 histidine operons".
 RL J. Mol. Biol. 203:565-606(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=86059230; Pubmed=2999081;
 RA Grisolia V., Carliomagn M.S., Nappo A.G., Bruni C.B.;
 RT "Cloning, structure, and expression of the Escherichia coli K-12 hisc
 RT gene".
 RL J. Bacteriol. 164:1317-1323(1985).
 RN [3]
 RP REVISIONS, SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=94260549; Pubmed=8201624;
 RA Jovanovic G., Kostic T., Jankovic M., Savic D.J.;
 RT "Nucleotide sequence of the Escherichia coli K12 histidine operon
 RT revalued".
 RL J. Mol. Biol. 239:433-435(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; Pubmed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12".
 RL Science 277:1453-1474(1997).
 RN [5]

RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97251358; Pubmed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isino K., Kasai H., Kikura S., Kitagawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H.,
 RA Takeda J., Takemoto K., Mada C., Yamamoto Y., Horiuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40,150,0 min region on the linkage map".
 RL DNA Res. 3:379-392(1996).
 CC -1- CATALYTIC ACTIVITY: L-HISTIDINOL-PHOSPHATE + 2-OXOGUTARATE -
 CC 3-(IMIDAZOL-4-YL)-2-OXOPROPYL PHOSPHATE + GLUTAMATE.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: EIGHTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC -----
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 CC -----
 DR EMBL; X03416; CAA27150.1; -
 DR EMBL; X13462; CAA31813.1; -
 DR EMBL; U02071; AAA19743.1; -
 DR EMBL; AE000293; AAC75082.1; -
 DR EMBL; D90840; CAB21779.1; -
 DR PIR; A30270; XNECHC.
 DR Ecogene; EG10446; hisc.
 DR InterPro; IPR001917; -
 DR Pfam; PF00222; aminotran_2; 1.
 DR PROSITE; PS00599; AA.TRANSFER.CLASS_2; 1.
 KW Histidine biosynthesis; Transferase; Aminotransferase;
 KW Pyridoxal phosphate.
 KM BINDING 214 PYRIDOXAL PHOSPHATE (PROBABLE).
 FT FT 130 L -> P (IN REF. 1 AND 2).
 FT CONFLICT 149 V -> A (IN REF. 1 AND 2).
 SQ SEQUENCE 356 AA; 39360 MW; 056CBB3CF894083F CRC64;
 OY 2 STPVA 6
 DB 246 STPVA 250
 Query Match 55.6%; Score 5; DB 1; Length 356;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 45
 HIS8_SALTY
 ID HIS8_SALTY STANDARD: PRT; 359 AA.
 AC P10369;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-
 DE PHOSPHATE TRANSAMINASE).
 OS HISC.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LT2;
 RX MEDLINE=89094829; Pubmed=3062174;

RA Carlomagno M.S., Chiarlotti L., Alfano P., Nappo A.G., Bruni C.B.;
 RT "Structure and function of the Salmonella typhimurium and Escherichia
 coli K-12 histidine operons";
 RL J. Mol. Biol. 203:585-606(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LT2;
 RA Barnes W.M., Hussen R.N., Whittier R.;
 RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-HISTIDINOL-PHOSPHATE + 2-OXOGUTARATE -
 3-(IMIDAZOL-4-YL)-2-OXOPROPYL PHOSPHATE + GLUTAMATE;
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE;
 CC -1- PATHWAY: EIGHTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 AMINOTRANSFERASES.
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 CC -----
 DR EMBL; X13464; CAA31824.1; -;
 DR EMBL; J01804; AAA88616.1; -;
 DR PIR; J50158; XNEBHC.
 DR StyGene; SG10159; h1sc.
 DR InterPro; IPR001917; -;
 DR Pfam; PF00222; aminotran_2; 1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
 KW Histidine biosynthesis; Transferase; Aminotransferase;
 KM Pyridoxal phosphate.
 FT BINDING 217 217 PYRIDOXAL PHOSPHATE (PROBABLE).
 FT CONFLICT 148 164 DGRVVFVCSFNNPTGQ -> TAAKWCSEVAPIILPDN
 FT CONFLICT 226 226 (IN REF. 2).
 FT CONFLICT 260 260 C -> R (IN REF. 1).
 FT CONFLICT 264 265 L -> S (IN REF. 1).
 FT CONFLICT 349 349 GI -> ES (IN REF. 1).
 FT CONFLICT 349 349 R -> P (IN REF. 1).
 SQ SEQUENCE 359 AA; 39715 MW; 6241506A59CBB2A7 CRC64;
 Query Match 55.6%; Score 5; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 STPVA 6
 Db 249 STPVA 253
 RESULT 46
 SRK2_SPOLA STANDARD; PRT; 362 AA.
 AC P42688;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TYROSINE-PROTEIN KINASE SRK2 (EC 2.7.1.112) (FRAGMENT).
 OS Spongilla lacustris (Freshwater sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haplosclerida; Spongillidae; Spongilla.
 OX NCBI_TaxID=6055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92334872; PubMed=1378585;
 RA Ollile S., Raulf F., Barnekow A., Hannig G., Scharf M.;
 RT "Multiple src-related kinase genes, srk1-4, in the fresh water sponge
 Spongilla lacustris";
 RL Oncogene 7:1625-1630(1992).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; X61602; CAA43799.1; -;
 DR HSSP; P00523; 2PTK.
 DR InterPro; IPR000719; -;
 DR InterPro; IPR000980; -;
 DR InterPro; IPR001245; -;
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00069; kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
 KM Phosphorylation.
 FT NON_TER 1 1
 FT DOMAIN 1 70 SH2.
 FT NP_BIND 95 348 PROTEIN KINASE.
 FT NP_BIND 101 109 ATP (BY SIMILARITY).
 FT BINDING 123 123 ATP (BY SIMILARITY).
 FT ACT_SITE 214 214 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40937 MW; D8C549E904EBBD0 CRC64;
 Query Match 55.6%; Score 5; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 STPVA 6
 Db 117 STPVA 121
 RESULT 47
 RPO_RECVD STANDARD; PRT; 366 AA.
 ID RPO_RECVD
 AC P03526;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (SIGMA NS PROTEIN) (CORE
 DE PROTEIN) (RNA-BINDING PROTEIN).
 OS Reovirus (type 3 / strain Deering).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 OX NCBI_TaxID=10886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84015379; PubMed=6312421;
 RA Richardson M.A., Furulich Y.;
 RT "Nucleotide sequence of reovirus genome segment S3, encoding non-
 RT structural protein sigma NS";
 RL Nucleic Acids Res. 11:6399-6408(1983).
 RN [2]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE=83017876; PubMed=6927854;
 RA Antczak J.B., Chmelo R.A., Pickup D.J., Joklik W.K.;
 RT "Sequence at both termini of the 10 genes of reovirus serotype 3
 (strain Deering)";
 RL Virology 121:307-319(1982).

```
CC -1- FUNCTION: THIS PROTEIN HAS A POLY(C)-DEPENDENT POLY(G) POLYMERASE
CC ACTIVITY, AND BINDS SINGLE-STRANDED, BUT NOT DOUBLE-STRANDED, RNA.
CC -1- SIMILARITY: 86.3% SIMILARITY TO REOVIRUS SEROTYPE 2 SIGMA NS
CC PROTEIN.
CC -----
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CC -----
DR EMBL: X01627; CAA25768.1; -
DR EMBL: J02330; AAA47280.1; -
DR PIR: A04126; MNXRSD.
DR InterPro: IPR002507; -
DR Pfam: PF01518; PolyG_pol; 1.
KW Core protein; RNA-binding; Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 366 AA; 41056 MW; 201A6223C4290D7D CRC64;

Query Match 55.6%; Score 5; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PVAPT 8
Db 189 PVAPT 193

RESULT 48
RPO_REOVL STANDARD: PRT: 366 AA.
AC P12002.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (SIGMA NS PROTEIN) (CORE
DE PROTEIN) (RNA-BINDING PROTEIN).
GN S3.
OS Reovirus (type 2 / strain D5/Jones).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID:10885;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-88072071; PubMed-3686825;
RA Wiener J.R., Joklik W.R.;
RT "Comparison of the reovirus serotype 1, 2, and 3 S3 genome segments
RT encoding the nonstructural protein sigma NS.";
RL Virology 161:332-339(1987)
CC -1- FUNCTION: THIS PROTEIN HAS A POLY(C)-DEPENDENT POLY(G) POLYMERASE
CC ACTIVITY, AND BINDS SINGLE-STRANDED, BUT NOT DOUBLE-STRANDED, RNA.
CC -----
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CC -----
DR EMBL: M18390; AAA47282.1; -
DR PIR: B27401; MNXRT2.
DR InterPro: IPR002507; -
DR Pfam: PF01518; PolyG_pol; 1.
KW Core protein; RNA-binding; Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 366 AA; 41334 MW; EF9202C3A6FC5085 CRC64;
```

```
Oy 4 PVAPT 8
Db 189 PVAPT 193

RESULT 49
RPO_REOVL STANDARD: PRT: 366 AA.
AC P07940.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (SIGMA NS PROTEIN) (CORE
DE PROTEIN) (RNA-BINDING PROTEIN).
GN S3.
OS Reovirus (type 1 / strain Lang).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID:10884;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87025802; PubMed-3767989;
RA George C.X., Atwater J.A., Samuel C.E.;
RT "Biosynthesis of reovirus-specified polypeptides. Molecular cDNA
RT cloning and nucleotide sequence of the reovirus serotype 1 Lang
RT strain s3 mRNA which encodes the nonstructural RNA-binding protein
RT sigma NS.";
RL Biochem. Biophys. Res. Commun. 139:845-851(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-88072071; PubMed-3686825;
RA Wiener J.R., Joklik W.R.;
RT "Comparison of the reovirus serotype 1, 2, and 3 S3 genome segments
RT encoding the nonstructural protein sigma NS.";
RL Virology 161:332-339(1987).
CC -1- FUNCTION: THIS PROTEIN HAS A POLY(C)-DEPENDENT POLY(G) POLYMERASE
CC ACTIVITY, AND BINDS SINGLE-STRANDED, BUT NOT DOUBLE-STRANDED, RNA.
CC -----
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CC -----
DR EMBL: M14325; AAA47273.1; -
DR EMBL: M18389; AAA47281.1; -
DR PIR: A25068; MNXRST.
DR InterPro: IPR002507; -
DR Pfam: PF01518; PolyG_pol; 1.
KW Core protein; RNA-binding; Transferase; RNA-directed RNA polymerase.
FT CONFLICT 250 V -> I (IN REF. 2).
SQ SEQUENCE 366 AA; 41188 MW; B9172A6A9251CC9A CRC64;

Query Match 55.6%; Score 5; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PVAPT 8
Db 189 PVAPT 193

RESULT 50
Y85_YEAST STANDARD: PRT: 366 AA.
AC 004806.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 42.4 KDA PROTEIN IN F4A4-HOR7 INTERGENIC REGION.
```

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GN YMR251W OR YM9920.05.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RA Hunt S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO THE YGR154C/YKR076W/YMR251W (YEAST) /
CC YOG (E.COLI) FAMILY.
CC -----
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CC -----
CC EMBL: Z48639; CAA88578.1; -.
DR SGD; S0004863; YMR251W.
KW Hypothetical protein.
SQ SEQUENCE 366 AA; 42403 MW; C0BF9FD3AB5C15B CRC64;

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Query Match          55.6%; Score 5; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 STPYA 6
   |||||
Db 109 STPYA 113

```

Search completed: August 15, 2001, 12:42:54
 Job time: 484 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:33:55 ; Search time 58.01 Seconds
(without alignments)
20.527 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 9

Sequence: 1 VSTRPVAPQTQ 9

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_16:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mmc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-unclassified:*
- 13: sp-vertebrate:*
- 14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	478	2	Q9RNU3 listeria mo
2	9	100.0	478	2	Q03493 listeria mo
3	7	77.8	530	13	Q9DEY2 Q9DEY2 coluturix co
4	6	66.7	102	2	Q9H1T7 Q9H1T7 pseudomonas
5	6	66.7	209	5	Q9YX73 Q9YX73 oryza sativ
6	6	66.7	237	10	Q9FU39 Q9FU39 chlamydia t
7	6	66.7	288	2	Q84512 Q84512 chlamydia t
8	6	66.7	289	2	Q9KYN4 Q9KYN4 streptomyc
9	6	66.7	293	2	Q9RW05 Q9RW05 delinococcus
10	6	66.7	447	2	Q86673 Q86673 streptomyc
11	6	66.7	460	3	Q9XTQ9 Q9XTQ9 caenorhabd
12	6	66.7	637	3	Q08484 Q08484 saccharomyc
13	6	66.7	652	5	Q9VW35 Q9VW35 dirosophila
14	6	66.7	748	3	Q9P5T7 Q9P5T7 neurospora
15	6	66.7	748	10	Q22907 Q22907 arabidopsis
16	6	66.7	750	3	Q9HFZ4 Q9HFZ4 candida alb
17	6	66.7	775	3	Q9VB49 Q9VB49 dirosophila
18	6	66.7	792	5	Q9VAG1 Q9VAG1 ephydattia f
19	6	66.7	819	5	Q9V48 dirosophila

20	6	66.7	904	5	Q9VEX7 Q9VEX7 dirosophila
21	6	66.7	912	5	Q9NHCI Q9NHCI dirosophila
22	6	66.7	912	5	Q9NHBP Q9NHBP dirosophila
23	6	66.7	916	5	Q9NHCC Q9NHCC dirosophila
24	6	66.7	916	5	Q9NHCO Q9NHCO dirosophila
25	6	66.7	1052	5	Q9VSS0 Q9VSS0 dirosophila
26	6	66.7	1094	4	Q00203 Q00203 homo sapien
27	6	66.7	1105	11	Q9Z1T1 Q9Z1T1 mus musculu
28	6	66.7	1653	2	Q9LPG3 Q9LPG3 streptococc
29	6	66.7	2037	13	Q9PVZ2 Q9PVZ2 xenopus lae
30	6	66.7	49	5	Q9Y1V2 Q9Y1V2 hydra magni
31	5	55.6	62	2	Q47006 Q47006 escherichia
32	5	55.6	75	2	Q9RRH1 Q9RRH1 delinococcus
33	5	55.6	82	5	Q17728 Q17728 caenorhabd
34	5	55.6	88	5	P91335 P91335 caenorhabd
35	5	55.6	94	14	Q67673 Q67673 porcine ade
36	5	55.6	95	11	Q9QYD6 Q9QYD6 mus musculu
37	5	55.6	95	14	Q68302 Q68302 hepatitis c
38	5	55.6	102	14	Q68301 Q68301 hepatitis c
39	5	55.6	108	13	Q93516 Q93516 glycydus ha
40	5	55.6	114	6	Q97949 Q97949 saginus oe
41	5	55.6	114	6	Q97935 Q97935 saginus oe
42	5	55.6	115	2	Q56724 Q56724 veillonella
43	5	55.6	115	5	Q9W2V1 Q9W2V1 dirosophila
44	5	55.6	115	13	Q90222 Q90222 agkistrodon
45	5	55.6	117	2	Q9X0K8 Q9X0K8 thermotoga
46	5	55.6	117	4	Q9NZE0 Q9NZE0 homo sapien
47	5	55.6	117	5	Q9VWMO Q9VWMO dirosophila
48	5	55.6	117	13	Q90221 Q90221 agkistrodon
49	5	55.6	121	5	Q9N3V1 Q9N3V1 caenorhabd
50	5	55.6	121	10	Q23980 Q23980 hordem vul
51	5	55.6	122	5	Q9YXZ8 Q9YXZ8 dirosophila
52	5	55.6	123	1	Q59455 Q59455 pyrococcus
53	5	55.6	126	7	Q29965 Q29965 homo sapien
54	5	55.6	126	7	Q78219 Q78219 homo sapien
55	5	55.6	132	10	Q04169 Q04169 zea mays. (m
56	5	55.6	133	2	Q87645 Q87645 methylococc
57	5	55.6	137	5	Q9N3U4 Q9N3U4 caenorhabd
58	5	55.6	138	14	Q9EBV4 Q9EBV4 foot-and-mo
59	5	55.6	138	14	Q9EBV2 Q9EBV2 foot-and-mo
60	5	55.6	138	14	Q9E8T3 Q9E8T3 foot-and-mo
61	5	55.6	141	1	Q9YAL8 Q9YAL8 aeropyrum p
62	5	55.6	141	3	Q05690 Q05690 saccharomyc
63	5	55.6	143	2	Q007266 Q007266 mycobacteri
64	5	55.6	148	6	Q9GK99 Q9GK99 bos taurus
65	5	55.6	149	14	Q68732 Q68732 hepatitis c
66	5	55.6	156	5	Q9N8J8 Q9N8J8 trypanosoma
67	5	55.6	156	14	Q69124 Q69124 human herpe
68	5	55.6	157	2	Q49991 Q49991 mycobacteri
69	5	55.6	158	14	Q69129 Q69129 human herpe
70	5	55.6	161	2	Q9FBC1 Q9FBC1 streptococc
71	5	55.6	161	10	Q9SSS3 Q9SSS3 arabidopsis
72	5	55.6	162	2	Q9K8Q7 Q9K8Q7 bacillus ha
73	5	55.6	163	5	Q9N3V0 Q9N3V0 caenorhabd
74	5	55.6	165	2	Q52819 Q52819 rhizobium l
75	5	55.6	166	4	Q9WRT0 Q9WRT0 homo sapien
76	5	55.6	166	10	Q9M4T9 Q9M4T9 triticum ae
77	5	55.6	170	2	Q9KCO1 Q9KCO1 bacillus ha
78	5	55.6	170	2	Q05551 Q05551 listeria mo
79	5	55.6	175	5	Q9VR96 Q9VR96 dirosophila
80	5	55.6	175	10	Q9XHF4 Q9XHF4 sorghum bic
81	5	55.6	177	10	Q43478 Q43478 hordem vul
82	5	55.6	179	10	Q9Z0M4 Q9Z0M4 arabidopsis
83	5	55.6	180	10	Q9W9M0 Q9W9M0 arabidopsis
84	5	55.6	185	5	Q9V916 Q9V916 dirosophila
85	5	55.6	185	10	Q9MA15 Q9MA15 arabidopsis
86	5	55.6	187	5	Q9N344 Q9N344 caenorhabd
87	5	55.6	191	2	Q9XCK6 Q9XCK6 streptococc
88	5	55.6	192	14	Q81390 Q81390 hepatitis c
89	5	55.6	193	10	Q9LKP5 Q9LKP5 zea mays (m
90	5	55.6	195	2	Q9L5W8 Q9L5W8 streptococc
91	5	55.6	197	2	Q9RKH2 Q9RKH2 streptomyc
92	5	55.6	199	2	Q9K531 Q9K531 pseudomonas

93	55.6	200	14	056247	056247 tobacco rat	166	5	55.6	315	5	018121	018121 caenorhabdi
94	55.6	201	3	P87261	P87261 saccharomyc	167	5	55.6	315	5	09XMA9	09XMA9 caenorhabdi
95	55.6	206	2	Q91651	Q91651 pseudomonas	168	5	55.6	318	2	066259	066259 actinobacil
96	55.6	206	2	Q9EX31	Q9EX31 streptomyc	169	5	55.6	318	2	005380	005380 actinobacil
97	55.6	209	5	Q9V794	Q9V794 drosophila	170	5	55.6	319	10	09SC08	09SC08 arabadopsi
98	55.6	210	2	Q9XCJ9	Q9XCJ9 streptococc	171	5	55.6	323	11	09R292	09R292 mus musculu
99	55.6	210	2	Q9RNU2	Q9RNU2 streptococc	172	5	55.6	324	5	09FEV8	09FEV8 caenorhabdi
100	55.6	211	2	Q9XU58	Q9XU58 caenorhabdi	173	5	55.6	324	5	022161	022161 caenorhabdi
101	55.6	212	2	Q9S4U5	Q9S4U5 streptococc	174	5	55.6	327	10	09LD07	09LD07 oryza sativ
102	55.6	212	11	Q9ERR0	Q9ERR0 mus musculu	175	5	55.6	327	14	069145	069145 human herpe
103	55.6	215	5	051491	051491 pseudomonas	176	5	55.6	329	5	09VY11	09VY11 drosophila
104	55.6	218	5	Q9V6P3	Q9V6P3 drosophila	177	5	55.6	331	2	069818	069818 streptomyc
105	55.6	220	11	Q9Z1E5	Q9Z1E5 rattus norv	178	5	55.6	332	5	023156	023156 caenorhabdi
106	55.6	223	2	Q9XCL1	Q9XCL1 streptococc	179	5	55.6	334	4	015008	015008 homo sapien
107	55.6	223	2	Q9KMN9	Q9KMN9 vibrio chol	180	5	55.6	334	4	09H7H8	09H7H8 homo sapien
108	55.6	224	5	Q9GPI4	Q9GPI4 drosophila	181	5	55.6	335	2	09RX81	09RX81 delnoccoc
109	55.6	224	2	Q9REJ3	Q9REJ3 streptococc	182	5	55.6	335	5	09NF70	09NF70 caenorhabdi
110	55.6	224	7	Q29967	Q29967 homo sapien	183	5	55.6	335	5	09NF69	09NF69 caenorhabdi
111	55.6	228	2	Q9RUB6	Q9RUB6 delnoccoc	184	5	55.6	335	5	09N6L3	09N6L3 caenorhabdi
112	55.6	228	2	Q9S456	Q9S456 shigella fl	185	5	55.6	339	2	09RXE8	09RXE8 delnoccoc
113	55.6	236	10	Q9LM00	Q9LM00 pinus taeda	186	5	55.6	342	2	09Z5F8	09Z5F8 mycobacteri
114	55.6	239	14	Q9IRJ1	Q9IRJ1 turkey herp	187	5	55.6	343	8	09Z238	09Z238 trichophyto
115	55.6	241	2	Q9X6G8	Q9X6G8 streptococc	188	5	55.6	347	5	09VRJ9	09VRJ9 drosophila
116	55.6	241	5	Q9GP13	Q9GP13 drosophila	189	5	55.6	351	5	09VST8	09VST8 drosophila
117	55.6	241	11	Q9Z135	Q9Z135 rattus norv	190	5	55.6	351	10	023142	023142 arabadopsi
118	55.6	241	14	Q84617	Q84617 paramedum	191	5	55.6	353	5	09W4Y8	09W4Y8 drosophila
119	55.6	244	5	Q9XZX6	Q9XZX6 leishmania	192	5	55.6	354	5	09NHR6	09NHR6 dictyostell
120	55.6	245	2	Q84764	Q84764 chlamydia t	193	5	55.6	355	4	006265	006265 homo sapien
121	55.6	250	7	019711	019711 homo sapien	194	5	55.6	356	2	09S5C6	09S5C6 escherichia
122	55.6	250	7	019714	019714 homo sapien	195	5	55.6	358	2	069960	069960 streptomyc
123	55.6	251	2	Q9K8B5	Q9K8B5 bacillus ha	196	5	55.6	359	2	09WMN3	09WMN3 synechococ
124	55.6	252	10	Q9LQL8	Q9LQL8 arabadopsi	197	5	55.6	359	8	037749	037749 cephalospor
125	55.6	255	7	019506	019506 homo sapien	198	5	55.6	362	4	09UR55	09UR55 homo sapien
126	55.6	256	2	Q9XG11	Q9XG11 streptococc	199	5	55.6	362	10	082054	082054 saccharum o
127	55.6	256	4	Q9NUR3	Q9NUR3 homo sapien	200	5	55.6	366	14	086313	086313 reovirus sp
128	55.6	258	2	Q9K410	Q9K410 streptomyc	201	5	55.6	366	14	086314	086314 reovirus sp
129	55.6	260	5	017625	017625 caenorhabdi	202	5	55.6	366	14	086315	086315 reovirus sp
130	55.6	260	7	P79531	P79531 homo sapien	203	5	55.6	366	14	086316	086316 reovirus sp
131	55.6	261	3	Q9P390	Q9P390 neurospora	204	5	55.6	366	14	086317	086317 reovirus sp
132	55.6	261	7	Q30096	Q30096 homo sapien	205	5	55.6	366	14	086318	086318 reovirus sp
133	55.6	261	7	Q30099	Q30099 homo sapien	206	5	55.6	366	14	086319	086319 reovirus sp
134	55.6	261	7	Q30061	Q30061 homo sapien	207	5	55.6	366	14	086320	086320 reovirus sp
135	55.6	261	7	Q31633	Q31633 homo sapien	208	5	55.6	366	14	086323	086323 reovirus sp
136	55.6	264	7	Q29826	Q29826 homo sapien	209	5	55.6	366	14	086307	086307 reovirus sp
137	55.6	264	7	Q29970	Q29970 homo sapien	210	5	55.6	366	14	086308	086308 reovirus sp
138	55.6	267	5	016704	016704 caenorhabdi	211	5	55.6	366	14	086309	086309 reovirus sp
139	55.6	267	14	087048	087048 semliki for	212	5	55.6	366	14	086310	086310 reovirus sp
140	55.6	269	7	Q30155	Q30155 homo sapien	213	5	55.6	366	14	086311	086311 reovirus sp
141	55.6	273	1	Q9HR52	Q9HR52 halobacteri	214	5	55.6	366	14	086312	086312 reovirus sp
142	55.6	273	2	005936	005936 pseudomonas	215	5	55.6	366	14	Q9ENM1	Q9ENM1 reovirus (t
143	55.6	276	2	P73137	P73137 synechocyst	216	5	55.6	367	14	041165	041165 paramedum
144	55.6	276	5	Q94215	Q94215 caenorhabdi	217	5	55.6	368	2	09LAV4	09LAV4 actinobact
145	55.6	282	2	Q9ZCX6	Q9ZCX6 rickettsia	218	5	55.6	368	2	Q9F0T0	Q9F0T0 pseudomonas
146	55.6	286	2	Q9R640	Q9R640 mycobacteri	219	5	55.6	368	10	082288	082288 arabadopsi
147	55.6	288	2	Q9UXE2	Q9UXE2 neisseria m	220	5	55.6	372	4	012863	012863 homo sapien
148	55.6	293	2	Q9ZU08	Q9ZU08 rhodococcus	221	5	55.6	372	14	Q9PYV0	Q9PYV0 xestia c-n1
149	55.6	293	2	Q9XAF7	Q9XAF7 streptomyc	222	5	55.6	375	10	Q39235	Q39235 arabadopsi
150	55.6	296	10	Q22812	Q22812 arabadopsi	223	5	55.6	375	10	049349	049349 arabadopsi
151	55.6	297	5	Q9VD14	Q9VD14 drosophila	224	5	55.6	376	5	Q9VR07	Q9VR07 drosophila
152	55.6	298	2	Q9XY66	Q9XY66 streptomyc	225	5	55.6	377	11	Q9Z2Z3	Q9Z2Z3 cricetus
153	55.6	298	5	Q9V090	Q9V090 drosophila	226	5	55.6	377	11	Q9QXJ0	Q9QXJ0 rattus norv
154	55.6	299	2	Q9KPI8	Q9KPI8 vibrio chol	227	5	55.6	380	1	Q9HRS8	Q9HRS8 halobacteri
155	55.6	302	10	Q9SAH7	Q9SAH7 arabadopsi	228	5	55.6	382	2	09HRS8	09HRS8 halobacteri
156	55.6	303	4	Q9UIC9	Q9UIC9 homo sapien	229	5	55.6	382	2	P77144	P77144 escherichia
157	55.6	304	14	Q9J4M8	Q9J4M8 human immun	230	5	55.6	382	5	09U3P1	09U3P1 caenorhabdi
158	55.6	306	10	Q9SDN3	Q9SDN3 prunus dulc	231	5	55.6	383	14	004397	004397 epstein-bar
159	55.6	307	2	Q9M5Q3	Q9M5Q3 petunia hyb	232	5	55.6	384	4	09S977	09S977 homo sapien
160	55.6	307	2	Q55410	Q55410 synechocyst	233	5	55.6	385	5	Q9GY42	Q9GY42 leishmania
161	55.6	307	5	Q22135	Q22135 caenorhabdi	234	5	55.6	387	2	Q9GL14	Q9GL14 microptamo
162	55.6	309	5	Q9VUY0	Q9VUY0 drosophila	235	5	55.6	387	2	Q9LAT2	Q9LAT2 rtemerella
163	55.6	310	11	Q9EQ47	Q9EQ47 mus musculu	236	5	55.6	387	2	Q9LANT	Q9LANT rtemerella
164	55.6	311	10	Q22805	Q22805 arabadopsi	237	5	55.6	387	4	Q9H8F7	Q9H8F7 homo sapien
165	55.6	314	10	Q9XKZ2	Q9XKZ2 pyrus pyrill	238	5	55.6	388	5	Q9VUD1	Q9VUD1 drosophila

239	5	55.6	392	4	Q9NPL5	Q9npl5 homo sapien	312	5	55.6	475	2	Q9EU22	Q9eu22 escherichia
240	5	55.6	392	5	Q9WM77	Q9wm77 drosophila	313	5	55.6	475	10	Q9LNM7	Q9lnm7 arabidopsis
241	5	55.6	393	4	Q9UPH5	Q9uph5 homo sapien	314	5	55.6	476	5	P91292	P91292 caenorhabdi
242	5	55.6	393	14	O41549	O41549 human immun	315	5	55.6	476	5	Q03996	Q03996 plasmodium
243	5	55.6	394	5	Q9XU00	Q9xu00 caenorhabdi	316	5	55.6	476	13	Q9Y119	Q9y119 agkistrodon
244	5	55.6	395	6	O77673	O77673 chaetophrac	317	5	55.6	477	2	O83494	O83494 treponema p
245	5	55.6	397	4	Q9UPH4	Q9uph4 homo sapien	318	5	55.6	478	5	O25684	O25684 plasmodium
246	5	55.6	398	4	Q9UGL3	Q9ugl3 homo sapien	319	5	55.6	478	13	Q98995	Q98995 vipera lebe
247	5	55.6	400	13	Q9IAY3	Q9iay3 agkistrodon	320	5	55.6	479	13	Q9PM70	Q9pm70 agkistrodon
248	5	55.6	400	13	Q9IAY1	Q9iay1 agkistrodon	321	5	55.6	479	13	Q9PW78	Q9pw78 agkistrodon
249	5	55.6	400	13	Q9IAY0	Q9iay0 agkistrodon	322	5	55.6	480	13	Q90220	Q90220 agkistrodon
250	5	55.6	402	2	P76102	P76102 escherichia	323	5	55.6	481	2	Q91408	Q91408 clostridium
251	5	55.6	404	2	O86687	O86687 streptomyce	324	5	55.6	481	3	Q91505	Q91505 trimeresuru
252	5	55.6	406	3	Q9UVD9	Q9uvd9 altermaria	325	5	55.6	481	13	O57413	O57413 trimeresuru
253	5	55.6	407	13	Q92032	Q92032 agkistrodon	326	5	55.6	482	5	O44196	O44196 caenorhabdi
254	5	55.6	408	4	Q9UGL4	Q9ugl4 homo sapien	327	5	55.6	482	5	Q9XV38	Q9xv38 acanthamoeb
255	5	55.6	410	2	O05446	O05446 mycobacteri	328	5	55.6	482	13	Q03998	Q03998 plasmodium
256	5	55.6	410	2	Q9F4K8	Q9f4k8 rhizobium l	329	5	55.6	482	13	Q9PVK9	Q9pvk9 agkistrodon
257	5	55.6	411	2	Q9MA98	Q9ma98 arabidopsis	330	5	55.6	483	13	Q9IAB0	Q9iab0 agkistrodon
258	5	55.6	411	2	Q9F4K7	Q9f4k7 rhizobium l	331	5	55.6	485	5	Q9N4N9	Q9n4n9 caenorhabdi
259	5	55.6	411	5	Q9Y943	Q9y943 drosophila	332	5	55.6	486	4	Q9UCX4	Q9ucx4 homo sapien
260	5	55.6	411	14	O81814	O81814 hepatitis c	333	5	55.6	487	13	Q92119	Q92119 trimeresuru
261	5	55.6	413	13	Q9PW35	Q9pw35 agkistrodon	334	5	55.6	488	10	Q9LNX1	Q9lnx1 arabidopsis
262	5	55.6	414	13	Q90391	Q90391 crocalus at	335	5	55.6	488	14	Q9WT03	Q9wt03 human herpe
263	5	55.6	414	13	Q90392	Q90392 crocalus at	336	5	55.6	491	2	Q9PF18	Q9pf18 altermonas
264	5	55.6	414	14	O81329	O81329 hepatitis c	337	5	55.6	496	5	O17537	O17537 caenorhabdi
265	5	55.6	414	14	P89958	P89958 hepatitis c	338	5	55.6	498	4	Q9H7A2	Q9h7a2 homo sapien
266	5	55.6	414	14	P89959	P89959 hepatitis c	339	5	55.6	499	11	O88714	O88714 mus musculu
267	5	55.6	415	14	O81554	O81554 hepatitis c	340	5	55.6	499	14	Q72860	Q72860 human immun
268	5	55.6	416	2	O31444	O31444 bacillus su	341	5	55.6	500	2	P73537	P73537 synechocyst
269	5	55.6	418	2	Q9K9F3	Q9k9f3 bacillus ha	342	5	55.6	503	11	Q9ROM4	Q9rom4 mus musculu
270	5	55.6	418	4	O75066	O75066 homo sapien	343	5	55.6	503	11	Q9ESZ1	Q9esz1 mus musculu
271	5	55.6	418	4	Q9WU48	Q9wu48 homo sapien	344	5	55.6	504	2	Q9ZBN5	Q9zbn5 streptomyce
272	5	55.6	420	10	Q9ZOC4	Q9zoc4 arabidopsis	345	5	55.6	505	4	O14395	O14395 homo sapien
273	5	55.6	421	2	Q90240	Q9j240 neisseria m	346	5	55.6	505	4	Q9UNR8	Q9unr8 homo sapien
274	5	55.6	421	2	Q9J0J3	Q9j0j3 neisseria m	347	5	55.6	505	13	O73795	O73795 glyoxydi ha
275	5	55.6	422	2	P96208	P96208 mycobacteri	348	5	55.6	508	5	O93227	O93227 caenorhabdi
276	5	55.6	423	1	O93642	O93642 halobacteri	349	5	55.6	508	6	O9CMC8	O9cmc8 fells silve
277	5	55.6	423	1	Q9HQT5	Q9hqt5 halobacteri	350	5	55.6	509	6	Q9GMC7	Q9gmc7 bison bison
278	5	55.6	423	2	Q49339	Q49339 mycobacteri	351	5	55.6	509	14	O56939	O56939 human papil
279	5	55.6	423	2	Q9U1M3	Q9u1m3 drosophila	352	5	55.6	509	14	O56945	O56945 human papil
280	5	55.6	428	2	O911M0	O911m0 pseudomonas	353	5	55.6	511	2	O52569	O52569 amycolatops
281	5	55.6	428	4	O9P245	O9p245 homo sapien	354	5	55.6	511	2	O76725	O76725 caenorhabdi
282	5	55.6	428	10	Q9FM92	Q9fm92 arabidopsis	355	5	55.6	512	5	O51313	O51313 aeropyrum p
283	5	55.6	429	2	O9K4B1	O9k4b1 escherichia	356	5	55.6	513	10	Q9YGB4	Q9ygb4 colobus mon
284	5	55.6	429	2	O9K2H0	O9k2h0 salmonella	357	5	55.6	514	10	Q9LLB6	Q9llb6 colobus mon
285	5	55.6	434	2	O9X6H2	O9x6h2 streptococc	358	5	55.6	516	14	O12670	O12670 colobus mon
286	5	55.6	435	5	O9VG46	O9vg46 drosophila	359	5	55.6	521	14	P88804	P88804 human papil
287	5	55.6	437	14	O69146	O69146 human herpe	360	5	55.6	530	2	O9KJPD	O9kjd0 arthropacte
288	5	55.6	444	1	O9H015	O9h015 halobacteri	361	5	55.6	530	2	O9I008	O9i008 pseudomonas
289	5	55.6	444	5	O9YV63	O9yv63 drosophila	362	5	55.6	534	1	O26459	O26459 methanobact
290	5	55.6	445	2	O45794	O45794 bacteroides	363	5	55.6	534	2	O9KJ53	O9kjs3 streptomyce
291	5	55.6	445	2	O9K199	O9k199 bacteroides	364	5	55.6	535	14	Q9OMK6	Q9omk6 chilla viru
292	5	55.6	446	5	O9N3V2	O9n3v2 caenorhabdi	365	5	55.6	540	4	O60230	O60230 human calic
293	5	55.6	448	5	O9GNF9	O9gnf9 drosophila	366	5	55.6	542	5	O23446	O23446 caenorhabdi
294	5	55.6	448	13	Q92019	Q92019 xenopus lae	367	5	55.6	543	10	Q92188	Q92188 arabidopsis
295	5	55.6	451	2	O9K801	O9k801 bacillus ha	368	5	55.6	543	10	Q43302	Q43302 arabidopsis
296	5	55.6	452	5	O27696	O27696 musca domes	369	5	55.6	543	10	Q9LY09	Q9ly09 arabidopsis
297	5	55.6	455	2	O914C1	O914c1 pseudomonas	370	5	55.6	544	13	O91349	O91349 xenopus lae
298	5	55.6	459	14	O9ZHC0	O9zhc0 streptococc	371	5	55.6	547	13	O91349	O91349 xenopus lae
299	5	55.6	460	5	O9IR53	O9ir53 human papil	372	5	55.6	548	2	O9ZEV1	O9zev1 listeria mo
300	5	55.6	462	10	O76464	O76464 drosophila	373	5	55.6	548	2	O9EXF6	O9exf6 listeria mo
301	5	55.6	462	10	O9LPW4	O9lpw4 arabidopsis	374	5	55.6	548	2	O9EXF6	O9exf6 listeria mo
302	5	55.6	464	2	P74828	P74828 splungomona	375	5	55.6	548	2	O9EXF6	O9exf6 listeria mo
303	5	55.6	465	14	Q90729	Q90729 human papil	376	5	55.6	550	2	Q9S4M6	Q9s4m6 escherichia
304	5	55.6	466	13	Q9IAX7	Q9iax7 agkistrodon	377	5	55.6	551	2	Q9KFS2	Q9kfs2 streptomyce
305	5	55.6	466	13	Q9IAX6	Q9iax6 agkistrodon	378	5	55.6	551	2	Q9KFS2	Q9kfs2 streptomyce
306	5	55.6	467	5	O9NXL1	O9nxl1 homo sapien	379	5	55.6	552	2	Q9RSN4	Q9rsn4 deinococcus
307	5	55.6	471	5	O9Y8B0	O9y8b0 drosophila	380	5	55.6	555	2	O9S612	O9s612 escherichia
308	5	55.6	473	2	O50210	O50210 synechococc	381	5	55.6	555	2	O9R3X4	O9r3x4 escherichia
309	5	55.6	475	2	O9X727	O9x727 escherichia	382	5	55.6	555	4	O9H4Z6	O9h4z6 homo sapien
310	5	55.6	475	2	O9F8R9	O9f8r9 escherichia	383	5	55.6	556	2	O9S4M3	O9s4m3 escherichia
311	5	55.6	475	2	O9F8R3	O9f8r3 escherichia	384	5	55.6	556	10	Q9M172	Q9m172 arabidopsis

385	5	55.6	556	10	09LFW2	Q9Lpw2 arabidopsis	458	5	55.6	739	5	Q9NB06	Q9NB06 trypanosoma
386	5	55.6	557	2	067869	067869 aquilex aeo	459	5	55.6	739	5	Q18221	Q18221 caenorhabdl
387	5	55.6	559	2	Q9RRY4	Q9RRY4 delinococcus	460	5	55.6	748	3	Q12311	Q12311 saccharomyc
388	5	55.6	560	2	Q9S4M5	Q9S4M5 escherichia	461	5	55.6	748	3	Q9P3D8	Q9P3D8 neurospora
389	5	55.6	561	4	Q92952	Q92952 homo sapien	462	5	55.6	750	2	P96256	P96256 mycobacteri
390	5	55.6	567	2	Q33932	Q33932 listeria mo	463	5	55.6	752	2	Q9K333	Q9K333 streptococc
391	5	55.6	570	2	Q66690	Q66690 aquilex aeo	464	5	55.6	753	5	Q22436	Q22436 caenorhabdl
392	5	55.6	572	3	Q26042	Q26042 penaeus jap	465	5	55.6	753	11	Q9JHW8	Q9JHW8 rattus norv
393	5	55.6	573	3	Q08179	Q08179 saccharomyc	466	5	55.6	757	10	Q9SR14	Q9SR14 arabidopsis
394	5	55.6	579	2	Q51504	Q51504 pseudomonas	467	5	55.6	760	4	Q00199	Q00199 homo sapien
395	5	55.6	581	2	Q9RU45	Q9RU45 delinococcus	468	5	55.6	763	2	Q9ZBR8	Q9ZBR8 mycobacteri
396	5	55.6	582	2	Q9ZNR9	Q9ZNR9 pseudomonas	469	5	55.6	781	10	Q9LKG6	Q9LKG6 arabidopsis
397	5	55.6	584	4	Q9UNR7	Q9UNR7 homo sapien	470	5	55.6	782	4	Q9UI94	Q9UI94 homo sapien
398	5	55.6	585	2	P71246	P71246 escherichia	471	5	55.6	784	5	Q9VIS7	Q9VIS7 drosophila
399	5	55.6	587	2	Q9L736	Q9L736 escherichia	472	5	55.6	796	5	Q16145	Q16145 caenorhabdl
400	5	55.6	588	2	Q9K2Y6	Q9K2Y6 escherichia	473	5	55.6	797	4	Q9S267	Q9S267 homo sapien
401	5	55.6	587	10	Q9MOT2	Q9MOT2 arabidopsis	474	5	55.6	797	4	Q9UNN9	Q9UNN9 homo sapien
402	5	55.6	596	10	Q9LSW2	Q9LSW2 arabidopsis	475	5	55.6	803	2	Q9RBR9	Q9RBR9 pseudomonas
403	5	55.6	599	2	Q9PEU0	Q9PEU0 campylobact	476	5	55.6	816	5	Q9VKJ9	Q9VKJ9 drosophila
404	5	55.6	604	2	Q00509	Q00509 streptomyce	477	5	55.6	817	3	Q07229	Q07229 saccharomyc
405	5	55.6	605	1	Q26511	Q26511 methanobact	478	5	55.6	822	5	Q9GUK3	Q9GUK3 leishmania
406	5	55.6	606	2	Q53561	Q53561 streptococc	479	5	55.6	823	5	Q25343	Q25343 leishmania
407	5	55.6	609	13	Q13027	Q13027 xenopus lae	480	5	55.6	829	5	Q61957	Q61957 caenorhabdl
408	5	55.6	612	4	Q93052	Q93052 homo sapien	481	5	55.6	831	4	Q9NKS6	Q9NKS6 homo sapien
409	5	55.6	613	2	Q9PE86	Q9PE86 xylella fas	482	5	55.6	831	11	Q9EP22	Q9EP22 mus musculu
410	5	55.6	614	3	Q12662	Q12662 panacochae	483	5	55.6	833	1	Q9S594	Q9S594 mycoplasma
411	5	55.6	620	5	Q9YOD4	Q9YOD4 penaeus mon	484	5	55.6	834	1	Q29217	Q29217 archaeoglob
412	5	55.6	620	5	Q9NEG8	Q9NEG8 leishmania	485	5	55.6	835	5	Q9V744	Q9V744 drosophila
413	5	55.6	624	4	Q9P2U4	Q9P2U4 homo sapien	486	5	55.6	835	4	Q9P230	Q9P230 homo sapien
414	5	55.6	626	4	Q9P2U3	Q9P2U3 homo sapien	487	5	55.6	842	2	Q52590	Q52590 pseudomonas
415	5	55.6	637	2	P72813	P72813 synechocyst	488	5	55.6	842	5	Q9VGC9	Q9VGC9 drosophila
416	5	55.6	637	5	Q9WDB6	Q9WDB6 drosophila	489	5	55.6	843	2	Q07289	Q07289 streptococc
417	5	55.6	642	2	Q9FC03	Q9FC03 streptomyce	490	5	55.6	846	5	Q9VZ10	Q9VZ10 drosophila
418	5	55.6	648	2	Q9EYC8	Q9EYC8 escherichia	491	5	55.6	847	14	Q41537	Q41537 human immun
419	5	55.6	648	4	Q14760	Q14760 homo sapien	492	5	55.6	849	4	Q9NVE4	Q9NVE4 homo sapien
420	5	55.6	651	4	Q9UW25	Q9UW25 homo sapien	493	5	55.6	859	14	Q9YVZ4	Q9YVZ4 human immun
421	5	55.6	651	5	Q18181	Q18181 caenorhabdl	494	5	55.6	864	4	Q9VGC8	Q9VGC8 drosophila
422	5	55.6	653	4	Q9NQ79	Q9NQ79 homo sapien	495	5	55.6	866	4	Q9H466	Q9H466 homo sapien
423	5	55.6	659	5	Q76517	Q76517 trypanosoma	496	5	55.6	870	5	Q9GRY4	Q9GRY4 leishmania
424	5	55.6	660	5	Q9VT63	Q9VT63 drosophila	497	5	55.6	872	2	Q9S4J3	Q9S4J3 streptococc
425	5	55.6	662	3	Q94041	Q94041 candida alb	498	5	55.6	875	4	Q60278	Q60278 homo sapien
426	5	55.6	665	10	Q65793	Q65793 pharbitis n	499	5	55.6	882	5	Q91752	Q91752 drosophila
427	5	55.6	666	4	Q9H907	Q9H907 homo sapien	500	5	55.6	883	2	Q9RF11	Q9RF11 myxococcus
428	5	55.6	668	5	Q9VWM7	Q9VWM7 drosophila	501	5	55.6	884	11	Q9JY22	Q9JY22 rattus norv
429	5	55.6	670	4	Q75714	Q75714 homo sapien	502	5	55.6	899	3	Q06132	Q06132 saccharomyc
430	5	55.6	670	4	Q9UPP5	Q9UPP5 homo sapien	503	5	55.6	920	3	P78953	P78953 schizosacch
431	5	55.6	670	4	Q9UNK7	Q9UNK7 homo sapien	504	5	55.6	929	1	Q9YDS4	Q9YDS4 aeropyrum p
432	5	55.6	670	6	Q9XT62	Q9XT62 cercopithe	505	5	55.6	929	10	Q23410	Q23410 arabidopsis
433	5	55.6	672	4	Q9H8W8	Q9H8W8 homo sapien	506	5	55.6	930	11	Q9JY23	Q9JY23 rattus norv
434	5	55.6	675	10	Q9EUI4	Q9EUI4 arabidopsis	507	5	55.6	930	11	Q9EY63	Q9EY63 mus musculu
435	5	55.6	681	4	Q75943	Q75943 homo sapien	508	5	55.6	930	11	Q9EQH2	Q9EQH2 mus musculu
436	5	55.6	682	1	Q9HPZ0	Q9HPZ0 halobacteri	509	5	55.6	931	10	Q04026	Q04026 arabidopsis
437	5	55.6	682	4	Q9NMX3	Q9NMX3 homo sapien	510	5	55.6	935	2	Q9XBP4	Q9XBP4 myxococcus
438	5	55.6	682	10	Q9M3E5	Q9M3E5 arabidopsis	511	5	55.6	939	14	Q9NRN1	Q9NRN1 macaca mula
439	5	55.6	683	10	Q9SK94	Q9SK94 arabidopsis	512	5	55.6	939	14	Q9JY19	Q9JY19 macaca mula
440	5	55.6	685	4	Q9NR61	Q9NR61 homo sapien	513	5	55.6	940	10	Q81471	Q81471 arabidopsis
441	5	55.6	685	11	Q9JH27	Q9JH27 mus musculu	514	5	55.6	941	4	Q9UKY2	Q9UKY2 homo sapien
442	5	55.6	686	11	Q9JY71	Q9JY71 mus musculu	515	5	55.6	941	4	Q9UHF8	Q9UHF8 homo sapien
443	5	55.6	687	11	Q89024	Q89024 mus musculu	516	5	55.6	941	4	Q9NZ08	Q9NZ08 caenorhabdl
444	5	55.6	687	14	Q88271	Q88271 simian parv	517	5	55.6	964	5	Q10953	Q10953 delinococcus
445	5	55.6	688	11	Q88934	Q88934 mus musculu	518	5	55.6	969	2	Q9RZ15	Q9RZ15 delinococcus
446	5	55.6	689	5	Q01719	Q01719 strongyloce	519	5	55.6	969	4	Q9Y214	Q9Y214 homo sapien
447	5	55.6	691	13	Q57658	Q57658 gallus gall	520	5	55.6	976	2	Q9EVI7	Q9EVI7 actinomyc
448	5	55.6	692	2	Q9F2J1	Q9F2J1 streptomyce	521	5	55.6	976	2	Q9EVI7	Q9EVI7 actinomyc
449	5	55.6	693	2	Q9K437	Q9K437 streptomyce	522	5	55.6	977	3	Q94540	Q94540 schizosacch
450	5	55.6	694	4	Q9P276	Q9P276 homo sapien	523	5	55.6	977	13	Q91925	Q91925 xenopus lae
451	5	55.6	700	5	Q96839	Q96839 drosophila	524	5	55.6	988	5	Q16851	Q16851 pluteia xy
452	5	55.6	700	5	Q9V887	Q9V887 drosophila	525	5	55.6	990	13	Q91803	Q91803 xenopus lae
453	5	55.6	708	5	Q9UAS6	Q9UAS6 drosophila	526	5	55.6	1004	2	P71719	P71719 mycobacteri
454	5	55.6	708	4	Q9NVU0	Q9NVU0 homo sapien	527	5	55.6	1006	5	Q9W3Y4	Q9W3Y4 drosophila
455	5	55.6	730	10	Q9EY38	Q9EY38 arabidopsis	528	5	55.6	1008	13	Q9DER7	Q9DER7 gallus gall
456	5	55.6	732	5	Q9YOC4	Q9YOC4 leishmania	529	5	55.6	1013	4	Q43897	Q43897 homo sapien
457	5	55.6	735	13	Q57381	Q57381 xenopus lae	530	5	55.6	1013	4	Q9NDS4	Q9NDS4 homo sapien

531	5	55.6	1022	5	061907	061907 caenorhabd	604	5	55.6	1719	11	P97789	P97789 mus musculu
532	5	55.6	1022	13	057460	057460 brachydantio	605	5	55.6	1723	11	060767	060767 mus musculu
533	5	55.6	1026	2	09X3R6	09X3r6 streptococc	606	5	55.6	1766	14	091599	091599 fowlpox vir
534	5	55.6	1030	4	014974	014974 homo sapien	607	5	55.6	1769	6	097758	097758 canis famli
535	5	55.6	1047	4	09NS20	09ns20 homo sapien	608	5	55.6	1777	14	09J5B3	09J5b3 fowlpox vir
536	5	55.6	1057	5	09W294	09w294 dtrosophila	609	5	55.6	1785	5	025685	025685 plasmodium
537	5	55.6	1066	4	09UGX4	09ugx4 homo sapien	610	5	55.6	1798	5	09VUB6	09vub6 dtrosophila
538	5	55.6	1070	5	094290	094290 caenorhabd	611	5	55.6	1799	5	018220	018220 caenorhabd
539	5	55.6	1074	5	09YU22	09yu22 dtrosophila	612	5	55.6	1802	5	018219	018219 caenorhabd
540	5	55.6	1103	9	09C0B5	09c0b5 bacteriopia	613	5	55.6	1802	14	09J5C2	09J5c2 fowlpox vir
541	5	55.6	1108	3	P87121	P87121 schizosacch	614	5	55.6	1822	2	007290	007290 streptococc
542	5	55.6	1112	10	09FH47	09fh47 arabidopsis	615	5	55.6	1829	5	019815	019815 caenorhabd
543	5	55.6	1113	2	09K6S8	09k6s8 bacillus ha	616	5	55.6	1846	10	09M0B6	09M0b6 arabidopsis
544	5	55.6	1115	4	09ULLO	09ul10 homo sapien	617	5	55.6	1848	5	09VUB6	09vub6 dtrosophila
545	5	55.6	1119	3	09P3N5	09p3n5 neurospora	618	5	55.6	1870	14	09J5A0	09J5a0 fowlpox vir
546	5	55.6	1124	5	09NDP3	09ndf3 apis mellif	619	5	55.6	1912	14	09J5C3	09J5c3 fowlpox vir
547	5	55.6	1135	3	09OVU5	09ovus pichia angu	620	5	55.6	1963	10	09LX79	09Lx79 arabidopsis
548	5	55.6	1140	3	09VTS5	09vts5 dtrosophila	621	5	55.6	1967	4	09P2D1	09P2d1 homo sapien
549	5	55.6	1159	4	09UF39	09uf39 homo sapien	622	5	55.6	1983	5	09M165	09m165 leishmania
550	5	55.6	1175	6	09TV66	09tv66 oxytelaqus	623	5	55.6	2001	10	09M659	09M659 arabidopsis
551	5	55.6	1182	14	002711	002711 murine endo	624	5	55.6	2001	10	09M658	09M658 arabidopsis
552	5	55.6	1187	5	09V7N3	09v7n3 dtrosophila	625	5	55.6	2164	13	09IAR9	09Iar9 galius gall
553	5	55.6	1188	4	09UQ26	09uq26 homo sapien	626	5	55.6	2210	5	0241B9	0241b9 dtrosophila
554	5	55.6	1191	5	09VJN7	09vjn7 dtrosophila	627	5	55.6	2217	5	09VW15	09vwl5 dtrosophila
555	5	55.6	1199	6	028139	028139 bos taurus	628	5	55.6	2254	10	09LN02	09ln02 arabidopsis
556	5	55.6	1201	5	09W1J0	09w1j0 dtrosophila	629	5	55.6	2271	5	09W1A9	09w1a9 dtrosophila
557	5	55.6	1208	2	09XD11	09xd11 legionella	630	5	55.6	2271	13	09I1909	09I1909 xenopus lae
558	5	55.6	1211	11	035223	035233 mus musculu	631	5	55.6	2280	5	09V8E6	09V8e6 dtrosophila
559	5	55.6	1212	2	09L1C8	09l1c8 streptomyce	632	5	55.6	2287	5	019761	019761 caenorhabd
560	5	55.6	1217	5	P91457	P91457 caenorhabd	633	5	55.6	2292	14	089272	089272 encephalomy
561	5	55.6	1217	11	088573	088573 mus musculu	634	5	55.6	2292	14	066763	066763 encephalomy
562	5	55.6	1219	5	09VT64	09vt64 dtrosophila	635	5	55.6	2292	14	066765	066765 encephalomy
563	5	55.6	1224	3	013637	013637 schizosacch	636	5	55.6	2292	14	066850	066850 encephalomy
564	5	55.6	1228	3	012754	012754 saccharomyc	637	5	55.6	2293	14	083422	083422 mengo encpe
565	5	55.6	1240	10	09T0B7	09t0b7 arabidopsis	638	5	55.6	2302	5	09N693	09N693 dtrosophila
566	5	55.6	1246	4	015052	015052 homo sapien	639	5	55.6	2310	5	09G9A9	09g9a9 dtrosophila
567	5	55.6	1254	4	09UBS9	09ubs9 homo sapien	640	5	55.6	2344	5	09N3Y8	09n3y8 caenorhabd
568	5	55.6	1255	5	09NK83	09nk83 dtrosophila	641	5	55.6	2382	4	09E4A3	09E4a3 homo sapien
569	5	55.6	1262	5	09N911	09n911 leishmania	642	5	55.6	2404	5	09VE34	09VE34 dtrosophila
570	5	55.6	1268	11	063623	063623 rattus norv	643	5	55.6	2446	4	09NS05	09ns05 homo sapien
571	5	55.6	1270	4	09HCG5	09hcg5 homo sapien	644	5	55.6	2447	5	022463	022463 caenorhabd
572	5	55.6	1276	11	P97260	P97260 cricetulus	645	5	55.6	2500	4	002646	002646 homo sapien
573	5	55.6	1277	4	012770	012770 homo sapien	646	5	55.6	2768	4	09VCO0	09vc00 dtrosophila
574	5	55.6	1300	11	09WTL4	09wtl4 mus musculu	647	5	55.6	2785	4	075691	075691 homo sapien
575	5	55.6	1322	5	09VYH2	09vyh2 dtrosophila	648	5	55.6	2796	2	048926	048926 mycobacteri
576	5	55.6	1331	1	09YEG3	09yeg3 aeropyrum p	649	5	55.6	2936	5	09NKP7	09Nkp7 leishmania
577	5	55.6	1341	4	09UFP8	09ufp8 homo sapien	650	5	55.6	2977	14	041892	041892 hepatitis g
578	5	55.6	1354	5	09VG11	09vg11 dtrosophila	651	5	55.6	2977	5	09VAP9	09vap9 dtrosophila
579	5	55.6	1357	5	09W4M4	09w4m4 dtrosophila	652	5	55.6	3016	14	092531	092531 hepatitis c
580	5	55.6	1400	11	09ESU6	09esu6 mus musculu	653	5	55.6	3131	3	000869	000869 fusarium eg
581	5	55.6	1405	4	09UL04	09ul04 homo sapien	654	5	55.6	3261	4	09Y556	09y556 homo sapien
582	5	55.6	1415	5	061442	061442 caenorhabd	655	5	55.6	3418	4	013879	013879 homo sapien
583	5	55.6	1418	5	09U6B9	09ub69 caenorhabd	656	5	55.6	3550	11	09UJN2	09Ujn2 mus musculu
584	5	55.6	1423	5	09W1A0	09w1a0 dtrosophila	657	5	55.6	3576	11	09Q2W2	09q2w2 mus musculu
585	5	55.6	1431	5	09U6R1	09ubr1 caenorhabd	658	5	55.6	4162	13	098918	098918 galius gall
586	5	55.6	1449	5	010922	010922 caenorhabd	659	5	55.6	4833	11	09OXY6	09oxy6 mus musculu
587	5	55.6	1457	5	09WY35	09wy35 dtrosophila	660	5	55.6	4857	4	014687	014687 homo sapien
588	5	55.6	1490	5	09U4B5	09u4b5 dtrosophila	661	5	55.6	5038	11	09QYX7	09Qyx7 mus musculu
589	5	55.6	1504	13	09PTW9	09ptw9 opsanus bet	662	5	55.6	5262	4	014686	014686 homo sapien
590	5	55.6	1534	6	028298	028298 canis famli	663	5	55.6	5388	5	09U1D0	09u1d0 leishmania
591	5	55.6	1543	5	09VWAO	09vwa0 dtrosophila	664	5	55.6	6831	5	023550	023550 caenorhabd
592	5	55.6	1566	2	053414	053414 streptococc	665	5	55.6	7160	5	023551	023551 caenorhabd
593	5	55.6	1566	2	055308	055308 streptococc	666	5	55.6	7160	14	09J168	09J168 tt virus.
594	5	55.6	1569	2	054183	054183 streptococc	667	5	55.6	7160	14	09J168	09J168 tt virus.
595	5	55.6	1576	13	09I1908	09i1908 xenopus lae	668	5	55.6	7160	14	09J168	09J168 tt virus.
596	5	55.6	1616	10	09M127	09m127 arabidopsis	669	5	55.6	7160	14	09J168	09J168 tt virus.
597	5	55.6	1624	5	09U679	09u679 strongyloe	670	5	55.6	7160	14	09J168	09J168 tt virus.
598	5	55.6	1663	4	09U001	09u001 homo sapien	671	5	55.6	7160	14	09J168	09J168 tt virus.
599	5	55.6	1687	11	035651	035651 mus musculu	672	5	55.6	7160	14	09J168	09J168 tt virus.
600	5	55.6	1688	5	09Y9D0	09y9d0 dtrosophila	673	5	55.6	7160	14	09J168	09J168 tt virus.
601	5	55.6	1694	5	0914N8	0914n8 pseudomonas	674	5	55.6	7160	14	09J168	09J168 tt virus.
602	5	55.6	1706	11	P97790	P97790 mus musculu	675	5	55.6	7160	14	09J168	09J168 tt virus.
603	5	55.6	1711	2	P96311	P96311 anaerocellu	676	5	55.6	7160	14	09J168	09J168 tt virus.

677	4	44.4	26	14	09MNU0	09wnj0	tt	virus.	p	750	4	44.4	40	7	09TN24	09tn24	rattus	norv
678	4	44.4	26	14	09W872	09w872	tt	virus.	p	751	4	44.4	41	7	09TN25	09tn25	rattus	norv
679	4	44.4	26	14	09J116	09j116	tt	virus.	o	752	4	44.4	43	2	09PE48	09pe48	xylella	fas
680	4	44.4	26	14	09J115	09j115	tt	virus.	o	753	4	44.4	43	7	09TN26	09tn26	rattus	norv
681	4	44.4	26	14	09J114	09j114	tt	virus.	o	754	4	44.4	44	5	061051	061051	trypanosoma	
682	4	44.4	26	14	09J113	09j113	tt	virus.	o	755	4	44.4	44	7	09S562	09s562	rattus	norv
683	4	44.4	26	14	09J112	09j112	tt	virus.	o	756	4	44.4	45	2	086765	086765	streptomyces	
684	4	44.4	26	14	09J110	09j110	tt	virus.	o	757	4	44.4	47	14	09YR02	09yr02	tt	virus. h
685	4	44.4	26	14	09J1H9	09j1H9	tt	virus.	o	758	4	44.4	47	14	09W754	09w754	tt	virus. h
686	4	44.4	26	14	09J1H8	09j1H8	tt	virus.	o	759	4	44.4	47	14	09PX67	09px67	watermelon	
687	4	44.4	26	14	09J1H3	09j1H3	tt	virus.	o	760	4	44.4	47	14	09DHM3	09dhm3	watermelon	
688	4	44.4	26	14	09J1H2	09j1H2	tt	virus.	o	761	4	44.4	49	2	045823	045823	corynebacte	
689	4	44.4	26	14	09J1H0	09j1H0	tt	virus.	o	762	4	44.4	49	6	09M2L9	09m2L9	canis	famil
690	4	44.4	26	14	09J1G5	09j1G5	tt	virus.	o	763	4	44.4	49	14	09JG73	09jg73	tt	virus. p
691	4	44.4	26	14	09J1G6	09j1G6	tt	virus.	o	764	4	44.4	49	14	09JG70	09jg70	tt	virus. p
692	4	44.4	26	14	09J1G4	09j1G4	tt	virus.	o	765	4	44.4	49	14	09DYC0	09dyc0	tt	virus. h
693	4	44.4	26	14	09J1G1	09j1G1	tt	virus.	o	766	4	44.4	51	5	017090	017090	ascaris	suu
694	4	44.4	26	14	09J1G0	09j1G0	tt	virus.	o	767	4	44.4	51	6	018724	018724	hylobates	s
695	4	44.4	26	14	09J1F9	09j1F9	tt	virus.	o	768	4	44.4	51	6	018725	018725	hylobates	s
696	4	44.4	26	14	09J1F8	09j1F8	tt	virus.	o	769	4	44.4	52	2	052864	052864	rhizobium	1
697	4	44.4	26	14	09J1F7	09j1F7	tt	virus.	o	770	4	44.4	52	8	0922U6	0922U6	littorina	s
698	4	44.4	26	14	09J1F6	09j1F6	tt	virus.	o	771	4	44.4	53	1	09YC81	09yc81	aeropyrum	p
699	4	44.4	26	14	09J1F5	09j1F5	tt	virus.	o	772	4	44.4	53	2	09RE85	09re85	staphylococ	
700	4	44.4	26	14	09J1F3	09j1F3	tt	virus.	o	773	4	44.4	53	8	09GB33	09gb33	quiscalus	q
701	4	44.4	26	14	09J1F2	09j1F2	tt	virus.	o	774	4	44.4	54	14	09E3W1	09e3W1	tomato	yell
702	4	44.4	26	14	09J1F1	09j1F1	tt	virus.	o	775	4	44.4	55	5	09ND27	09nd27	leishmania	
703	4	44.4	26	14	09J1F0	09j1F0	tt	virus.	o	776	4	44.4	55	6	018722	018722	pan	troglod
704	4	44.4	26	14	09J1E8	09j1E8	tt	virus.	o	777	4	44.4	55	8	09T3G7	09t3G7	icterus	obe
705	4	44.4	26	14	09J1E7	09j1E7	tt	virus.	o	778	4	44.4	55	8	09MDP1	09mdp1	quiscalus	1
706	4	44.4	26	14	09J1E6	09j1E6	tt	virus.	o	779	4	44.4	55	8	09MDP9	09mdp9	quiscalus	1
707	4	44.4	26	14	09J1E4	09j1E4	tt	virus.	o	780	4	44.4	55	11	063761	063761	rattus	norv
708	4	44.4	26	14	09J1E3	09j1E3	tt	virus.	o	781	4	44.4	57	6	028471	028471	macaca	fasc
709	4	44.4	26	14	09J1E1	09j1E1	tt	virus.	o	782	4	44.4	58	2	09E4B6	09e4B6	human	adeno
710	4	44.4	26	14	09J1E0	09j1E0	tt	virus.	o	783	4	44.4	58	2	09S4C7	09s4C7	porphyromon	
711	4	44.4	26	14	09J1D9	09j1D9	tt	virus.	o	784	4	44.4	59	14	003812	003812	human	immun
712	4	44.4	26	14	09J1D6	09j1D6	tt	virus.	o	785	4	44.4	60	2	086035	086035	rhizobium	m
713	4	44.4	26	14	09J1D4	09j1D4	tt	virus.	o	786	4	44.4	60	4	014889	014889	homo	sapien
714	4	44.4	26	14	09J1D3	09j1D3	tt	virus.	o	787	4	44.4	61	4	09NU88	09nu88	homo	sapien
715	4	44.4	26	14	09J1D2	09j1D2	tt	virus.	o	788	4	44.4	61	14	P89262	P89262	xestla	c-n1
716	4	44.4	26	14	09J1D1	09j1D1	tt	virus.	o	789	4	44.4	62	5	09XWL6	09xwl6	caenorhabdi	
717	4	44.4	26	14	09J1D0	09j1D0	tt	virus.	o	790	4	44.4	62	6	09XS88	09xs88	equus	cabal
718	4	44.4	28	14	09WNI9	09wni9	tt	virus.	o	791	4	44.4	63	5	09NMES	09nmes	leishmania	
719	4	44.4	28	14	09WNI7	09wni7	tt	virus.	o	792	4	44.4	63	10	09XGK9	09xgK9	euglena	gra
720	4	44.4	28	14	09WNI4	09wni4	tt	virus.	o	793	4	44.4	64	2	057026	057026	borrelia	af
721	4	44.4	28	14	09WNI3	09wni3	tt	virus.	o	794	4	44.4	65	5	09GXM2	09gxM2	leishmania	
722	4	44.4	28	14	09QRTJ7	09qrlJ7	tt	virus.	o	795	4	44.4	66	5	09NFS5	09nfs5	drosophila	
723	4	44.4	28	14	09QRTJ6	09qrlJ6	tt	virus.	o	796	4	44.4	66	7	029916	029916	homo	sapien
724	4	44.4	28	14	09QRTJ5	09qrlJ5	tt	virus.	o	797	4	44.4	66	8	096802	096802	skeletonema	
725	4	44.4	28	14	09QRTJ3	09qrlJ3	tt	virus.	o	798	4	44.4	67	2	09WYU9	09wyU9	thermotoga	
726	4	44.4	28	14	09QRTJ2	09qrlJ2	tt	virus.	o	799	4	44.4	68	2	048848	048848	lactobacilli	
727	4	44.4	29	14	086257	086257	human	rotav		800	4	44.4	68	2	09KZG1	09kzG1	streptomyces	
728	4	44.4	29	14	086259	086259	human	rotav		801	4	44.4	68	14	09YK4	09yk4	tomato	yell
729	4	44.4	29	14	086262	086262	human	rotav		802	4	44.4	69	2	09RCV0	09rcV0	streptomyces	
730	4	44.4	29	14	086256	086256	human	rotav		803	4	44.4	69	2	09KMY2	09kmy2	vibrio	chol
731	4	44.4	29	14	086260	086260	human	rotav		804	4	44.4	69	11	09JMB7	09jmb7	mus	musculu
732	4	44.4	29	14	086261	086261	human	rotav		805	4	44.4	69	14	P89655	P89655	murid	herpe
733	4	44.4	29	14	086263	086263	human	rotav		806	4	44.4	69	14	09PE27	09pe27	simlan	herp
734	4	44.4	29	14	086264	086264	human	rotav		807	4	44.4	70	14	089817	089817	borna	disea
735	4	44.4	29	14	086265	086265	human	rotav		808	4	44.4	71	2	09PAR8	09par8	xylella	fas
736	4	44.4	29	14	086266	086266	human	rotav		809	4	44.4	71	10	09PTW6	09ptw6	oryza	sativ
737	4	44.4	29	14	086267	086267	human	rotav		810	4	44.4	71	14	087616	087616	chimpanzee	
738	4	44.4	31	14	09IMY6	09imY6	tt	virus.	h	811	4	44.4	72	10	09LX10	09lx10	arabidopsis	
739	4	44.4	31	14	09IMY5	09imY5	tt	virus.	h	812	4	44.4	72	14	085982	085982	methanobact	
740	4	44.4	31	14	09IMY4	09imY4	tt	virus.	h	813	4	44.4	73	1	027331	027331	human	immun
741	4	44.4	31	14	09IMY2	09imY2	tt	virus.	h	814	4	44.4	73	2	09PFS8	09pfs8	xylella	fas
742	4	44.4	32	2	047657	047657	escherichia			815	4	44.4	73	2	09KX54	09kx54	streptomyces	
743	4	44.4	32	14	09WNI5	09wni5	tt	virus.	o	816	4	44.4	73	4	000247	000247	homo	sapien
744	4	44.4	32	14	09UG31	09ug31	tt	virus.	o	817	4	44.4	73	5	09XU39	09xu39	caenorhabdi	
745	4	44.4	32	14	09JG27	09jg27	tt	virus.	o	818	4	44.4	73	14	P87655	P87655	europcan	br
746	4	44.4	35	14	09YM29	09ym29	human	immun		819	4	44.4	74	2	09ZHW8	09zhw8	bruceella	me
747	4	44.4	37	11	060704	060704	mus	musculu		820	4	44.4	74	14	056576	056576	hepatitis	c
748	4	44.4	38	8	09T2N6	09t2n6	spiniacia	ol		821	4	44.4	74	14	081723	081723	hepatitis	c
749	4	44.4	39	10	040959	040959	physcomlfire			822	4	44.4	74	14	081743	081743	hepatitis	c

823	4	44.4	74	14	081744	081744 hepatitis c	896	4	44.4	85	14	070695	070695 human immun
824	4	44.4	74	14	081745	081745 hepatitis c	897	4	44.4	85	14	090298	090298 odocolleus
825	4	44.4	74	14	09YP05	09YP05 hepatitis c	898	4	44.4	86	2	049372	049372 mycoplasma
826	4	44.4	74	14	09YP04	09YP04 hepatitis c	899	4	44.4	86	2	P94196	P94196 agrobacteri
827	4	44.4	74	14	09YP03	09YP03 hepatitis c	900	4	44.4	86	6	09YV23	09YV23 oryctolagus
828	4	44.4	74	14	09YP02	09YP02 hepatitis c	901	4	44.4	86	6	P82672	P82672 bos taurus
829	4	44.4	74	14	09YPP3	09YPP3 hepatitis c	902	4	44.4	86	10	Q42283	Q42283 arabidopsis
830	4	44.4	74	14	09YPP1	09YPP1 hepatitis c	903	4	44.4	87	2	09L8H3	09L8H3 streptomyce
831	4	44.4	74	14	09YJB8	09YJB8 hepatitis c	904	4	44.4	87	5	09W216	09W216 drosophila
832	4	44.4	74	14	09YJN5	09YJN5 hepatitis c	905	4	44.4	87	5	09NAC9	09NAC9 caenorhabdi
833	4	44.4	74	14	09YID0	09YID0 hepatitis c	906	4	44.4	87	5	09GWT4	09GWT4 leishmania
834	4	44.4	74	14	09WK43	09WK43 hepatitis c	907	4	44.4	88	2	09RGW7	09RGW7 acinetobact
835	4	44.4	74	14	09WK42	09WK42 hepatitis c	908	4	44.4	88	10	Q41185	Q41185 arabidopsis
836	4	44.4	75	2	044892	044892 hepatitis c	909	4	44.4	88	14	09QPS0	09QPS0 hepatitis c
837	4	44.4	75	2	09XW66	09XW66 borrelia bu	910	4	44.4	88	14	09QPS9	09QPS9 hepatitis c
838	4	44.4	75	14	069312	069312 gallid herp	911	4	44.4	88	14	09QPR4	09QPR4 hepatitis c
839	4	44.4	76	2	045627	045627 bacillus st	912	4	44.4	89	2	09ZNI3	09ZNI3 pseudomonas
840	4	44.4	76	2	09RS66	09RS66 delnoccocus	913	4	44.4	89	2	09LOV2	09LOV2 streptomyce
841	4	44.4	76	2	09KGR1	09KGR1 vibrio para	914	4	44.4	89	2	030687	030687 rhodococcus
842	4	44.4	76	9	09MBW6	09MBW6 bacterioph	915	4	44.4	91	2	09Z982	09Z982 chlamydia p
843	4	44.4	76	10	022492	022492 oenanthel	916	4	44.4	91	2	09ZSJ1	09ZSJ1 chlamydia p
844	4	44.4	76	10	082581	082581 pimpinella	917	4	44.4	91	5	09N3U7	09N3U7 caenorhabdi
845	4	44.4	76	10	09XIK9	09XIK9 arabidopsis	918	4	44.4	91	5	09GWN3	09GWN3 ostercagia
846	4	44.4	76	14	084503	084503 paramecium	919	4	44.4	92	2	09ZBZ9	09ZBZ9 streptomyce
847	4	44.4	77	5	09PBV2	09PBV2 xylella fas	920	4	44.4	92	10	09LGS9	09LGS9 oryza sativ
848	4	44.4	77	5	09N3U6	09N3U6 caenorhabdi	921	4	44.4	93	2	052948	052948 bacillus su
849	4	44.4	77	14	09QPC7	09QPC7 tomato yell	922	4	44.4	93	2	09Z9G9	09Z9G9 chlamydia p
850	4	44.4	78	2	086789	086789 streptomyce	923	4	44.4	94	6	09N030	09N030 macaca fasc
851	4	44.4	78	2	034155	034155 microcystis	924	4	44.4	94	10	09SIN7	09SIN7 arabidopsis
852	4	44.4	78	2	049654	049654 mycobacteri	925	4	44.4	95	14	005535	005535 equine herp
853	4	44.4	78	7	095413	095413 ovis aries	926	4	44.4	96	2	033423	033423 pseudomonas
854	4	44.4	79	2	047383	047383 escherichia	927	4	44.4	96	5	019828	019828 caenorhabdi
855	4	44.4	79	5	017013	017013 anopheles g	928	4	44.4	96	5	09VZB7	09VZB7 drosophila
856	4	44.4	79	5	094188	094188 caenorhabdi	929	4	44.4	96	5	09GWE7	09GWE7 leishmania
857	4	44.4	79	5	09W7T5	09W7T5 leishmania	930	4	44.4	96	10	09LJU3	09LJU3 arabidopsis
858	4	44.4	80	10	09ZT55	09ZT55 zea mays (m	931	4	44.4	97	2	09ZNP5	09ZNP5 comamonas t
859	4	44.4	80	10	09M697	09M697 brassica ol	932	4	44.4	97	5	09VHF4	09VHF4 drosophila
860	4	44.4	81	5	094209	094209 caenorhabdi	933	4	44.4	98	2	09WX46	09WX46 escherichia
861	4	44.4	81	5	09NMKO	09NMKO leishmania	934	4	44.4	98	5	09N616	09N616 drosophila
862	4	44.4	81	6	028856	028856 sus scrofa	935	4	44.4	98	11	061369	061369 mus muscu
863	4	44.4	82	2	P95312	P95312 mycobacteri	936	4	44.4	99	1	09UX22	09UX22 sulfobodu
864	4	44.4	82	2	035239	035239 escherichia	937	4	44.4	99	2	044464	044464 agrobacteri
865	4	44.4	82	5	094210	094210 caenorhabdi	938	4	44.4	99	14	09E586	09E586 human immun
866	4	44.4	82	5	094212	094212 caenorhabdi	939	4	44.4	100	1	09YBJ1	09YBJ1 aeropyrum p
867	4	44.4	82	5	094214	094214 caenorhabdi	940	4	44.4	100	1	09UWS1	09UWS1 sulfobodu
868	4	44.4	82	5	061784	061784 caenorhabdi	941	4	44.4	100	5	P92194	P92194 drosophila
869	4	44.4	83	2	09WTG3	09WTG3 escherichia	942	4	44.4	100	14	040501	040501 human immun
870	4	44.4	83	7	019724	019724 homo sapien	943	4	44.4	100	14	069359	069359 feline herp
871	4	44.4	83	10	09FW11	09FW11 oryza sativ	944	4	44.4	100	14	09J7Y9	09J7Y9 feline aden
872	4	44.4	84	5	016803	016803 paracentrot	945	4	44.4	100	14	09DIZ8	09DIZ8 human adeno
873	4	44.4	84	10	024072	024072 medicago sa	946	4	44.4	100	14	09DIZ7	09DIZ7 human adeno
874	4	44.4	84	14	090694	090694 unidentified	947	4	44.4	100	14	09DIZ6	09DIZ6 human adeno
875	4	44.4	84	14	092612	092612 unidentified	948	4	44.4	100	14	09DIZ5	09DIZ5 human adeno
876	4	44.4	84	14	092613	092613 unidentified	949	4	44.4	100	14	09DIZ4	09DIZ4 human adeno
877	4	44.4	84	14	09QPU4	09QPU4 human adeno	950	4	44.4	100	14	09DIZ3	09DIZ3 human adeno
878	4	44.4	84	14	09QPU3	09QPU3 human adeno	951	4	44.4	100	14	09DIZ2	09DIZ2 human adeno
879	4	44.4	84	14	09QPU2	09QPU2 human adeno	952	4	44.4	100	14	09DIZ1	09DIZ1 human adeno
880	4	44.4	84	14	09QPU1	09QPU1 human adeno	953	4	44.4	100	14	09DIZ0	09DIZ0 human adeno
881	4	44.4	84	14	09QPU0	09QPU0 human adeno	954	4	44.4	100	14	09DIT9	09DIT9 human adeno
882	4	44.4	84	14	09QPT9	09QPT9 human adeno	955	4	44.4	100	14	09DIT8	09DIT8 human adeno
883	4	44.4	84	14	09QPT8	09QPT8 human adeno	956	4	44.4	100	14	09DIT7	09DIT7 human adeno
884	4	44.4	84	14	09QPT7	09QPT7 human adeno	957	4	44.4	100	14	09DIT6	09DIT6 human adeno
885	4	44.4	84	14	09QPT6	09QPT6 human adeno	958	4	44.4	101	2	09Z8B1	09Z8B1 chlamydia p
886	4	44.4	84	14	09QPT5	09QPT5 human adeno	959	4	44.4	101	5	017614	017614 caenorhabdi
887	4	44.4	84	14	09QPT4	09QPT4 human adeno	960	4	44.4	101	5	090IT3	090IT3 caenorhabdi
888	4	44.4	84	14	09QPT3	09QPT3 human adeno	961	4	44.4	101	14	065385	065385 unidentified
889	4	44.4	84	14	09QPT2	09QPT2 human adeno	962	4	44.4	101	14	065432	065432 unidentified
890	4	44.4	84	14	09QPT1	09QPT1 human adeno	963	4	44.4	101	14	065659	065659 unidentified
891	4	44.4	84	14	09QPT0	09QPT0 human adeno	964	4	44.4	101	14	065679	065679 unidentified
892	4	44.4	84	14	09QPS9	09QPS9 human adeno	965	4	44.4	102	2	09PK42	09PK42 chlamydia m
893	4	44.4	84	14	09QPS8	09QPS8 human adeno	966	4	44.4	102	5	0917C6	0917C6 drosophila
894	4	44.4	84	14	09QPS7	09QPS7 human adeno	967	4	44.4	102	10	004341	004341 arabidopsis
895	4	44.4	85	2	09Z432	09Z432 pseudomonas	968	4	44.4	102	10	P93057	P93057 bromus iner

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969 4 44.4 102 10 Q9FEZ8 Q9FEZ8 glycine max
970 4 44.4 103 2 Q9RX39 Q9RX39 delinococcus
971 4 44.4 103 5 P90571 P90571 plasmodium
972 4 44.4 103 5 P90572 P90572 plasmodium
973 4 44.4 103 14 Q71233 Q71233 human immun
974 4 44.4 103 14 Q71244 Q71244 human immun
975 4 44.4 103 14 Q71226 Q71226 human immun
976 4 44.4 103 14 Q71231 Q71231 human immun
977 4 44.4 103 14 P88761 P88761 human immun
978 4 44.4 103 14 P88762 P88762 human immun
979 4 44.4 103 14 P88763 P88763 human immun
980 4 44.4 103 14 Q39135 Q39135 human immun
981 4 44.4 103 14 Q39137 Q39137 human immun
982 4 44.4 103 14 Q71228 Q71228 human immun
983 4 44.4 103 14 Q9MFM8 Q9MFM8 human immun
984 4 44.4 104 4 Q9P0E3 Q9P0E3 homo sapien
985 4 44.4 104 5 P92184 P92184 drosophila
986 4 44.4 104 5 Q96905 Q96905 drosophila
987 4 44.4 104 5 P92192 P92192 drosophila
988 4 44.4 105 2 Q54742 Q54742 streptococc
989 4 44.4 105 2 Q87035 Q87035 vibrio chol
990 4 44.4 105 2 Q9X8C6 Q9X8C6 streptomyce
991 4 44.4 105 2 Q9PEK4 Q9PEK4 xyella fas
992 4 44.4 105 4 P78449 P78449 homo sapien
993 4 44.4 105 4 Q17410 Q17410 lucilia cup
994 4 44.4 105 5 P92201 P92201 drosophila
995 4 44.4 105 5 Q91706 Q91706 drosophila
996 4 44.4 105 8 Q32712 Q32712 nicotiana t
997 4 44.4 105 8 Q9MG34 Q9MG34 actinonyx ju
998 4 44.4 105 9 Q80231 Q80231 bacterioph
999 4 44.4 105 10 Q41031 Q41031 picea sitch
1000 4 44.4 105 11 Q9R1P8 Q9R1P8 mus musculu

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ALIGNMENTS

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RESULT 1
Q9RNU3 PRELIMINARY; PRT; 86 AA.
ID Q9RNU3;
AC Q9RNU3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE P60 PROTEIN (FRAGMENT).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RX MEDLINE=90256283; PubMed=2111287;
RA Kohler S., Leimister-Wachter M., Chakraborty T., Lottspeich F.,
RA Goebel W.;
RT "The gene coding for protein p60 of Listeria monocytogenes and its use
RT as a specific probe for Listeria monocytogenes.";
RL Infect. Immun. 58:1943-1950(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Park S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF179003; AAD5089.1; -.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9194 MM; 71F649A817D697F6 CRC64;

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Query Match 100.0%; Score 9; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0 0046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSTPVAPRO 9

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Db 29 VSTPVAPRO 37
|||||||
RESULT 2
ID Q03493 PRELIMINARY; PRT; 478 AA.
AC Q03493;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN).
GN IAP.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RX MEDLINE=93094153; PubMed=1459966;
RP Buber A., Kuhn M., Goebel W., Koehler S.;
RT "Structural and functional properties of the p60 proteins from
RT different Listeria species."
RL J. Bacteriol. 174:8166-8171(1992).
CC -1- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE
CC INVASION OF NONPROFESSIONAL PHAGOCYTIC CELLS BY LISTERIA.
DR EMBL: M80351; AAA25280.1; -.
DR InterPro: IPR000064; -.
DR InterPro: IPR002482; -.
DR Pfam: PF00877; NUPC_P60; 1.
DR Pfam: PF01476; LysM; 2.
DR SMART: SM00257; LysM; 1.
KW SIGNAL.
FT CHAIN 1 27 BY SIMILARITY.
FT SIGNAL 1 27
FT CHAIN 28 478 PROTEIN P60.
SQ SEQUENCE 478 AA; 49997 MM; D46D050507402344 CRC64;

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Query Match 100.0%; Score 9; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0 018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSTPVAPRO 9
Db 145 VSTPVAPRO 153
RESULT 3
Q9DEV2 PRELIMINARY; PRT; 530 AA.
ID Q9DEV2;
AC Q9DEV2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TARGET OF JUN 3.
GN TOJ3.
OS Cuturnix coturnix (common quail).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Cuculix.
OX NCBI_TaxID=9091;
RX MEDLINE=9091;
RP SEQUENCE FROM N.A.
RA Bader A.G., Hartl M., Bister K.;
RT "TOJ3, a novel potential target of the oncogenic transcription factor
RT Jun."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY007310; AAG16624.1; -.
SQ SEQUENCE 530 AA; 57929 MM; E460DB89D9FF490B CRC64;

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Query Match 77.8%; Score 7; DB 13; Length 530;
Best Local Similarity 100.0%; Pred. No. 3;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VSTPVP 7
    1111111
Db 169 VSTPVP 175

RESULT 4
O9HYT7 PRELIMINARY; PRT; 102 AA.
ID O9HYT7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN PA3307.
GN PA3307.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey R.L., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Golty L., Tolentino E., Westbrook-Wadman S., Yan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiser J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT *Complete genomic sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.*;
RL Nature 406:959-964(2000).
DR EMBL; AE004733; AAG0695.1; -.
KW Hypothetical protein.
SQ SEQUENCE 102 AA; 11114 MW; D92FE4B8B95286B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 PVAPQ 9
    11111
Db 27 PVAPQ 32

RESULT 5
O9VX73 PRELIMINARY; PRT; 209 AA.
ID O9VX73;
AC O9VX73;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG5070.0 PROTEIN.
GN CG5070.0.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Modaray C., Morris J., Moshireli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003504; AAF48705.1; -.
DR FlyBase; FBgn0030824; CG5070.
SQ SEQUENCE 209 AA; 19129 MW; E9F5084CDE0E638A CRC64;

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Query Match 66.7%; Score 6; DB 5; Length 209;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VSTPVA 6
    11111
Db 135 VSTPVA 140

RESULT 6
O9FU39 PRELIMINARY; PRT; 237 AA.
ID O9FU39;
AC O9FU39;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE P0001B06.23 PROTEIN.
GN P0001B06.23.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacridae; Oryzae;
OC Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone: P0001B06.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002537; BAB16870.1; -.
SQ SEQUENCE 237 AA; 25810 MW; 972E4FC57C2E39A CRC64;

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Query Match 66.7%; Score 6; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 TPVAPT 8
 Db 220 TPVAPT 225
 RESULT 7
 ID 084512 PRELIMINARY; PRT; 288 AA.
 AC 084512;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHEICAL 32.2 KDA PROTEIN.
 GN C7504.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiales; Chlamydia.
 CX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/UM-3/CX;
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."
 RL Science 282:754-759(1998).
 DR EMBL: AE001323; AAC68105.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 288 AA; 32191 MW; 9B5CAE26D04028B5 CRC64;
 Query Match 66.7%; Score 6; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 STPVAP 7
 Db 131 STPVAP 136
 RESULT 8
 ID 09KYNA PRELIMINARY; PRT; 289 AA.
 AC 09KYNA;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PUTATIVE ARAC-FAMILY TRANSCRIPTIONAL REGULATOR.
 GN SC9H11.05.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteriales; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 CX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA MEDLINE-97000351; PubMed-8843436;
 RA Regenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).

CC -1- SIMILARITY: BELONGS TO THE ARAC/XYLIS FAMILY OF TRANSCRIPTIONAL REGULATORS.
 DR EMBL: AL356592; CAB92194.1; -.
 DR InterPro: IPR000005; -.
 DR Pfam: PF00165; HTH_ARAC. 1.
 DR PRINTS: PR00032; HTHARAC.
 DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
 DR SMART: SM00342; HTH_ARAC; 1.
 KW DNA-binding; Transcription regulation.
 SQ SEQUENCE 289 AA; 31511 MW; F709F9CE93C73F56 CRC64;
 Query Match 66.7%; Score 6; DB 2; Length 289;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TPVAPT 8
 Db 37 TPVAPT 42
 RESULT 9
 ID 09RW05 PRELIMINARY; PRT; 293 AA.
 AC 09RW05;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HYPOTHEICAL 30.8 KDA PROTEIN.
 GN DR0864.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 CX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RI;
 RA MEDLINE-20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.R., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1."
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001940; AAF10447.1; -.
 DR TIGR: DR0864; -.
 KW Hypothetical protein.
 SQ SEQUENCE 293 AA; 30849 MW; 4FA7BFEFF12A0E83 CRC64;
 Query Match 66.7%; Score 6; DB 2; Length 293;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 STPVAP 7
 Db 227 STPVAP 232
 RESULT 10
 ID 086673 PRELIMINARY; PRT; 447 AA.
 AC 086673;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PUTATIVE LIPOPROTEIN.
 GN SCA42.17C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteriales; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 -RC STRAIN-A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Parthill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA MEDLINE-97000351; PubMed-8843436;
 RX Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb streptomycetes cellicoar A3(2) chromosome.";
 RL MOL. Microbiol. 21:77-96(1996).
 DR EMBL: AL031182; CAA20169.1; -;
 KM Lipoprotein.
 SQ SEQUENCE 447 AA; 46712 MW; 809E0091B7834D80 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
 DB 63 TPVAPT 68

RESULT 11
 O9XTQ9 PRELIMINARY; PRT; 460 AA.
 AC O9XTQ9;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE H13N06.2 PROTEIN.
 GN H13N06.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Leonard N.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons N., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Thierly-Mieg J., Thomas C., Sonhammer E., Staden R., Sulston J.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: 299942; CAB17068.1; -;
 DR InterPro: IPR002035; -;
 DR Pfam: PF00092; vva; 1;
 SQ SEQUENCE 460 AA; 49872 MW; 54FA0FAC48B8AD8A CRC64;

Query Match 66.7%; Score 6; DB 5; Length 460;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
 DB 73 TPVAPT 78

RESULT 12
 ID 008484 PRELIMINARY; PRT; 637 AA.
 AC 008484: 000028;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CHROMOSOME XV READING FRAME ORF YOR070C.
 GN YOR29-21 OR GYPL.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bohn C., Bolotin-Fukuhara M., Daignan-Fornier B., Dang D.V.,
 RA Valens M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97279235; PubMed-9133743;
 RA Valens M., Bohn C., Daignan-Fornier B., Dang V., Bolotin-Fukuhara M.;
 RT "The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the
 presence of two tRNAs and 24 new open reading frames.";
 RL Yeast 13:379-390(1997).
 DR EMBL: 274978; CAA99263.1; -;
 DR EMBL: 270678; CAA94555.1; -;
 DR SGD: S0005596; GYPL.
 DR InterPro: IPR00195; -;
 DR Pfam: PR00566; TBC; 1;
 DR SMART: SM00164; TBC; 1;
 SQ SEQUENCE 637 AA; 73289 MW; 08C1A26B6ED37E13 CRC64;

Query Match 66.7%; Score 6; DB 3; Length 637;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
 DB 181 TPVAPT 186

RESULT 13
 ID 09VW35 PRELIMINARY; PRT; 652 AA.
 AC 09VW35;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE CG8743 PROTEIN.
 GN CG8743.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY; PubMed-10731132;
 RA MEDLINE-20196006; Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adams M.D., Celisner S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolashkov S.,
 RA Borkova D., Botchan M.R., Boucek J., Brokstein P., Brothier P.,
 RA Butts K.C., Butnam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hosteln D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mecklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E.C., Spadling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003516; AAF49118.1; -
 DR FlyBase; FBgn0036904; CG8743.
 DR InterPro; IPR001682; -
 DR InterPro; IPR002111; -
 SQ SEQUENCE 652 AA; 74251 MW; 21989FCE490235E4 CRC64;

Query Match 66.7%; Score 6; DB 5; Length 652;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STVPAP 7
 |||||
 Db 51 STVPAP 56

RESULT 14
 09P5T7 PRELIMINARY; PRT; 748 AA.
 ID 09P5T7;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE GLUCAN 1, 4-ALPHA-GLUCOSIDASE RELATED PROTEIN.
 GN B5022.150.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 ON NCBI_Taxid=5141;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Schulte U., Algen V., Hohnsels J., Brandt P., Fartmann B., Holland R.,
 RA Nykatura G., Kewes H.W., Mannhaupt G.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN 12;
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL355932; CAB91434.1; -
 SQ SEQUENCE 748 AA; 79293 MW; 39316E2D4C37848A CRC64;

Query Match 66.7%; Score 6; DB 3; Length 748;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVA 6
 |||||
 Db 506 VSTPVA 511

RESULT 15
 022907 PRELIMINARY; PRT; 748 AA.
 ID 022907;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 GN RNA HELICASE ISOLG.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_Taxid=3702;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV COLUMBIA;
 RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
 RA Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
 RA Venter J.C.;
 RL submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
 CC -1- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
 DR EMBL: AC002337; AAB63833.1; -
 DR Mendel; 26537; Atacth; 26537.
 DR InterPro; IPR000629; -
 DR InterPro; IPR001410; -
 DR InterPro; IPR001650; -
 DR Pfam; PF002270; DEAD_1;
 DR Pfam; PF002271; helicase_C_1;
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 DR SMART; SM00490; HELIC_C; 1.
 KW ATP-binding; Helicase; RNA-binding.
 SQ SEQUENCE 748 AA; 81590 MW; 3F2FD0D5722D7364 CRC64;

Query Match 66.7%; Score 6; DB 10; Length 748;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPQ 9
 |||||
 Db 725 PVAPQ 730

RESULT 16
 09HF24 PRELIMINARY; PRT; 750 AA.
 ID 09HF24;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE REPRSED BY TUP1 PROTEIN 1.
 GN RB1.

OS *Candida albicans* (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; *Candida*.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20253093; PubMed=10790384;
 RA Braun B.R., Johnson A.D.;
 RT "TUP1, CPH1 and ERG1 make independent contributions to filamentation
 in *Candida albicans*.";
 RL Genetics 155:57-67(2000).
 RP [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20435724; PubMed=10978273;
 RA Braun B.R., Head W.S., Wang M.X., Johnson A.D.;
 RT "Identification and characterization of TUP1-regulated genes in
Candida albicans.";
 RL Genetics 156:31-44(2000).
 DR EMBL: AF254142; AAG09787.1;
 SQ SEQUENCE 750 AA; 76351 MW; 3B1C0C8EEAFCD72 CRC64;

Query Match 66.7%; Score 6; DB 3; Length 750;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STRVAP 7
 Db 650 STRVAP 655

RESULT 17
 O9VB49 PRELIMINARY; PRT; 775 AA.
 AC O9VB49;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CG3361 PROTEIN.
 GN CG3361.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Neilson C.R., Milos G.L.G.,
 RA Abell J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Boltskov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wattam D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003760; AAF5694.1;
 DR Flybase: FBgn0039507; CG3361.
 SQ SEQUENCE 775 AA; 85777 MW; AA3D5C6D6F871160 CRC64;

Query Match 66.7%; Score 6; DB 5; Length 775;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STRVAP 7
 Db 358 STRVAP 363

RESULT 18
 O9UAG1 PRELIMINARY; PRT; 792 AA.
 ID O9UAG1;
 AC O9UAG1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SALX-5.
 DE Ephydatta fluviatilis.
 OS Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haptosclerida; Spongillidae; Ephydatta.
 OX NCBI_TaxID=31350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99332084; PubMed=10405173;
 RA Suga H., Ono K., Miyata T.;
 RT "Multiple TGF-beta receptor related genes in sponge and ancient gene
 duplication before the parazoan-eumetazoan split.";
 RL FEBS Lett. 453:346-350(1999).
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB026828; BAA82605.1;
 DR InterPro: IPR000719;
 DR InterPro: IPR002290;
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR SMART: SM00220; S_TKc; 1.
 KW ATP-binding, Serine/threonine-protein kinase, Transferase.
 SQ SEQUENCE 792 AA; 85470 MW; CEDICFOCFCE523 CRC64;

Query Match 66.7%; Score 6; DB 5; Length 792;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 8
 Db 575 TPVAPT 580

RESULT 19
 O9VVA8 PRELIMINARY; PRT; 819 AA.
 ID O9VVA8;
 AC O9VVA8;

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DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE CG16807 PROTEIN.
GN CG16807.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisl M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RC Science 287:2185-2195(2000).
CL -1- SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.
DR EMBL: AE003527; AAF49474.1; -
DR FlyBase: FBgn0036621; CG16807.
DR InterPro: IPR000571; -
DR InterPro: IPR001841; -
DR Pfam: PF00097; 2f-C3HC4; 1.
DR Pfam: PF00642; 2f-CCCH; 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR ZINC_Finger.
SQ SEQUENCE 819 AA; 90376 MW; 33DA29076EDE7E2E CRC64;

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Query Match 66.7%: Score 6; DB 5; Length 819;
Best Local Similarity 100.0%; Pred. NO. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PVAPTO 9
|11111|
DB 563 PVAPTO 568

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RESULT 20
ID 09VEX7 PRELIMINARY; PRT; 904 AA.
AC 09VEX7;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE CG6889 PROTEIN.
GN CG6889.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisl M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RC Science 287:2185-2195(2000).
DR EMBL: AE003712; AAF55288.1; -
DR FlyBase: FBgn0040071; tara.
DR InterPro: IPR00104; -
DR PRINTS: PR00308; ANTIFREEZE1.
SQ SEQUENCE 904 AA; 94862 MW; 084F49645F5A6998 CRC64;

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Query Match 66.7%: Score 6; DB 5; Length 904;
Best Local Similarity 100.0%; Pred. NO. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TPVAPT 8
|11111|
DB 706 TPVAPT 711

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RESULT 21

Q9NHC1 PRELIMINARY; PRT; 912 AA.
AC Q9NHC1: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TARA 1B ISOFORM.
GN TARA OR CG6889.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Calgano S.T., Boube M., Cribbs D.L., Bourbon H.M.;
RT "taranis, a novel trithorax-group of homeotic gene activators, encodes
RT two protein isoforms related to the human cell-cycle regulator
RT p34(Sei-1).";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF227212; AAF43018.1; -
DR Flybase: FBgn0040071; tara.
DR InterPro: IPR000104; -
DR PRINTS: PR00308; ANTIFREEZE1.
SQ SEQUENCE 912 AA; 95728 MW; 0DBA6C2FE6B8F3E CRC64;

Query Match 66.7%; Score 6; DB 5; Length 912;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TPVAPT 8
Db 714 TPVAPT 719

RESULT 22

Q9NHB9 PRELIMINARY; PRT; 912 AA.
AC Q9NHB9: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TARA 1B ISOFORM.
GN TARA OR CG6889.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Calgano S.T., Boube M., Cribbs D.L., Bourbon H.M.;
RT "taranis, a novel member of the trithorax-group of homeotic gene
RT activators from Drosophila, encodes two protein isoforms related to
RT the human cell-cycle regulator p34(Sei-1).";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF227213; AAF43020.1; -
DR Flybase: FBgn0040071; tara.
DR InterPro: IPR000104; -
DR PRINTS: PR00308; ANTIFREEZE1.
SQ SEQUENCE 912 AA; 95698 MW; 1CAB7D3EFF7F544E CRC64;

Query Match 66.7%; Score 6; DB 5; Length 912;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TPVAPT 8
Db 714 TPVAPT 719

RESULT 23

Q9NHC2 PRELIMINARY; PRT; 916 AA.
AC Q9NHC2: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TARA 1A ISOFORM.
GN TARA OR CG6889.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Calgano S.T., Boube M., Cribbs D.L., Bourbon H.M.;
RT "taranis, a novel member of the trithorax-group of homeotic gene
RT activators, encodes two protein isoforms related to the human cell-
RT cycle regulator p34(Sei-1).";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF227211; AAF43017.1; -
DR Flybase: FBgn0040071; tara.
DR InterPro: IPR000104; -
DR PRINTS: PR00308; ANTIFREEZE1.
SQ SEQUENCE 916 AA; 96272 MW; A67D331E012FA39E CRC64;

Query Match 66.7%; Score 6; DB 5; Length 916;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TPVAPT 8
Db 718 TPVAPT 723

RESULT 24

Q9NHC0 PRELIMINARY; PRT; 916 AA.
AC Q9NHC0: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TARA 1A ISOFORM.
GN TARA OR CG6889.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Calgano S.T., Boube M., Cribbs D.L., Bourbon H.M.;
RT "taranis, a novel member of the trithorax-group of homeotic gene
RT activators from Drosophila, encodes two protein isoforms related to
RT the human cell-cycle regulator p34(Sei-1).";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF227213; AAF43019.1; -
DR Flybase: FBgn0040071; tara.
DR InterPro: IPR000104; -
DR PRINTS: PR00308; ANTIFREEZE1.
SQ SEQUENCE 916 AA; 96242 MW; B76C220F103B98EE CRC64;

Query Match 66.7%; Score 6; DB 5; Length 916;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TPVAPT 8
Db 718 TPVAPT 723

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RESULT 25
ID 09VS50 PRELIMINARY: PRT: 1052 AA.
AC 09VS50:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CG8598 PROTEIN.
GN CG8598
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abmayant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein J., Brotler P.,
RA Botkin D.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de la Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Goddek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houtlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani B.E., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodali C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gidbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003559; AAF50579.1; -
DR FlyBase: FBgn0035766; CG8598.
DR InterPro: IPR001969; -
DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 1052 AA; 117413 MW; 5DAAE81BB3B12580 CRC64;

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Query Match 66.7%; Score 6; DB 5; Length 1052;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 STVPAP 7
|11111|
Db 383 STVPAP 388

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RESULT 26
ID 000203 PRELIMINARY: PRT: 1094 AA.
AC 000203: 000580;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE BETA-ADAPTIN 3A (AP-3 COMPLEX BETA3A SUBUNIT) (CEREBELLAR DEGENERATION
DE ANTIGEN BETA-NAP HOMOLOG BETA-3A).
GN ADB3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=HEART;
RX MEDLINE=97296491; PubMed=9151686;
RA Simpson F., Peden A.A., Christopoulou L., Robinson M.S.;
RT "Characterization of the adaptor-related protein complex, AP-3.";
RL J. Cell Biol. 137:835-845(1997).
[2]
RN
RP SEQUENCE FROM N.A., PHOSPHORYLATION, AND TISSUE SPECIFICITY.
RC TISSUE=PANCREAS;
RX MEDLINE=97326075; PubMed=9182526;
RA Dell'Angelica E.C., Ooi C.E., Bonifacio J.S.;
RT "Beta3A-adaptin, a subunit of the adaptor-like complex AP-3.";
RL J. Biol. Chem. 272:15078-15084(1997).
[3]
RN
RP HERMANSKY-PUDLAK SYNDROME (HPS) DISEASE.
RC TISSUE=SKIN FIBROBLAST, AND PERIPHERAL BLOOD;
RX MEDLINE=99149014; PubMed=10024875;
RA Dell'Angelica E.C., Shetlerauk V., Aguilar R.C., Gahl W.A.,
RA Bonifacio J.S.;
RT "Altered trafficking of lysosomal proteins in Hermansky-Pudlak
RT syndrome due to mutations in the beta 3a subunit of the AP-3
RT adaptor.";
RL Mol. Cell 3:11-21(1999).
CC -1- FUNCTION: PART OF THE AP-3 COMPLEX, AN ADAPTOR-RELATED COMPLEX
CC WHICH IS NOT CLATHRIN-ASSOCIATED. THE COMPLEX IS ASSOCIATED WITH
CC THE GOLGI REGION AS WELL AS MORE PERIPHERAL STRUCTURES. IT
CC FACILITATES THE BUDDING OF VESICLES FROM THE GOLGI MEMBRANE AND
CC MAY BE DIRECTLY INVOLVED IN TRAFFICKING TO LYOSOMES.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 3 (AP-3) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (DELTA AND BETA3), A MEDIUM CHAIN
CC (WU3) AND A SMALL CHAIN (SIGMA3). EXPRESSED.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- PTM: PHOSPHORYLATED ON SERINE.
CC -1- DISEASE: DEFECTS IN ADB3A ARE THE CAUSE OF HERMANSKY-PUDLAK
CC SYNDROME (HPS), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY
CC OCULOCUTANEOUS ALBINISM AND PLATELET STORAGE POOL DEFICIENCY.
CC -1- SIMILARITY: BELONGS TO THE ADAPTER COMPLEXES LARGE SUBUNITS
CC FAMILY.
CC EMBL: U01931; AAD03778.1; -
CC EMBL: U81504; AAB61638.1; -
CC MIM: 203300; -
CC MIM: 603401; -
CC InterPro: IPR002553; -
CC Pfam: PF01602; Adaptin_N; 1.
CC Albinism; Disease mutation; Golgi stack; phosphorylation;
CC Polymorphism; Protein transport; transport.
CC VARIANT 390 410 MISSING (IN HPS).
CC VARIANT 580 580 L->R (IN HPS).
CC CONFLICT 804 804 MISSING (IN REF. 1).
CC SEQUENCE 1094 AA; 121349 MW; AC683CE1BEFE3EB6 CRC64;

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Query Match 66.7%; Score 6; DB 4; Length 1094;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VSTPVA 6

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Db 827 VSTRPA 832

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RESULT 27
ID Q921T1 PRELIMINARY; PRT: 1105 AA.
AC Q921T1:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE AP-3 COMPLEX BETA3A SUBUNIT (ADAPTOR-RELATED PROTEIN COMPLEX AP-3 BETA
DE 1 SUBUNIT).
GN AP3b1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ;
RA Peng L., Seymour A.B., Jiang S.Y., To A., Peden A.A., Novak E.K.,
RA Zhen L., Rusliak M.E., Elcher E.M., Robinson M.S., Gorin M.B.,
RA Swank R.T.;
RT "The Beta3A Subunit Gene (Ap3b1) of the AP-3 Complex is Altered in the
RT Mouse Hypopigmentation Mutant Pearl, a Model for Hermansky Pudlak
RT Syndrome and Night Blindness.";
RL Hum. Mol. Genet. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129S6/SVEVYAC;
RX MEDLINE=20512043; PubMed=11056055;
RA Feng L., Rigatti B.W., Novak E.K., Gorin M.B., Swank R.T.;
RT "Genomic Structure of the Mouse Ap3b1 Gene in Normal and Pearl Mice.";
RL Genomics 69:370-379(2000).
DR EMBL; AF103809; AAC78338.1; -.
DR EMBL; AF255589; AAG23622.1; JOINED.
DR EMBL; AF255567; AAG23622.1; JOINED.
DR EMBL; AF255566; AAG23622.1; JOINED.
DR EMBL; AF255569; AAG23622.1; JOINED.
DR EMBL; AF255570; AAG23622.1; JOINED.
DR EMBL; AF255576; AAG23622.1; JOINED.
DR EMBL; AF255571; AAG23622.1; JOINED.
DR EMBL; AF255572; AAG23622.1; JOINED.
DR EMBL; AF255573; AAG23622.1; JOINED.
DR EMBL; AF255574; AAG23622.1; JOINED.
DR EMBL; AF255575; AAG23622.1; JOINED.
DR EMBL; AF255576; AAG23622.1; JOINED.
DR EMBL; AF255577; AAG23622.1; JOINED.
DR EMBL; AF255578; AAG23622.1; JOINED.
DR EMBL; AF255579; AAG23622.1; JOINED.
DR EMBL; AF255580; AAG23622.1; JOINED.
DR EMBL; AF255581; AAG23622.1; JOINED.
DR EMBL; AF255582; AAG23622.1; JOINED.
DR EMBL; AF255583; AAG23622.1; JOINED.
DR EMBL; AF255584; AAG23622.1; JOINED.
DR EMBL; AF255585; AAG23622.1; JOINED.
DR EMBL; AF255586; AAG23622.1; JOINED.
DR EMBL; AF255587; AAG23622.1; JOINED.
DR EMBL; AF255588; AAG23622.1; JOINED.
DR MGD; MGI:133879; Ap3b1.
DR InterPro; IPR000130; -.
DR InterPro; IPR002553; -.
DR Pfam; PF01602; Adaplin_N.1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 1105 AA; 122869 MW; 586B818CE4FB5ABE CRC64;

```

Query Match 66.7%; Score 6; DB 11; Length 1105;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTRPA 6

Db 838 VSTRPA 843

|||||

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RESULT 28
ID Q9LBG3 PRELIMINARY; PRT: 1653 AA.
AC Q9LBG3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PAA.
GN PAA.
OS Streptococcus criceti.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1333;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E49;
RA Tamura H., Kato H.;
RT "Cell surface antigen I/II - Streptococcus cricetus.";
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042239; BAA95000.1; -.
DR InterPro; IPR001899; -.
DR InterPro; IPR002965; -.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SQ SEQUENCE 1653 AA; 180862 MW; 93F28E215BF598DE CRC64;

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Query Match 66.7%; Score 6; DB 2; Length 1653;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPQ 9
 Db 955 PVAPQ 960

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RESULT 29
ID Q9PVZ2 PRELIMINARY; PRT: 2037 AA.
AC Q9PVZ2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NUCLEOPORIN CAN.
GN CAN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99384295; PubMed=10454574;
RA Askjaer P., Bachl A., Wilm M., Bischoff R., Weeks D.L., Ogniewski V.,
RA Ohno M., Niehrs C., Kjems J., Matlej I.W., Forrester M.;
RT "RangRP-regulated interactions of CRM1 with nucleoporins and a
RT shuttling DEAD-box helicase.";
RL Mol. Cell. Biol. 19:6276-6285(1999).
DR EMBL; AJ243889; CAB53357.1; -.
DR InterPro; IPR000515; -.
DR InterPro; IPR001680; -.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; UNKNOWN_1.
DR SMART; SM00320; WD40; 1.
DR Pfam; PF01602; Adaplin_N.1.
SQ SEQUENCE 2037 AA; 208931 MW; 225DEA49A0435635 CRC64;

```

Query Match 66.7%; Score 6; DB 13; Length 2037;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVAP 7
Db 1052 STPVAP 1057

RESULT 30

09YIV2 PRELIMINARY; PRT; 49 AA.
ID 09YIV2
AC 09YIV2;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE PEDIBIN PRECURSOR.
GN PED.
OS Hydra magnipapillata (Hydra), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Hydrozoa; Hydroids; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_Taxid=6085, 6087;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-H.magnipapillata; STRAIN-105;
RA Takahashi T., Hotta M., Fujisawa T.;
RT "Foot dominant expression of the foot activating peptide, Hym-346/Pedibin, in hydra."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-H.magnipapillata; STRAIN-105;
RA MEDLINE=99094877; PubMed=9876180;
RX Greens A., Shimizu H., Hoffmeister S., Bode H., Fujisawa T.;
RT "The novel signal peptides, pedibin and Hym-346, lower positional
value thereby enhancing foot formation in hydra."
RL Development 126:517-524(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-H.attenuata;
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
peptides from Hydra vulgaris."
RL Development 122:1941-1948(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-H.attenuata;
RA Hoffmeister S.A.H., Herrmann D.;
RT "Cloning of the foot-formation activating peptide pedibin from Hydra
vulgaris."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-H.attenuata; S.A.H., Herrmann D.;
RA Hoffmeister-Ullrich S.A.H., Herrmann D.;
RL EMBL; AB030084; BAA82554.1; -;
DR EMBL; AF179908; AAF01282.1; -;
KM Signal.
FT SIGNAL. 1 28 POTENTIAL.
FT CHAIN 29 49 PEDIBIN.
SQ SEQUENCE 49 AA; 5373 MW; FAF5543F0DF3B92A CRC64;

Query Match 55.6%; Score 5; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPV 5
Db 7 STPV 11

RESULT 31

047006 PRELIMINARY; PRT; 62 AA.
ID 047006
AC 047006;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE FLAGELLIN (FRAGMENT).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=045:H23 (ECRC H23);
RA Kwang J., Wilson R., Yang S., He T.;
RL Clin. Diagn. Lab. Immunol. 0:0-0(0).
DR EMBL; U57313; AAB01993.1; -;
FT NON_TER 1 1
FT NON_TER 62 62
SQ SEQUENCE 62 AA; 6217 MW; 6BF545C9F2134414 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
Db 15 TPVAP 19

RESULT 32

09RRH1 PRELIMINARY; PRT; 75 AA.
ID 09RRH1
AC 09RRH1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 7.7 KDA PROTEIN.
GN DR2520.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_Taxid=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE002081; AAF12064.1; -;
DR TIGR; DR2520; -;
KM Hypothetical protein.
SQ SEQUENCE 75 AA; 7704 MW; EBE47B7BAE33B0E CRC64;

Query Match 55.6%; Score 5; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VAPRO 9
Db 24 VAPRO 28


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RESULT 33
ID 017728 PRELIMINARY: PRT: 82 AA.
AC 017728:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C06E4.2 PROTEIN.
GN C06E4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaiden N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mleg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Du Z., Gattung S.;
RA Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Waterston R.;
RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U41277; AAA82477.1;
SQ SEQUENCE 82 AA; 9058 MW; EECAC722EBB12586 CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 5; Length 82;
Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPTO 9
DB 40 VAPTO 44

RESULT 34
ID P91335 PRELIMINARY: PRT: 88 AA.
AC P91335:
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C05MID F55C7.
GN F55C7.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaiden N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mleg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Du Z., Le T.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U80436; AAC71107.1;
SQ SEQUENCE 88 AA; 9771 MW; 59FB61FDD7C0CE3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 5; Length 88;
Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
DB 31 STPVA 35

RESULT 35
ID 067673 PRELIMINARY: PRT: 94 AA.
AC 067673:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE HEXON PROTEIN (FRAGMENT).
OS porcine adenovirus sp.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=47901;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LUNG;
RA Pring-Akerdrom P.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X95630; CAA64884.1;
DR HSSP: P03277; IDHX.
DR InterPro: IPR000736;
DR Pfam: PF01065; Adeno_hexon; 1.
KW Hexon Protein.
FT NON_TER 1 1
FT NON_TER 94 94
SQ SEQUENCE 94 AA; 10807 MW; 2646FBEB97DDCC9FD CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 14; Length 94;
Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPTO 9
DB 39 VAPTO 43

RESULT 36
ID 090YD6 PRELIMINARY: PRT: 95 AA.
AC 090YD6:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

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RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaiden N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mleg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Du Z., Le T.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U80436; AAC71107.1;
SQ SEQUENCE 88 AA; 9771 MW; 59FB61FDD7C0CE3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 5; Length 88;
Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
DB 31 STPVA 35

RESULT 35
ID 067673 PRELIMINARY: PRT: 94 AA.
AC 067673:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE HEXON PROTEIN (FRAGMENT).
OS porcine adenovirus sp.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=47901;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LUNG;
RA Pring-Akerdrom P.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X95630; CAA64884.1;
DR HSSP: P03277; IDHX.
DR InterPro: IPR000736;
DR Pfam: PF01065; Adeno_hexon; 1.
KW Hexon Protein.
FT NON_TER 1 1
FT NON_TER 94 94
SQ SEQUENCE 94 AA; 10807 MW; 2646FBEB97DDCC9FD CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 14; Length 94;
Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VAPTO 9
DB 39 VAPTO 43

RESULT 36
ID 090YD6 PRELIMINARY: PRT: 95 AA.
AC 090YD6:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

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DE SMALL INDUCIBLE CYTOKINE A12 PRECURSOR.
GN SCYA12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JL/J; TISSUE=SPLEEN;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RT Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
RT candidates for ae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
DR EMBL; AF065938; AAF15368.1; -.
DR HSSP; P13500; IDOL.
DR MGD; MGI:108224; Scya12.
DR InterPro; IPR000476; -.
DR InterPro; IPR000827; -.
DR InterPro; IPR001811; -.
DR Pfam; PF00048; IL8; 1.
DR ProDom; PD002047; -; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 95 AA; 10727 MW; 9DB56B029729D0B0 CRC64;

Query Match 55.6%; Score 5; DB 11; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
DB 27 VSTPV 31

RESULT 37
068302 PRELIMINARY; PRT; 95 AA.
AC 068302;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35)]
DE (FRAGMENT).
GN E1.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HCV-BB43;
RA Songsiyilai S., Kanistanon D.;
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL; U23396; AAA64862.1; -.
DR InterPro; IPR002519; -.
DR Pfam; PF01539; HCV_env; 1.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 95 AA; 10305 MW; 86270AA69397533A CRC64;

Query Match 55.6%; Score 5; DB 14; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAP 8
DB 23 PVAP 27

RESULT 38
068301 PRELIMINARY; PRT; 102 AA.
AC 068301;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35)]
DE (FRAGMENT).
GN E1.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HCV-BB8;
RA Songsiyilai S., Kanistanon D.;
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL; U23395; AAA64861.1; -.
DR InterPro; IPR002519; -.
DR Pfam; PF01539; HCV_env; 1.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 11040 MW; 2C560825E0AD043E CRC64;

Query Match 55.6%; Score 5; DB 14; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAP 8
DB 24 PVAP 28

RESULT 39
093516 PRELIMINARY; PRT; 108 AA.
AC 093516;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE SALMOSIN2 (FRAGMENT).
OS Gloydius halys brevicaudus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=66175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Park D.S., Kim H.D., Chung K.H., Kim D.S., Yun Y.D.;
RT "Cloning and Characterization of Novel Disintegrins from Agkistrodon
RT halys venom.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF055337; AAC42597.1; -.
DR HSSP; P18619; IFVL.
DR InterPro; IPR001762; -.
DR Pfam; PF00200; disintegrin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR SMART; SM00050; DISIN; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 11726 MW; 573F0B6918970C8C CRC64;

Query Match
Best Local Similarity 55.6%; Score 5; DB 13; Length 108;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
11111
DB 25 VSTPV 29

RESULT 40

O97949 PRELIMINARY; PRT; 114 AA.
AC O97949:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE BETA-MICROSEMINOPROTEIN PRECURSOR.
GN MSP-J1.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxId=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundwall A., Makinen M.;
RT "Molecular cloning of genes encoding beta-microseminoprotein from the cotton-top tamarin."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010155; CAB38123.1; -.
DR EMBL; AJ010156; CAB38123.1; JOINED.
DR EMBL; AJ010157; CAB38123.1; JOINED.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 114 AA; 12746 MW; F3F05B013445BAD4 CRC64;

Query Match
Best Local Similarity 55.6%; Score 5; DB 6; Length 114;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
11111
DB 73 VSTPV 77

RESULT 41

O97935 PRELIMINARY; PRT; 114 AA.
AC O97935:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE BETA-MICROSEMINOPROTEIN PRECURSOR.
GN MSP-E1.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxId=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundwall A., Makinen M.;
RT "Molecular cloning of genes encoding beta-microseminoprotein from the cotton-top tamarin."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010154; CAB38105.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 114 AA; 12738 MW; 05E7A410125C94B2 CRC64;

Query Match
Best Local Similarity 55.6%; Score 5; DB 6; Length 114;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
11111
DB 73 VSTPV 77

RESULT 42

O56724 PRELIMINARY; PRT; 115 AA.
AC O56724; O56723;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE DELTA-SUBUNIT, METHYLMALONYL-COA DECARBOXYLASE.
OS Veillonella parvula.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Sporomusa subbranch; Veillonella.
OX NCBI_TaxId=29466;
RN [1]
RP SEQUENCE FROM N.A.
RA Huder J.B., Dimroth P.;
RL J. Biol. Chem. 0:0-0(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94043308; PubMed=8227015;
RA Huder J.B., Dimroth P.;
RT "Sequence of the sodium ion pump methylmalonyl-CoA decarboxylase from Veillonella parvula."
RT J. Biol. Chem. 268:24564-24571(1993).
DR EMBL; Z24754; CA80873.1; -.
DR EMBL; U22208; AAC36821.1; -.
SQ SEQUENCE 115 AA; 11951 MW; 3F873586E596EC26 CRC64;

Query Match
Best Local Similarity 55.6%; Score 5; DB 2; Length 115;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
11111
DB 60 TPVAP 64

RESULT 43

O9W2V1 PRELIMINARY; PRT; 115 AA.
AC O9W2V1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CG12640 PROTEIN.
GN CG12640.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abigail J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbagam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svrstkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gldbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003450; AAF6587.1; -
 DR FlyBase: FBgn0030202; CG12640.
 DR InterPro: IPR001745; -
 DR PROSITE: PS00627; GHMP_KINASES_ATP; UNKNOWN.1.
 SQ SEQUENCE 115 AA; 12840 MW; 7975280AB7AFBD79 CRC64;

Query Match 55.6%; Score 5; DB 5; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
 Db 32 TPVAP 36

RESULT 44
 ID 090222 PRELIMINARY; PRT: 115 AA.
 AC 090222;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 PR PRO-HALYSTATIN 3 (FRAGMENT).
 OS Agkistrodon halys pallas (Chinese water moccasin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Gloydius.
 OC NCBI_Taxid=8714;
 OX 1;
 RN SEQUENCE FROM N.A.
 RP TISSUE=LIVER.
 RC Fujisawa Y., Kuroda S., Notoya K., Konishi H., Terashita Z.,
 RA "Halystatin, a novel disintegrin from agkistrodon halys, is a potent
 RT inhibitor of bone resorption and platelet aggregation.";
 RL Takeida Kenkusho Ho 53:39-56(1994).
 CC -1- STIMILARITY: CONTAINS A DISINTEGRIN DOMAIN.
 DR EMBL: D28871; BAA06026.1; -
 DR HSSP: P18619; IFLV.
 DR MEROPS: M12.134; -
 DR InterPro: IPR001590; -
 DR InterPro: IPR001762; -
 DR Pfam: PF00200; disintegrin.1.
 DR PRINTS: PR00289; DISINTEGRIN.

DR PROSITE: PS50215; ADAM_MEROP; 1.
 DR PROSITE: PS00427; DISINTEGRIN.1; 1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR SMART: SM00050; DISIN: 1.
 KW Blood coagulation; Platelet; Cell adhesion; Venom.
 FT NON_TER 1
 SQ SEQUENCE 115 AA; 12389 MW; 00C085D94635A274 CRC64;

Query Match 55.6%; Score 5; DB 13; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 Db 34 VSTPV 38

RESULT 45
 ID 09X0K8 PRELIMINARY; PRT: 117 AA.
 AC 09X0K8;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN TM1124.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OC NCBI_Taxid=2336;
 OX 1;
 RN SEQUENCE FROM N.A.
 RP STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RL genome sequence of *Thermotoga maritima*.";
 RL Nature 399:323-329(1999).
 DR EMBL: AE001770; AAD36200.1; -
 DR TIGR: TM1124; -
 SQ SEQUENCE 117 AA; 13692 MW; BDB44AF940E1A95 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
 Db 30 STPVA 34

RESULT 46
 ID 09NZE0 PRELIMINARY; PRT: 117 AA.
 AC 09NZE0;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE BM-016.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX 1;
 RN SEQUENCE FROM N.A.
 RP TISSUE=BONE MARROW;
 RC Zhao M., Song H., Li N., Peng Y., Han Z., Chen Z.;

RT "A novel gene expressed in human bone marrow."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF208858; AAF64272.1; -
 SQ SEQUENCE 117 AA: 12834 MW: D7A64D8378BD7983 CRC64:

Query Match 55.6%; Score 5; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 |||||
 DB 43 VSTPV 47

RESULT 47
 O9VWMO PRELIMINARY: PRT: 117 AA.
 AC O9VWMO:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG15883 PROTEIN.
 GN CG15883.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champé M., Pfeiffer G.L.G.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Adair J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borovica D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li Z., Liang Y., Lin X.,
 RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Modary C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relbert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spirdling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter L., Wang A.H., Wang X.,
 RA Wang Z.-Y., Weissman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 DR EMBL: AE003511; AAF48918.1; -
 DR Flybase: FBgn0030985; CG15883.

SQ SEQUENCE 117 AA: 12897 MW: 085AA0062082827E CRC64:

Query Match 55.6%; Score 5; DB 5; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
 |||||
 DB 35 STPVA 39

RESULT 48
 O90221 PRELIMINARY: PRT: 117 AA.
 AC O90221:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PREPRO-HALYSTATIN 2 (FRAGMENT).
 OS Agkistrodon halys palas (Chinese water moccasin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperae; Crotalinae; Gloydius.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Fujisawa Y., Kuroda S., Notoya K., Konishi H., Terashita Z.,
 RT "Halystatin, a novel disintegrin from agkistrodon halys, is a potent
 RT inhibitor of bone resorption and platelet aggregation.";
 RL Takeda Kenkyusho Ho 53:39-56(1994).
 CC -1- SIMILARITY: CONTAINS A DISINTEGRIN DOMAIN.
 DR EMBL: D28871; BA06027.1; -
 DR HSP: P18619; IFWL.
 DR MEROPS: M12.134; -
 DR Interpro: IPR001590; -
 DR Interpro: IPR001762; -
 DR Pfam: PF00200; disintegrin.1.
 DR PRINTS: PR00289; DISINTEGRIN.
 DR PROSITE: PS50215; ADAM_MEROP.1.
 DR PROSITE: PS50427; DISINTEGRIN.1.
 DR PROSITE: PS50214; DISINTEGRIN.2; 1.
 DR SMART: SM00050; DISIN.1.
 KW Blood coagulation; Platelet; Cell adhesion; Venom.
 FT NON-TER 1
 SQ SEQUENCE 117 AA: 12686 MW: B1F9A98056BAB07B CRC64:

Query Match 55.6%; Score 5; DB 13; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
 |||||
 DB 34 VSTPV 38

RESULT 49
 O9N3V1 PRELIMINARY: PRT: 121 AA.
 AC O9N3V1:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL PROTEIN Y47D7A.H.
 GN Y47D7A.H.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Felodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;
 RX MEDLINE-99069613; PubMed-9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 EMBL: AC024790; AAF0636.1;
 SQ SEQUENCE 121 AA; 13441 MW; FF21FD197434C60F CRC64;

Query Match 55.6%; Score 5; DB 5; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
 |||||
 Db 46 PVAPT 50

RESULT 50
 O23980 PRELIMINARY; PRT; 121 AA.
 AC O23980;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE COLD-REGULATED PROTEIN (FRAGMENT).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
 OC Hordeum.
 OX NCBI_TaxID-4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. GIORGIE; TISSUE-LEAF;
 RA Cattiveili L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. GIORGIE; TISSUE-LEAF;
 RA Cattiveili L.; Bartels D.;
 RL Plant Physiol. 93:1504-1510(1990).
 DR EMBL: AJ000100; CAA03925.1;
 DR Mendel; 25606; Horvu;1290;25606.
 FT NON_TER 1
 SQ SEQUENCE 121 AA; 12484 MW; 1B2A44C69C189735 CRC64;

Query Match 55.6%; Score 5; DB 10; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
 |||||
 Db 84 TPVAP 88

Search completed: August 15, 2001, 12:42:32
 Job time: 517 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2001, 12:32:55 ; Search time 31.32 Seconds
(without alignments)
5.917 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 9

Sequence: 1 VSTPVAPTQ 9

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 197339 seqs, 20590346 residues

Word size : 0

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Issued Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	2	US-08-456-670B-26
2	9	100.0	21	1	US-08-127-499A-27
3	9	100.0	21	1	US-08-482-847-27
4	9	100.0	232	2	US-08-456-670B-39
5	9	100.0	478	2	US-08-456-670B-40
6	9	100.0	484	1	US-08-127-499A-26
7	9	100.0	484	1	US-08-482-847-26
8	8	88.9	12	2	US-08-456-670B-30
9	6	66.7	10	2	US-08-456-670B-31
10	6	66.7	20	2	US-08-456-670B-17
11	5	55.6	11	4	US-09-001-984C-55
12	5	55.6	94	1	US-07-899-535A-1
13	5	55.6	192	1	US-08-086-428B-57
14	5	55.6	192	1	US-08-440-103-44
15	5	55.6	192	1	US-08-440-542-44
16	5	55.6	192	1	US-08-231-368-44
17	5	55.6	192	1	US-08-440-210-44
18	5	55.6	192	2	US-08-468-570-57
19	5	55.6	192	2	US-08-290-665A-57
20	5	55.6	192	4	US-08-444-818-167
21	5	55.6	192	5	PCR-US95-10398-57
22	5	55.6	264	3	US-08-969-644-12
23	5	55.6	264	3	US-08-444-189-12
24	5	55.6	264	4	US-08-465-465-2
25	5	55.6	264	4	US-08-468-544-12
26	5	55.6	286	1	US-08-382-184-3
27	5	55.6	286	2	US-08-641-356-3

28	5	55.6	286	4	US-09-132-528-4	Sequence 4, Appl
29	5	55.6	286	4	US-08-875-494-3	Sequence 3, Appl
30	5	55.6	325	1	US-08-382-184-2	Sequence 2, Appl
31	5	55.6	325	2	US-08-641-356-2	Sequence 2, Appl
32	5	55.6	325	4	US-09-132-528-2	Sequence 2, Appl
33	5	55.6	325	4	US-09-132-528-3	Sequence 3, Appl
34	5	55.6	325	4	US-08-875-494-2	Sequence 2, Appl
35	5	55.6	339	4	US-08-444-818-152	Sequence 152, App
36	5	55.6	339	4	US-08-444-818-156	Sequence 156, App
37	5	55.6	359	1	US-08-137-627-4	Sequence 4, Appl
38	5	55.6	359	2	US-08-865-348-4	Sequence 4, Appl
39	5	55.6	370	3	US-08-969-644-23	Sequence 23, Appl
40	5	55.6	370	3	US-08-444-189-23	Sequence 23, Appl
41	5	55.6	370	4	US-08-468-544-23	Sequence 23, Appl
42	5	55.6	377	2	US-08-853-659A-41	Sequence 41, Appl
43	5	55.6	384	3	US-08-852-824-4	Sequence 4, Appl
44	5	55.6	396	1	US-08-769-309A-15	Sequence 15, Appl
45	5	55.6	396	3	US-08-994-570-15	Sequence 15, Appl
46	5	55.6	401	2	US-08-839-008-5	Sequence 5, Appl
47	5	55.6	422	1	US-08-403-545-4	Sequence 4, Appl
48	5	55.6	422	4	US-08-404-381-4	Sequence 4, Appl
49	5	55.6	428	1	US-08-353-550-1	Sequence 1, Appl
50	5	55.6	428	2	US-08-551-687-1	Sequence 1, Appl
51	5	55.6	431	3	US-08-807-342B-5	Sequence 5, Appl
52	5	55.6	434	2	US-08-710-249-4	Sequence 4, Appl
53	5	55.6	453	1	US-08-769-309A-14	Sequence 14, Appl
54	5	55.6	453	2	US-08-994-570-14	Sequence 14, Appl
55	5	55.6	468	2	US-08-839-008-7	Sequence 7, Appl
56	5	55.6	468	4	US-09-032-523-8	Sequence 8, Appl
57	5	55.6	469	1	US-08-353-550-6	Sequence 6, Appl
58	5	55.6	469	2	US-08-551-687-6	Sequence 6, Appl
59	5	55.6	486	3	US-08-889-841-8	Sequence 8, Appl
60	5	55.6	491	3	US-08-889-841-10	Sequence 10, Appl
61	5	55.6	498	1	US-08-496-885A-6	Sequence 6, Appl
62	5	55.6	498	2	US-08-466-589-12	Sequence 12, Appl
63	5	55.6	498	2	US-08-700-636-12	Sequence 12, Appl
64	5	55.6	498	3	US-08-467-574-12	Sequence 12, Appl
65	5	55.6	501	2	US-08-845-566-1	Sequence 1, Appl
66	5	55.6	501	3	US-08-921-408-4	Sequence 4, Appl
67	5	55.6	605	2	US-08-687-958A-1	Sequence 1, Appl
68	5	55.6	651	1	US-08-769-309A-17	Sequence 17, Appl
69	5	55.6	651	3	US-08-994-570-17	Sequence 17, Appl
70	5	55.6	655	1	US-07-736-178C-2	Sequence 2, Appl
71	5	55.6	670	2	US-08-366-547-2	Sequence 2, Appl
72	5	55.6	671	2	US-08-737-716-13	Sequence 13, Appl
73	5	55.6	685	3	US-08-872-855-2	Sequence 2, Appl
74	5	55.6	739	3	US-09-035-648-24	Sequence 24, Appl
75	5	55.6	739	4	US-09-001-925-24	Sequence 24, Appl
76	5	55.6	788	1	US-08-572-225-1	Sequence 1, Appl
77	5	55.6	933	4	US-08-764-870-14	Sequence 14, Appl
78	5	55.6	1009	2	US-08-680-326-31	Sequence 31, Appl
79	5	55.6	1013	2	US-08-866-650-5	Sequence 5, Appl
80	5	55.6	1013	2	US-09-021-287-5	Sequence 5, Appl
81	5	55.6	1013	2	US-09-021-287-5	Sequence 2, Appl
82	5	55.6	1148	2	US-08-313-185-58	Sequence 58, Appl
83	5	55.6	1148	2	US-09-082-614A-58	Sequence 58, Appl
84	5	55.6	1213	1	US-08-188-582-20	Sequence 20, Appl
85	5	55.6	1213	1	US-08-646-715-20	Sequence 20, Appl
86	5	55.6	1222	2	US-08-682-517-15	Sequence 15, Appl
87	5	55.6	1252	2	US-08-682-517-9	Sequence 9, Appl
88	5	55.6	1253	1	US-07-920-281C-3	Sequence 3, Appl
89	5	55.6	1253	4	US-08-466-277-3	Sequence 3, Appl
90	5	55.6	1449	3	US-08-840-062-6	Sequence 6, Appl
91	5	55.6	1466	2	US-08-687-956A-23	Sequence 23, Appl
92	5	55.6	1627	1	US-07-665-792E-9	Sequence 9, Appl
93	5	55.6	1780	1	US-08-769-309A-5	Sequence 5, Appl
94	5	55.6	2476	3	US-08-994-570-5	Sequence 5, Appl
95	5	55.6	2476	2	US-08-276-967-2	Sequence 2, Appl
96	5	55.6	3418	2	US-08-639-501-2	Sequence 2, Appl
97	5	55.6	3418	2	US-08-603-753D-4	Sequence 4, Appl
98	5	55.6	3418	3	US-09-044-946-2	Sequence 2, Appl
99	5	55.6	3418	3	US-08-755-587-44	Sequence 44, Appl
100	5	55.6	3418	3	US-09-044-908-2	Sequence 2, Appl

101	5	55.6	3418	4	US-09-099-753-4	Sequence 4, Appl1	174	4	44.4	28	2	US-08-392-816-4	Sequence 4, Appl1
102	5	55.6	3418	4	US-08-986-106-4	Sequence 4, Appl1	175	4	44.4	31	1	US-07-829-462-4	Sequence 4, Appl1
103	4	44.4	4	4	US-08-973-462-28	Sequence 28, Appl1	176	4	44.4	31	1	US-08-340-812-4	Sequence 4, Appl1
104	4	44.4	7	1	US-08-261-206A-18	Sequence 18, Appl1	177	4	44.4	31	1	US-08-459-064B-4	Sequence 4, Appl1
105	4	44.4	7	2	US-08-350-260A-421	Sequence 421, App	178	4	44.4	31	1	US-08-488-252-14	Sequence 34, Appl1
106	4	44.4	8	2	US-08-769-745-11	Sequence 11, Appl1	179	4	44.4	31	2	US-08-460-421A-4	Sequence 4, Appl1
107	4	44.4	8	3	US-08-335-733D-38	Sequence 38, Appl1	180	4	44.4	31	2	US-08-023-980B-30	Sequence 30, Appl1
108	4	44.4	8	3	US-08-335-733D-39	Sequence 39, Appl1	181	4	44.4	31	2	US-08-486-953A-25	Sequence 25, Appl1
109	4	44.4	8	3	US-08-335-733D-40	Sequence 40, Appl1	182	4	44.4	31	3	US-08-466-368-16	Sequence 16, Appl1
110	4	44.4	8	3	US-08-335-733D-41	Sequence 41, Appl1	183	4	44.4	31	5	PCT-US93-00909-4	Sequence 4, Appl1
111	4	44.4	8	3	US-08-335-733D-42	Sequence 42, Appl1	184	4	44.4	31	6	512648-2	Patent No. 512648
112	4	44.4	9	1	US-08-338-634-7	Sequence 7, Appl1	185	4	44.4	33	1	US-08-086-428B-137	Sequence 137, App
113	4	44.4	9	1	US-08-244-855-14	Sequence 14, Appl1	186	4	44.4	33	2	US-08-468-570-137	Sequence 137, App
114	4	44.4	9	3	US-08-335-733D-5	Sequence 5, Appl1	187	4	44.4	33	2	US-08-468-570-137	Sequence 137, App
115	4	44.4	9	3	US-09-001-984C-17	Sequence 17, Appl1	188	4	44.4	33	5	US-08-290-665A-241	Sequence 241, App
116	4	44.4	10	4	US-08-836-075A-188	Sequence 188, App	189	4	44.4	35	4	PCT-US95-10398-241	Sequence 241, App
117	4	44.4	11	1	US-08-336-343A-29	Sequence 29, Appl1	190	4	44.4	35	4	US-09-001-984C-11	Sequence 11, Appl1
118	4	44.4	11	1	US-08-338-634-8	Sequence 8, Appl1	191	4	44.4	37	1	US-08-001-984C-42	Sequence 42, Appl1
119	4	44.4	11	1	US-08-436-670B-35	Sequence 35, Appl1	192	4	44.4	37	1	US-08-463-660-8	Sequence 8, Appl1
120	4	44.4	11	2	US-08-456-670B-38	Sequence 38, Appl1	193	4	44.4	37	1	US-08-678-280-8	Sequence 8, Appl1
121	4	44.4	11	2	US-08-705-875A-11	Sequence 11, Appl1	194	4	44.4	38	1	US-08-176-500-85	Sequence 85, Appl1
122	4	44.4	11	3	US-08-652-877-29	Sequence 29, Appl1	195	4	44.4	38	1	US-08-471-052A-85	Sequence 85, Appl1
123	4	44.4	11	4	US-08-476-515A-29	Sequence 29, Appl1	196	4	44.4	38	1	US-08-189-331-85	Sequence 85, Appl1
124	4	44.4	11	4	US-09-001-984C-7	Sequence 7, Appl1	197	4	44.4	38	2	US-08-471-939-85	Sequence 85, Appl1
125	4	44.4	11	4	US-09-001-984C-23	Sequence 23, Appl1	198	4	44.4	38	2	US-08-471-800-85	Sequence 85, Appl1
126	4	44.4	11	5	PCT-US95-16415-18	Sequence 18, Appl1	199	4	44.4	38	2	US-08-488-161-3	Sequence 85, Appl1
127	4	44.4	12	4	US-08-602-999A-255	Sequence 255, App	200	4	44.4	38	2	US-08-146-028-18	Sequence 18, Appl1
128	4	44.4	13	3	US-08-705-875A-12	Sequence 12, Appl1	201	4	44.4	38	2	US-08-146-028-18	Sequence 18, Appl1
129	4	44.4	13	4	US-09-001-984C-8	Sequence 8, Appl1	202	4	44.4	38	3	US-09-273-685-3	Sequence 3, Appl1
130	4	44.4	13	4	US-09-001-984C-9	Sequence 9, Appl1	203	4	44.4	38	4	US-08-723-425A-18	Sequence 18, Appl1
131	4	44.4	13	4	US-09-001-984C-20	Sequence 20, Appl1	204	4	44.4	38	4	US-09-112-206-18	Sequence 18, Appl1
132	4	44.4	13	4	US-09-001-984C-25	Sequence 25, Appl1	205	4	44.4	38	5	PCT-US95-11934-3	Sequence 3, Appl1
133	4	44.4	14	3	US-08-705-875A-13	Sequence 13, Appl1	206	4	44.4	39	2	US-08-455-625-3	Sequence 3, Appl1
134	4	44.4	15	1	US-08-408-604A-31	Sequence 31, Appl1	207	4	44.4	39	2	US-08-455-625-29	Sequence 29, Appl1
135	4	44.4	15	2	US-08-687-956A-3	Sequence 3, Appl1	208	4	44.4	39	4	US-08-455-685-3	Sequence 3, Appl1
136	4	44.4	15	2	US-08-687-956A-6	Sequence 6, Appl1	209	4	44.4	39	4	US-08-455-685-29	Sequence 29, Appl1
137	4	44.4	15	2	US-08-602-999A-410	Sequence 410, App	210	4	44.4	39	5	PCT-US94-05142-29	Sequence 29, Appl1
138	4	44.4	15	5	PCT-US93-09626-31	Sequence 31, Appl1	211	4	44.4	42	1	PCT-US94-05142-29	Sequence 29, Appl1
139	4	44.4	16	1	US-08-447-925-5	Sequence 5, Appl1	212	4	44.4	42	1	US-08-450-945-61	Sequence 61, Appl1
140	4	44.4	16	2	US-08-102-385G-35	Sequence 35, Appl1	213	4	44.4	48	3	US-08-976-161-61	Sequence 61, Appl1
141	4	44.4	16	3	US-08-705-875A-14	Sequence 14, Appl1	214	4	44.4	48	3	US-08-665-259-6	Sequence 6, Appl1
142	4	44.4	16	4	US-08-602-999A-179	Sequence 179, App	215	4	44.4	49	3	US-08-762-500-6	Sequence 6, Appl1
143	4	44.4	18	1	US-08-441-354A-6	Sequence 6, Appl1	216	4	44.4	49	3	US-08-665-259-5	Sequence 5, Appl1
144	4	44.4	18	1	US-08-629-752-6	Sequence 6, Appl1	217	4	44.4	49	3	US-08-762-500-5	Sequence 5, Appl1
145	4	44.4	18	2	US-08-802-991-6	Sequence 6, Appl1	218	4	44.4	52	1	US-08-294-189-17	Sequence 17, Appl1
146	4	44.4	19	2	US-08-284-391B-39	Sequence 39, Appl1	219	4	44.4	53	2	US-08-238-821B-53	Sequence 53, Appl1
147	4	44.4	19	2	US-08-284-391B-41	Sequence 41, Appl1	220	4	44.4	53	2	PCT-US95-05744-53	Sequence 53, Appl1
148	4	44.4	20	1	US-08-218-025A-72	Sequence 72, Appl1	221	4	44.4	54	2	US-08-400-159-16	Sequence 16, Appl1
149	4	44.4	20	2	US-08-934-915-10	Sequence 10, Appl1	222	4	44.4	54	2	US-08-611-729A-16	Sequence 16, Appl1
150	4	44.4	21	1	US-08-273-776-1	Sequence 1, Appl1	223	4	44.4	58	2	US-08-152-721B-19	Sequence 19, Appl1
151	4	44.4	21	5	PCT-US92-10432-1	Sequence 1, Appl1	224	4	44.4	59	1	US-08-306-671-25	Sequence 25, Appl1
152	4	44.4	22	2	US-08-833-546-9	Sequence 9, Appl1	225	4	44.4	59	1	US-08-569-959-25	Sequence 25, Appl1
153	4	44.4	22	4	US-09-388-664-9	Sequence 9, Appl1	226	4	44.4	59	3	US-08-651-136C-66	Sequence 66, Appl1
154	4	44.4	23	1	US-08-493-235-40	Sequence 132, App	227	4	44.4	60	1	US-08-447-925-1	Sequence 1, Appl1
155	4	44.4	23	2	US-08-492-027A-3	Sequence 40, Appl1	228	4	44.4	60	1	US-08-099-354-7	Sequence 7, Appl1
156	4	44.4	23	2	US-08-485-324-15	Sequence 3, Appl1	229	4	44.4	60	2	US-08-288-059-3	Sequence 3, Appl1
157	4	44.4	23	3	US-08-447-506-15	Sequence 15, Appl1	230	4	44.4	61	1	US-07-734-534A-5	Sequence 3, Appl1
158	4	44.4	23	3	US-08-235-437-15	Sequence 15, Appl1	231	4	44.4	65	4	US-09-188-930-297	Sequence 297, App
159	4	44.4	23	3	US-08-447-515-15	Sequence 15, Appl1	232	4	44.4	69	1	US-08-477-383-40	Sequence 40, Appl1
160	4	44.4	24	1	US-08-488-252-31	Sequence 31, Appl1	233	4	44.4	69	1	US-08-487-174-10	Sequence 40, Appl1
161	4	44.4	24	2	US-08-407-252-4	Sequence 4, Appl1	234	4	44.4	69	1	US-08-480-750-40	Sequence 40, Appl1
162	4	44.4	24	2	US-08-705-875A-15	Sequence 15, Appl1	235	4	44.4	70	2	US-08-935-450-12	Sequence 12, Appl1
163	4	44.4	25	1	US-08-451-405A-3	Sequence 3, Appl1	236	4	44.4	80	1	US-08-137-800-41	Sequence 41, Appl1
164	4	44.4	25	2	US-08-474-696A-4	Sequence 4, Appl1	237	4	44.4	80	1	US-08-477-383-11	Sequence 11, Appl1
165	4	44.4	25	2	US-08-455-625-25	Sequence 25, Appl1	238	4	44.4	80	1	US-08-477-174-11	Sequence 41, Appl1
166	4	44.4	25	4	US-08-455-625-25	Sequence 25, Appl1	239	4	44.4	80	1	US-08-480-750-41	Sequence 41, Appl1
167	4	44.4	25	5	PCT-US94-05142-25	Sequence 25, Appl1	240	4	44.4	80	1	US-08-341-219-23	Sequence 23, Appl1
168	4	44.4	26	1	US-08-383-753-26	Sequence 26, Appl1	241	4	44.4	80	4	US-08-912-514A-23	Sequence 23, Appl1
169	4	44.4	26	2	US-08-586-772-26	Sequence 26, Appl1	242	4	44.4	82	1	US-08-225-757B-12	Sequence 12, Appl1
170	4	44.4	26	2	US-08-959-512-26	Sequence 26, Appl1	243	4	44.4	82	1	US-08-446-338B-14	Sequence 14, Appl1
171	4	44.4	26	3	US-08-705-875A-16	Sequence 16, Appl1	244	4	44.4	82	2	US-08-446-100B-14	Sequence 14, Appl1
172	4	44.4	26	3	US-08-335-733D-1	Sequence 1, Appl1	245	4	44.4	82	2	US-08-805-445-14	Sequence 14, Appl1
173	4	44.4	26	3	US-08-335-733D-1	Sequence 1, Appl1	246	4	44.4	82	2	US-08-064-067D-14	Sequence 14, Appl1

247	4	44.4	82	2	US-09-066-208-14	Sequence 14, Appl	320	4	44.4	124	5	PCT-US95-08743-131	Sequence 131, App
248	4	44.4	83	1	US-08-370-225-21	Sequence 21, Appl	321	4	44.4	127	2	US-08-137-117D-37	Sequence 37, Appl
249	4	44.4	83	1	US-08-461-859-21	Sequence 21, Appl	322	4	44.4	127	2	US-08-436-717-37	Sequence 37, Appl
250	4	44.4	83	5	PCT-US93-10069-721	Sequence 21, Appl	323	4	44.4	138	1	US-08-686-878A-14	Sequence 14, Appl
251	4	44.4	84	3	US-08-648-342-10	Sequence 10, Appl	324	4	44.4	139	1	US-07-718-274A-2	Sequence 2, Appl
252	4	44.4	94	1	US-08-167-035-23	Sequence 23, Appl	325	4	44.4	139	1	US-08-163-877-10	Sequence 10, Appl
253	4	44.4	94	1	US-08-208-887A-23	Sequence 23, Appl	326	4	44.4	139	1	US-08-149-106-2	Sequence 2, Appl
254	4	44.4	94	2	US-08-539-005-23	Sequence 23, Appl	327	4	44.4	139	1	US-08-298-021-2	Sequence 2, Appl
255	4	44.4	94	2	US-08-238-821B-46	Sequence 46, Appl	328	4	44.4	139	1	US-08-278-729A-5	Sequence 5, Appl
256	4	44.4	94	5	PCT-US95-05744-46	Sequence 46, Appl	329	4	44.4	139	1	US-08-278-729A-6	Sequence 6, Appl
257	4	44.4	100	3	US-09-034-916-13	Sequence 13, Appl	330	4	44.4	139	1	US-08-155-343A-5	Sequence 5, Appl
258	4	44.4	100	4	US-08-973-462-11	Sequence 11, Appl	331	4	44.4	139	1	US-08-155-343A-6	Sequence 6, Appl
259	4	44.4	102	1	US-08-335-583C-47	Sequence 47, Appl	332	4	44.4	139	1	US-08-406-672-6	Sequence 6, Appl
260	4	44.4	102	2	US-08-808-982-8	Sequence 8, Appl	333	4	44.4	139	1	US-08-643-563A-5	Sequence 5, Appl
261	4	44.4	102	3	US-08-288-508C-18	Sequence 18, Appl	334	4	44.4	139	1	US-08-643-563A-6	Sequence 6, Appl
262	4	44.4	102	3	US-08-478-097A-16	Sequence 16, Appl	335	4	44.4	139	1	US-08-643-563A-5	Sequence 5, Appl
263	4	44.4	102	3	US-08-289-222E-27	Sequence 27, Appl	336	4	44.4	139	1	US-08-643-763A-5	Sequence 5, Appl
264	4	44.4	102	4	US-09-054-526B-27	Sequence 27, Appl	337	4	44.4	139	1	US-08-643-763A-6	Sequence 6, Appl
265	4	44.4	102	4	US-08-931-858E-161	Sequence 161, App	338	4	44.4	139	1	US-08-462-623-5	Sequence 5, Appl
266	4	44.4	102	4	US-08-981-739-161	Sequence 161, App	339	4	44.4	139	1	US-08-462-623-6	Sequence 6, Appl
267	4	44.4	104	1	US-07-764-731B-8	Sequence 8, Appl	340	4	44.4	139	1	US-08-451-953A-5	Sequence 5, Appl
268	4	44.4	105	1	US-08-422-101-9	Sequence 9, Appl	341	4	44.4	139	1	US-08-451-953A-6	Sequence 6, Appl
269	4	44.4	105	1	US-08-422-091-9	Sequence 9, Appl	342	4	44.4	139	1	US-08-360-914B-10	Sequence 10, Appl
270	4	44.4	105	2	US-08-422-092-9	Sequence 9, Appl	343	4	44.4	139	1	US-08-741-589A-10	Sequence 10, Appl
271	4	44.4	105	2	US-08-788-800-6	Sequence 6, Appl	344	4	44.4	139	2	US-08-445-468A-5	Sequence 5, Appl
272	4	44.4	105	3	US-08-422-093-9	Sequence 9, Appl	345	4	44.4	139	2	US-08-445-468A-6	Sequence 6, Appl
273	4	44.4	105	3	US-08-422-112-9	Sequence 9, Appl	346	4	44.4	139	2	US-08-461-397A-5	Sequence 5, Appl
274	4	44.4	107	2	US-08-810-572A-4	Sequence 4, Appl	347	4	44.4	139	2	US-08-461-397A-6	Sequence 6, Appl
275	4	44.4	109	1	US-07-829-462-1	Sequence 1, Appl	348	4	44.4	139	2	US-08-912-088-5	Sequence 5, Appl
276	4	44.4	109	1	US-08-340-812-1	Sequence 1, Appl	349	4	44.4	139	2	US-08-912-088-6	Sequence 6, Appl
277	4	44.4	109	1	US-08-459-064B-1	Sequence 1, Appl	350	4	44.4	139	3	US-08-912-088-6	Sequence 6, Appl
278	4	44.4	109	2	US-08-460-421A-1	Sequence 1, Appl	351	4	44.4	139	3	US-08-278-730A-5	Sequence 5, Appl
279	4	44.4	109	2	US-08-717-169-1	Sequence 1, Appl	352	4	44.4	139	3	US-08-278-730A-6	Sequence 6, Appl
280	4	44.4	109	2	US-08-761-277A-51	Sequence 51, Appl	353	4	44.4	139	3	US-08-445-467-5	Sequence 5, Appl
281	4	44.4	109	3	US-08-646-322-5	Sequence 5, Appl	354	4	44.4	139	3	US-08-443-676-1	Sequence 6, Appl
282	4	44.4	109	5	PCT-US93-00909-1	Sequence 1, Appl	355	4	44.4	139	3	US-08-480-515A-5	Sequence 5, Appl
283	4	44.4	110	1	US-07-849-389-7	Sequence 7, Appl	356	4	44.4	139	3	US-08-480-515A-6	Sequence 6, Appl
284	4	44.4	111	3	US-08-545-809A-111	Sequence 111, App	357	4	44.4	139	4	US-08-414-033A-5	Sequence 5, Appl
285	4	44.4	113	4	US-08-836-075A-70	Sequence 70, Appl	358	4	44.4	139	4	US-08-414-033A-6	Sequence 6, Appl
286	4	44.4	113	4	US-08-836-075A-72	Sequence 72, Appl	359	4	44.4	139	4	US-08-271-556A-3	Sequence 3, Appl
287	4	44.4	113	4	US-08-836-075A-74	Sequence 74, Appl	360	4	44.4	139	4	US-08-271-556A-4	Sequence 4, Appl
288	4	44.4	113	4	US-08-836-075A-78	Sequence 78, Appl	361	4	44.4	139	4	US-08-905-223-44	Sequence 44, App
289	4	44.4	114	4	US-09-188-930-161	Sequence 161, App	362	4	44.4	139	5	PCT-US92-01968-5	Sequence 5, Appl
290	4	44.4	114	4	US-09-188-930-288	Sequence 288, App	363	4	44.4	139	5	PCT-US92-01968-6	Sequence 6, Appl
291	4	44.4	115	2	US-07-903-029-6	Sequence 6, Appl	364	4	44.4	139	5	PCT-US93-07190-5	Sequence 5, Appl
292	4	44.4	115	3	US-08-478-097A-30	Sequence 30, Appl	365	4	44.4	139	5	PCT-US93-07190-6	Sequence 6, Appl
293	4	44.4	116	1	US-08-636-253-2	Sequence 2, Appl	366	4	44.4	139	5	PCT-US93-07231-5	Sequence 5, Appl
294	4	44.4	117	1	US-08-448-196A-2	Sequence 2, Appl	367	4	44.4	139	5	PCT-US93-07231-6	Sequence 6, Appl
295	4	44.4	118	1	US-08-481-377-12	Sequence 12, Appl	368	4	44.4	139	5	PCT-US93-08742-5	Sequence 5, Appl
296	4	44.4	118	2	US-08-491-835-10	Sequence 10, Appl	369	4	44.4	139	5	PCT-US93-08742-6	Sequence 6, Appl
297	4	44.4	118	3	US-08-392-794A-4	Sequence 4, Appl	370	4	44.4	139	5	PCT-US93-08808-5	Sequence 5, Appl
298	4	44.4	118	3	US-09-153-733A-12	Sequence 12, Appl	371	4	44.4	139	5	PCT-US93-08808-6	Sequence 6, Appl
299	4	44.4	118	3	US-08-946-092A-10	Sequence 10, Appl	372	4	44.4	139	5	PCT-US93-08885-5	Sequence 5, Appl
300	4	44.4	118	4	US-09-172-062-10	Sequence 10, Appl	373	4	44.4	139	5	PCT-US93-08885-6	Sequence 6, Appl
301	4	44.4	118	5	PCT-US94-00665-12	Sequence 12, Appl	374	4	44.4	139	5	PCT-US94-13181-10	Sequence 10, Appl
302	4	44.4	118	5	PCT-US94-00665-10	Sequence 10, Appl	375	4	44.4	142	2	US-08-805-117-3	Sequence 3, Appl
303	4	44.4	119	1	US-08-581-552B-12	Sequence 12, Appl	376	4	44.4	151	2	US-08-722-050-8	Sequence 8, Appl
304	4	44.4	119	1	US-08-455-558-18	Sequence 18, Appl	377	4	44.4	153	3	US-08-851-843A-177	Sequence 177, App
305	4	44.4	119	2	US-08-525-596B-22	Sequence 22, Appl	378	4	44.4	153	3	US-08-974-549A-296	Sequence 296, App
306	4	44.4	119	2	US-08-581-528A-12	Sequence 12, Appl	379	4	44.4	154	2	US-08-330-394A-29	Sequence 29, Appl
307	4	44.4	119	3	US-09-097-616-12	Sequence 12, Appl	380	4	44.4	155	3	US-08-950-720A-10	Sequence 10, Appl
308	4	44.4	119	3	US-09-177-860A-22	Sequence 22, Appl	381	4	44.4	156	2	US-08-330-394A-22	Sequence 22, Appl
309	4	44.4	119	4	US-09-156-316-9	Sequence 9, Appl	382	4	44.4	158	1	US-08-611-107-4	Sequence 4, Appl
310	4	44.4	119	4	US-08-624-635-13	Sequence 13, Appl	383	4	44.4	158	2	US-08-422-560A-4	Sequence 4, Appl
311	4	44.4	119	4	US-09-145-060-18	Sequence 18, Appl	384	4	44.4	158	4	US-08-468-793-4	Sequence 4, Appl
312	4	44.4	119	5	PCT-US94-00657-18	Sequence 18, Appl	385	4	44.4	161	1	US-08-450-257-56	Sequence 56, Appl
313	4	44.4	119	5	PCT-US94-07762-12	Sequence 12, Appl	386	4	44.4	161	1	US-08-450-246-56	Sequence 56, Appl
314	4	44.4	119	5	PCT-US94-07799-12	Sequence 12, Appl	387	4	44.4	161	1	US-08-450-098-56	Sequence 56, Appl
315	4	44.4	121	6	US-08-805-117-1	Sequence 1, Appl	388	4	44.4	161	1	US-08-451-223-56	Sequence 56, Appl
316	4	44.4	122	6	530466-3	Patent No. 530466	389	4	44.4	161	1	US-08-450-236-56	Sequence 56, Appl
317	4	44.4	124	1	US-08-276-852-131	Sequence 131, App	390	4	44.4	161	2	US-08-621-803-249	Sequence 249, App
318	4	44.4	124	1	US-08-899-575-131	Sequence 131, App	391	4	44.4	161	3	US-09-045-764A-4	Sequence 4, Appl
319	4	44.4	124	1	US-08-899-575-131	Sequence 131, App	392	4	44.4	161	4	US-09-271-970-2	Sequence 2, Appl

393	4	44.4	152	1	US-08-048-164A-2	Sequence 2, App11	466	4	44.4	216	2	US-08-929-418-2	Sequence 2, App11
394	4	44.4	152	1	US-08-460-462-2	Sequence 2, App11	467	4	44.4	220	2	US-08-726-306A-29	Sequence 2, App1
395	4	44.4	152	1	US-08-460-457-2	Sequence 2, App11	468	4	44.4	221	1	US-08-032-848C-13	Sequence 19, App1
396	4	44.4	152	1	US-08-460-458-2	Sequence 2, App11	469	4	44.4	221	2	US-08-861-659-6	Sequence 6, App11
397	4	44.4	152	2	US-08-460-455-2	Sequence 2, App11	470	4	44.4	221	2	US-09-134-596-6	Sequence 6, App11
398	4	44.4	152	2	US-08-330-394A-2	Sequence 2, App11	471	4	44.4	221	3	US-09-293-273-6	Sequence 6, App11
399	4	44.4	152	3	US-08-983-045-2	Sequence 2, App11	472	4	44.4	224	1	US-08-553-516-2	Sequence 2, App11
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402	4	44.4	156	2	US-08-483-695-3	Sequence 3, App11	475	4	44.4	229	4	US-08-751-359-22	Sequence 22, App1
403	4	44.4	156	2	US-07-965-285-3	Sequence 3, App11	476	4	44.4	233	4	US-08-523-894-6	Sequence 6, App11
404	4	44.4	156	2	US-08-487-231-3	Sequence 3, App11	477	4	44.4	234	4	US-08-487-550-2	Sequence 6, App11
405	4	44.4	156	4	US-09-201-912-3	Sequence 3, App11	478	4	44.4	235	2	US-08-378-939-12	Sequence 12, App1
406	4	44.4	159	1	US-07-841-646-9	Sequence 9, App11	479	4	44.4	235	4	US-09-049-672A-10	Sequence 10, App1
407	4	44.4	159	1	US-08-147-023-9	Sequence 9, App11	480	4	44.4	235	4	US-09-049-672A-12	Sequence 12, App1
408	4	44.4	159	1	US-08-447-570-9	Sequence 9, App11	481	4	44.4	235	4	US-09-329-350-31	Sequence 31, App1
409	4	44.4	159	2	US-08-449-700-9	Sequence 9, App11	482	4	44.4	236	3	US-08-487-550-10	Sequence 10, App1
410	4	44.4	159	2	US-08-449-699A-9	Sequence 9, App11	483	4	44.4	236	4	US-09-049-672A-7	Sequence 7, App11
411	4	44.4	174	2	US-08-683-562B-45	Sequence 45, App1	484	4	44.4	236	4	US-08-961-083-96	Sequence 96, App1
412	4	44.4	174	2	US-08-683-562B-48	Sequence 48, App1	485	4	44.4	237	2	US-08-672-564-3	Sequence 3, App11
413	4	44.4	176	6	US-08-392-794A-8	Sequence 8, App11	486	4	44.4	238	4	US-09-216-295-12	Sequence 12, App1
414	4	44.4	176	6	5185440-7	Sequence 8, App11	487	4	44.4	240	3	US-09-248-335-42	Sequence 42, App1
415	4	44.4	177	1	US-08-450-257-61	Sequence 61, App1	488	4	44.4	240	4	US-09-049-672A-11	Sequence 11, App1
416	4	44.4	177	1	US-08-450-246-61	Sequence 61, App1	489	4	44.4	245	2	US-08-912-129A-48	Sequence 48, App1
417	4	44.4	177	1	US-08-450-098-61	Sequence 61, App1	490	4	44.4	248	1	US-08-238-130-2	Sequence 2, App11
418	4	44.4	177	1	US-08-451-233-61	Sequence 61, App1	491	4	44.4	248	2	US-08-921-426-4	Sequence 4, App11
419	4	44.4	177	1	US-08-450-236-61	Sequence 61, App1	492	4	44.4	248	5	US-08-816-915-4	Sequence 4, App11
420	4	44.4	178	3	US-08-705-875A-8	Sequence 8, App11	493	4	44.4	248	5	PCT-US95-07743-4	Sequence 4, App1
421	4	44.4	178	3	US-09-122-443-9	Sequence 9, App11	494	4	44.4	249	1	US-08-450-257-57	Sequence 57, App1
422	4	44.4	178	4	US-09-220-731-23	Sequence 23, App1	495	4	44.4	249	1	US-08-450-246-57	Sequence 57, App1
423	4	44.4	178	4	US-09-220-731-24	Sequence 24, App1	496	4	44.4	249	1	US-08-450-098-57	Sequence 57, App1
424	4	44.4	178	4	US-09-211-970-8	Sequence 8, App11	497	4	44.4	249	1	US-08-451-233-57	Sequence 57, App1
425	4	44.4	179	2	US-08-621-803-257	Sequence 257, App	498	4	44.4	249	1	US-08-450-236-57	Sequence 57, App1
426	4	44.4	179	2	US-08-621-803-261	Sequence 261, App	499	4	44.4	249	2	US-08-991-946A-1	Sequence 1, App11
427	4	44.4	180	1	US-07-953-230A-12	Sequence 12, App1	500	4	44.4	251	4	US-08-944-483-28	Sequence 28, App1
428	4	44.4	180	6	5405942-4	Sequence 12, App1	501	4	44.4	251	2	US-08-310-912A-106	Sequence 106, App
429	4	44.4	181	4	US-08-961-083-114	Sequence 114, App	502	4	44.4	255	2	US-08-841-089-106	Sequence 106, App
430	4	44.4	186	1	US-08-928-443-3	Sequence 3, App11	503	4	44.4	255	3	PCT-US95-04570-106	Sequence 106, App
431	4	44.4	186	3	US-09-129-055-3	Sequence 3, App11	504	4	44.4	255	5	PCT-US95-04589-106	Sequence 106, App
432	4	44.4	187	1	US-08-450-257-62	Sequence 62, App1	505	4	44.4	257	2	US-08-715-204-6	Sequence 6, App11
433	4	44.4	187	1	US-08-450-246-62	Sequence 62, App1	506	4	44.4	257	3	US-09-162-597-6	Sequence 6, App11
434	4	44.4	187	1	US-08-450-098-62	Sequence 62, App1	507	4	44.4	257	3	US-07-721-761A-29	Sequence 29, App1
435	4	44.4	187	1	US-08-451-233-62	Sequence 62, App1	508	4	44.4	258	1	US-07-978-687-29	Sequence 29, App1
436	4	44.4	187	1	US-08-450-236-62	Sequence 62, App1	509	4	44.4	258	4	US-08-961-083-90	Sequence 90, App1
437	4	44.4	189	3	US-08-779-764A-18	Sequence 28, App1	510	4	44.4	258	5	PCT-US91-05801-29	Sequence 29, App1
438	4	44.4	190	4	US-09-271-970-14	Sequence 14, App1	511	4	44.4	259	4	US-09-216-295-5	Sequence 5, App11
439	4	44.4	192	1	US-08-086-428B-53	Sequence 53, App1	512	4	44.4	262	2	US-07-857-224B-64	Sequence 64, App1
440	4	44.4	192	1	US-08-086-428B-58	Sequence 58, App1	513	4	44.4	262	2	US-08-494-907-6	Sequence 6, App11
441	4	44.4	192	1	US-08-086-428B-85	Sequence 85, App1	514	4	44.4	264	5	PCT-US96-10986-6	Sequence 6, App11
442	4	44.4	192	2	US-08-468-570-53	Sequence 53, App1	515	4	44.4	267	4	US-08-454-928A-10	Sequence 10, App1
443	4	44.4	192	2	US-08-468-570-58	Sequence 58, App1	516	4	44.4	269	1	US-08-241-766-4	Sequence 4, App11
444	4	44.4	192	2	US-08-468-570-85	Sequence 85, App1	517	4	44.4	269	1	US-08-241-766-5	Sequence 5, App11
445	4	44.4	192	2	US-08-290-665A-53	Sequence 53, App1	518	4	44.4	269	1	US-08-241-766-6	Sequence 6, App11
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447	4	44.4	192	2	US-08-290-665A-85	Sequence 85, App1	520	4	44.4	269	1	US-08-241-766-14	Sequence 14, App1
448	4	44.4	192	4	US-09-475-316A-23	Sequence 23, App1	521	4	44.4	269	2	US-08-484-905-116	Sequence 116, App
449	4	44.4	192	5	PCT-US94-05795-3	Sequence 3, App11	522	4	44.4	269	3	US-08-481-985B-116	Sequence 116, App
450	4	44.4	192	5	PCT-US95-10398-53	Sequence 53, App1	523	4	44.4	269	3	US-08-370-476-116	Sequence 116, App
451	4	44.4	192	5	PCT-US95-10398-58	Sequence 58, App1	524	4	44.4	270	2	US-08-370-476-116	Sequence 116, App
452	4	44.4	192	5	PCT-US95-10398-85	Sequence 85, App1	525	4	44.4	270	2	US-09-031-485-7	Sequence 7, App11
453	4	44.4	193	2	US-08-536-626A-39	Sequence 39, App1	526	4	44.4	270	2	US-08-847-429A-7	Sequence 7, App11
454	4	44.4	194	2	US-08-621-803-255	Sequence 255, App	527	4	44.4	270	2	US-07-857-224B-31	Sequence 31, App1
455	4	44.4	195	2	US-08-621-803-263	Sequence 263, App	528	4	44.4	272	2	US-09-065-474-7	Sequence 7, App11
456	4	44.4	196	4	US-09-383-586-11	Sequence 11, App1	529	4	44.4	272	2	US-08-160-524A-7	Sequence 7, App11
457	4	44.4	201	2	US-08-531-525-13	Sequence 13, App1	530	4	44.4	275	2	US-08-492-027A-4	Sequence 4, App11
458	4	44.4	201	2	US-08-916-901-3	Sequence 3, App11	531	4	44.4	278	1	US-07-921-807B-10	Sequence 10, App1
459	4	44.4	201	2	US-08-916-901-8	Sequence 8, App11	532	4	44.4	278	1	US-08-441-944A-10	Sequence 10, App1
460	4	44.4	201	2	US-08-918-270A-13	Sequence 13, App1	533	4	44.4	282	5	PCT-US95-13335-1	Sequence 1, App11
461	4	44.4	208	4	US-08-097-869-6	Sequence 6, App11	534	4	44.4	283	3	US-08-658-469-2	Sequence 2, App11
462	4	44.4	210	4	US-07-667-276A-2	Sequence 2, App11	535	4	44.4	283	3	US-09-081-420-2	Sequence 2, App11
463	4	44.4	212	4	US-08-973-462-25	Sequence 25, App1	536	4	44.4	284	2	US-08-767-096-3	Sequence 3, App11
464	4	44.4	214	1	US-08-217-327-4	Sequence 4, App11	537	4	44.4	287	2	US-09-065-474-145	Sequence 145, App
465	4	44.4	215	2	US-08-912-129A-58	Sequence 58, App1	538	4	44.4	293	2	US-08-810-572A-2	Sequence 2, App11

539	4	44.4	293	3	US-09-203-716-2	Sequence 2, Appli	612	4	44.4	303	3	US-08-876-398A-20	Sequence 20, Appl
540	4	44.4	294	2	US-08-874-347-26	Sequence 26, Appl	613	4	44.4	303	3	US-08-876-398A-22	Sequence 22, Appl
541	4	44.4	294	3	US-09-093-532-26	Sequence 26, Appl	614	4	44.4	303	3	US-08-876-398A-24	Sequence 24, Appl
542	4	44.4	297	1	US-08-176-620A-16	Sequence 16, Appl	615	4	44.4	303	3	US-08-876-398A-26	Sequence 26, Appl
543	4	44.4	297	2	US-08-874-347-23	Sequence 23, Appl	616	4	44.4	303	3	US-08-876-398A-28	Sequence 28, Appl
544	4	44.4	297	2	US-08-874-347-24	Sequence 24, Appl	617	4	44.4	303	3	US-08-876-398A-30	Sequence 30, Appl
545	4	44.4	297	2	US-08-461-985-16	Sequence 16, Appl	618	4	44.4	303	3	US-08-876-398A-32	Sequence 32, Appl
546	4	44.4	297	3	US-09-093-522-23	Sequence 23, Appl	619	4	44.4	303	3	US-08-876-398A-34	Sequence 34, Appl
547	4	44.4	297	3	US-09-093-522-24	Sequence 24, Appl	620	4	44.4	303	3	US-08-876-398A-36	Sequence 36, Appl
548	4	44.4	298	1	US-08-348-792-4	Sequence 4, Appli	621	4	44.4	303	3	US-08-876-398A-38	Sequence 38, Appl
549	4	44.4	298	2	US-08-462-738-4	Sequence 4, Appli	622	4	44.4	303	3	US-08-876-398A-40	Sequence 40, Appl
550	4	44.4	299	2	US-08-872-437-2	Sequence 2, Appli	623	4	44.4	303	3	US-08-876-398A-42	Sequence 42, Appl
551	4	44.4	299	3	US-08-651-136C-12	Sequence 12, Appl	624	4	44.4	303	3	US-08-876-398A-44	Sequence 44, Appl
552	4	44.4	300	1	US-07-640-029-5	Sequence 5, Appli	625	4	44.4	303	3	US-08-876-398A-46	Sequence 46, Appl
553	4	44.4	300	3	US-08-705-875A-4	Sequence 4, Appli	626	4	44.4	303	3	US-08-876-398A-48	Sequence 48, Appl
554	4	44.4	300	3	US-08-705-875A-6	Sequence 6, Appli	627	4	44.4	303	3	US-08-876-398A-50	Sequence 50, Appl
555	4	44.4	300	4	US-09-220-731-21	Sequence 21, Appl	628	4	44.4	303	3	US-08-876-398A-52	Sequence 52, Appl
556	4	44.4	300	4	US-08-439-992A-5	Sequence 5, Appli	629	4	44.4	303	3	US-08-876-398A-54	Sequence 54, Appl
557	4	44.4	301	2	US-08-355-844-2	Sequence 2, Appli	630	4	44.4	303	3	US-08-876-398A-56	Sequence 56, Appl
558	4	44.4	301	5	PCT-US95-16126-2	Sequence 2, Appli	631	4	44.4	303	3	US-08-876-398A-58	Sequence 58, Appl
559	4	44.4	302	1	US-07-640-029-6	Sequence 6, Appli	632	4	44.4	303	3	US-08-876-398A-60	Sequence 60, Appl
560	4	44.4	302	1	US-07-921-807B-7	Sequence 7, Appli	633	4	44.4	303	3	US-08-876-398A-62	Sequence 62, Appl
561	4	44.4	302	1	US-07-921-807B-8	Sequence 8, Appli	634	4	44.4	303	3	US-08-876-398A-64	Sequence 64, Appl
562	4	44.4	302	1	US-08-441-944A-7	Sequence 7, Appli	635	4	44.4	303	3	US-08-876-398A-66	Sequence 66, Appl
563	4	44.4	302	1	US-08-441-944A-8	Sequence 8, Appli	636	4	44.4	303	3	US-08-876-398A-68	Sequence 68, Appl
564	4	44.4	302	1	US-08-439-992A-6	Sequence 6, Appli	637	4	44.4	304	1	US-08-900-711-5	Sequence 5, Appli
565	4	44.4	303	1	US-07-917-111-2	Sequence 3, Appli	638	4	44.4	304	2	US-08-815-336-2	Sequence 2, Appli
566	4	44.4	303	1	US-07-917-111-3	Sequence 3, Appli	639	4	44.4	304	2	US-08-415-343B-5	Sequence 5, Appli
567	4	44.4	303	1	US-08-479-638-2	Sequence 2, Appli	640	4	44.4	304	2	US-08-762-433-1	Sequence 1, Appli
568	4	44.4	303	1	US-08-479-638-3	Sequence 3, Appli	641	4	44.4	304	2	US-09-001-219-1	Sequence 1, Appli
569	4	44.4	303	2	US-08-294-871A-2	Sequence 2, Appli	642	4	44.4	305	1	US-08-348-792-6	Sequence 6, Appli
570	4	44.4	303	2	US-08-294-871A-4	Sequence 4, Appli	643	4	44.4	305	2	US-08-853-659A-47	Sequence 47, Appli
571	4	44.4	303	2	US-08-294-871A-6	Sequence 6, Appli	644	4	44.4	305	2	US-08-462-728-6	Sequence 6, Appli
572	4	44.4	303	2	US-08-294-871A-8	Sequence 8, Appli	645	4	44.4	306	1	US-08-454-136-11	Sequence 11, Appl
573	4	44.4	303	2	US-08-294-871A-10	Sequence 10, Appl	646	4	44.4	306	2	US-08-286-819A-33	Sequence 33, Appl
574	4	44.4	303	2	US-08-294-871A-12	Sequence 12, Appl	647	4	44.4	306	3	US-08-980-357-83	Sequence 33, Appl
575	4	44.4	303	2	US-08-294-871A-14	Sequence 14, Appl	648	4	44.4	306	3	US-09-064-033-11	Sequence 11, Appl
576	4	44.4	303	2	US-08-294-871A-16	Sequence 16, Appl	649	4	44.4	307	1	US-08-348-792-8	Sequence 8, Appli
577	4	44.4	303	2	US-08-294-871A-18	Sequence 18, Appl	650	4	44.4	307	2	US-08-462-738-8	Sequence 8, Appli
578	4	44.4	303	2	US-08-294-871A-20	Sequence 20, Appl	651	4	44.4	307	4	US-09-177-249-13	Sequence 13, Appl
579	4	44.4	303	2	US-08-294-871A-22	Sequence 22, Appl	652	4	44.4	308	3	US-08-705-875A-10	Sequence 10, Appl
580	4	44.4	303	2	US-08-294-871A-24	Sequence 24, Appl	653	4	44.4	311	2	US-08-602-359A-41	Sequence 41, Appl
581	4	44.4	303	2	US-08-294-871A-26	Sequence 26, Appl	654	4	44.4	312	1	US-08-094-128A-27	Sequence 27, Appl
582	4	44.4	303	2	US-08-294-871A-28	Sequence 28, Appl	655	4	44.4	312	1	US-08-455-674-27	Sequence 27, Appl
583	4	44.4	303	2	US-08-294-871A-30	Sequence 30, Appl	656	4	44.4	312	1	US-08-455-992-27	Sequence 27, Appl
584	4	44.4	303	2	US-08-294-871A-32	Sequence 32, Appl	657	4	44.4	312	1	US-08-455-992-27	Sequence 27, Appl
585	4	44.4	303	2	US-08-294-871A-34	Sequence 34, Appl	658	4	44.4	312	1	US-08-455-992-27	Sequence 27, Appl
586	4	44.4	303	2	US-08-294-871A-36	Sequence 36, Appl	659	4	44.4	312	2	US-09-031-485-2	Sequence 2, Appli
587	4	44.4	303	2	US-08-294-871A-38	Sequence 38, Appl	660	4	44.4	312	2	US-08-847-429A-2	Sequence 2, Appli
588	4	44.4	303	2	US-08-294-871A-40	Sequence 40, Appl	661	4	44.4	312	3	US-08-894-017-10	Sequence 10, Appl
589	4	44.4	303	2	US-08-294-871A-42	Sequence 42, Appl	662	4	44.4	312	3	US-09-065-474-2	Sequence 2, Appli
590	4	44.4	303	2	US-08-294-871A-44	Sequence 44, Appl	663	4	44.4	312	3	US-09-084-813-6	Sequence 6, Appli
591	4	44.4	303	2	US-08-294-871A-46	Sequence 46, Appl	664	4	44.4	312	4	US-09-216-295-21	Sequence 21, Appl
592	4	44.4	303	2	US-08-294-871A-48	Sequence 48, Appl	665	4	44.4	312	5	PCT-US92-00652-27	Sequence 27, Appl
593	4	44.4	303	2	US-08-294-871A-50	Sequence 50, Appl	666	4	44.4	312	5	PCT-US92-09662-6	Sequence 6, Appli
594	4	44.4	303	2	US-08-294-871A-52	Sequence 52, Appl	667	4	44.4	315	4	US-09-434-774-16	Sequence 16, Appl
595	4	44.4	303	2	US-08-294-871A-54	Sequence 54, Appl	668	4	44.4	317	1	US-07-841-646-11	Sequence 11, Appl
596	4	44.4	303	2	US-08-294-871A-56	Sequence 56, Appl	669	4	44.4	317	1	US-08-147-023-11	Sequence 11, Appl
597	4	44.4	303	2	US-08-294-871A-58	Sequence 58, Appl	670	4	44.4	317	1	US-07-709-949-2	Sequence 2, Appli
598	4	44.4	303	2	US-08-294-871A-60	Sequence 60, Appl	671	4	44.4	317	1	US-08-447-570-11	Sequence 11, Appl
599	4	44.4	303	2	US-08-294-871A-62	Sequence 62, Appl	672	4	44.4	317	2	US-08-449-700-11	Sequence 11, Appl
600	4	44.4	303	2	US-08-294-871A-64	Sequence 64, Appl	673	4	44.4	317	2	US-08-449-699A-11	Sequence 11, Appl
601	4	44.4	303	2	US-08-294-871A-66	Sequence 66, Appl	674	4	44.4	318	4	US-08-878-474-3	Sequence 4, Appli
602	4	44.4	303	2	US-08-294-871A-68	Sequence 68, Appl	675	4	44.4	319	4	US-08-836-075A-44	Sequence 44, Appl
603	4	44.4	303	3	US-08-876-398A-2	Sequence 2, Appli	676	4	44.4	323	2	US-08-435-149-2	Sequence 4, Appli
604	4	44.4	303	3	US-08-876-398A-4	Sequence 4, Appli	677	4	44.4	323	4	US-09-172-063-21	Sequence 21, Appl
605	4	44.4	303	3	US-08-876-398A-6	Sequence 6, Appli	678	4	44.4	323	4	US-09-172-063-22	Sequence 22, Appl
606	4	44.4	303	3	US-08-876-398A-8	Sequence 8, Appli	679	4	44.4	323	4	US-08-643-212-18	Sequence 18, Appl
607	4	44.4	303	3	US-08-876-398A-10	Sequence 10, Appl	680	4	44.4	323	4	US-08-643-212-20	Sequence 20, Appl
608	4	44.4	303	3	US-08-876-398A-12	Sequence 12, Appl	681	4	44.4	323	4	US-08-643-212-22	Sequence 22, Appl
609	4	44.4	303	3	US-08-876-398A-14	Sequence 14, Appl	682	4	44.4	323	4	US-08-643-212-24	Sequence 24, Appl
610	4	44.4	303	3	US-08-876-398A-16	Sequence 16, Appl	683	4	44.4	323	4	US-08-643-212-26	Sequence 26, Appl
611	4	44.4	303	3	US-08-876-398A-18	Sequence 18, Appl	684	4	44.4	323	4	US-08-643-212-28	Sequence 28, Appl

685	4	44.4	324	1	US-08-310-416A-14	Sequence 14, Appl	758	4	44.4	367	2	US-08-737-045-14	Sequence 14, Appl
686	4	44.4	324	2	US-08-888-171-14	Sequence 14, Appl	759	4	44.4	367	3	US-08-932-871B-2	Sequence 2, Appl1
687	4	44.4	325	1	US-08-447-500-8	Sequence 8, Appl1	760	4	44.4	367	3	US-09-476-819-2	Sequence 2, Appl1
688	4	44.4	325	1	US-08-454-097-8	Sequence 8, Appl1	761	4	44.4	368	4	US-08-961-083-76	Sequence 76, Appl
689	4	44.4	325	1	US-08-453-866-8	Sequence 8, Appl1	762	4	44.4	368	4	US-09-413-574-4	Sequence 4, Appl1
690	4	44.4	325	3	US-08-185-359-8	Sequence 8, Appl1	763	4	44.4	368	4	US-08-991-677-6	Sequence 6, Appl1
691	4	44.4	326	1	US-07-603-133B-28	Sequence 28, Appl	764	4	44.4	369	4	US-09-108-020-40	Sequence 40, Appl
692	4	44.4	326	2	US-08-786-606-8	Sequence 8, Appl1	765	4	44.4	370	2	US-08-878-989-19	Sequence 19, Appl
693	4	44.4	328	1	US-08-414-926A-9	Sequence 9, Appl1	766	4	44.4	370	3	US-08-369-822C-2	Sequence 2, Appl1
694	4	44.4	328	2	US-08-926-922-9	Sequence 9, Appl1	767	4	44.4	370	3	US-08-582-776C-2	Sequence 2, Appl1
695	4	44.4	328	2	US-08-956-012-1	Sequence 1, Appl1	768	4	44.4	370	3	US-09-248-835-26	Sequence 26, Appl
696	4	44.4	328	3	US-09-253-682-9	Sequence 9, Appl1	769	4	44.4	370	3	US-08-434-831B-2	Sequence 2, Appl1
697	4	44.4	328	6	5212074-4	Patent No. 5212074	770	4	44.4	370	4	US-09-272-796-19	Sequence 19, Appl
698	4	44.4	331	2	US-08-986-217-7	Sequence 7, Appl1	771	4	44.4	371	4	US-09-104-308-11	Sequence 11, Appl1
699	4	44.4	332	2	US-08-637-763B-6	Sequence 6, Appl1	772	4	44.4	372	1	US-08-196-618-33	Sequence 33, Appl
700	4	44.4	332	2	US-08-637-763B-8	Sequence 8, Appl1	773	4	44.4	372	1	US-08-681-953-33	Sequence 33, Appl
701	4	44.4	332	3	US-09-170-354-6	Sequence 6, Appl1	774	4	44.4	373	2	US-08-812-129A-52	Sequence 52, Appl
702	4	44.4	332	3	US-09-170-354-8	Sequence 8, Appl1	775	4	44.4	374	1	US-07-914-281-11	Sequence 11, Appl
703	4	44.4	333	2	US-08-869-506-3	Sequence 3, Appl1	776	4	44.4	374	1	US-08-393-246-11	Sequence 11, Appl
704	4	44.4	333	3	US-09-128-967-3	Sequence 3, Appl1	777	4	44.4	374	1	US-08-525-058A-11	Sequence 11, Appl
705	4	44.4	335	1	US-08-348-792-2	Sequence 2, Appl1	778	4	44.4	374	2	US-08-696-731-11	Sequence 11, Appl
706	4	44.4	335	2	US-08-462-738-2	Sequence 2, Appl1	779	4	44.4	374	4	US-09-042-531-11	Sequence 11, Appl
707	4	44.4	336	2	US-08-474-379C-88	Sequence 88, Appl	780	4	44.4	375	1	US-07-803-622E-7	Sequence 7, Appl1
708	4	44.4	336	4	US-08-235-836C-52	Sequence 52, Appl	781	4	44.4	375	1	US-07-803-622E-9	Sequence 9, Appl1
709	4	44.4	337	1	US-08-447-500-10	Sequence 10, Appl	782	4	44.4	378	2	US-09-055-097-1	Sequence 1, Appl1
710	4	44.4	337	1	US-08-454-097-12	Sequence 12, Appl	783	4	44.4	379	1	US-08-347-029-2	Sequence 2, Appl1
711	4	44.4	337	1	US-08-453-866-10	Sequence 10, Appl	784	4	44.4	379	1	US-08-350-859-2	Sequence 2, Appl1
712	4	44.4	337	1	US-09-100-664A-11	Sequence 11, Appl	785	4	44.4	379	1	US-08-490-803-2	Sequence 2, Appl1
713	4	44.4	337	3	US-09-100-664A-12	Sequence 12, Appl	786	4	44.4	379	1	US-08-484-246-2	Sequence 2, Appl1
714	4	44.4	337	3	US-08-185-359-12	Sequence 12, Appl	787	4	44.4	379	2	US-08-457-254-2	Sequence 2, Appl1
715	4	44.4	339	1	US-08-248-629A-5	Sequence 5, Appl1	788	4	44.4	379	2	US-08-999-927-4	Sequence 2, Appl1
716	4	44.4	339	1	US-08-451-932-5	Sequence 5, Appl1	789	4	44.4	379	3	US-08-999-927-4	Sequence 2, Appl1
717	4	44.4	339	1	US-08-452-260-5	Sequence 5, Appl1	790	4	44.4	379	5	PCT-US94-08806-2	Sequence 2, Appl1
718	4	44.4	339	1	US-08-326-785-5	Sequence 5, Appl1	791	4	44.4	379	5	PCT-US95-01775-2	Sequence 2, Appl1
719	4	44.4	339	2	US-08-612-788-5	Sequence 5, Appl1	792	4	44.4	379	5	PCT-US95-01829-4	Sequence 4, Appl1
720	4	44.4	339	2	US-08-605-598B-5	Sequence 5, Appl1	793	4	44.4	379	5	PCT-US95-14933-2	Sequence 2, Appl1
721	4	44.4	339	2	US-08-429-743-5	Sequence 5, Appl1	794	4	44.4	379	5	PCT-US95-16626-2	Sequence 2, Appl1
722	4	44.4	339	2	US-08-866-735-5	Sequence 5, Appl1	795	4	44.4	382	4	US-09-142-551A-2	Sequence 2, Appl1
723	4	44.4	339	3	US-09-066-028-5	Sequence 5, Appl1	796	4	44.4	384	1	US-09-277-716-22	Sequence 22, Appl
724	4	44.4	339	5	PCT-US95-05107-5	Sequence 5, Appl1	797	4	44.4	384	1	US-07-688-532C-40	Sequence 40, Appl
725	4	44.4	341	4	US-09-196-293-14	Sequence 14, Appl	798	4	44.4	384	2	US-08-474-379C-40	Sequence 40, Appl
726	4	44.4	341	4	US-08-209-603E-14	Sequence 14, Appl	799	4	44.4	384	3	US-09-146-249E-40	Sequence 40, Appl
727	4	44.4	344	3	US-08-858-003-33	Sequence 33, Appl	800	4	44.4	386	6	US-08-206-188B-40	Sequence 40, Appl
728	4	44.4	344	3	US-09-078-166-33	Sequence 33, Appl	801	4	44.4	386	6	5171840-5	Patent No. 5171840
729	4	44.4	344	4	US-08-997-467-33	Sequence 33, Appl	802	4	44.4	387	1	US-08-314-596-40	Patent No. 5480796
730	4	44.4	344	6	5171840-7	Patent No. 5171840	803	4	44.4	387	1	US-08-314-596-42	Sequence 42, Appl
731	4	44.4	344	6	5480796-7	Patent No. 5480796	804	4	44.4	387	1	US-08-320-982-40	Sequence 40, Appl
732	4	44.4	345	1	US-08-102-942A-2	Sequence 2, Appl1	805	4	44.4	387	1	US-08-320-982-42	Sequence 42, Appl
733	4	44.4	346	2	US-08-602-359A-34	Sequence 34, Appl	806	4	44.4	387	2	US-08-872-302-6	Sequence 6, Appl1
734	4	44.4	349	2	US-08-483-926A-12	Sequence 12, Appl	807	4	44.4	387	2	US-08-819-037-40	Sequence 40, Appl
735	4	44.4	351	5	PCT-US93-05703-2	Sequence 2, Appl1	808	4	44.4	387	3	US-08-819-037-42	Sequence 42, Appl
736	4	44.4	352	2	US-08-483-926A-11	Sequence 11, Appl	809	4	44.4	390	1	US-08-347-792-15	Sequence 15, Appl
737	4	44.4	352	2	US-08-737-045-12	Sequence 12, Appl	810	4	44.4	390	1	US-08-431-357-15	Sequence 15, Appl
738	4	44.4	352	3	US-08-921-887-52	Sequence 52, Appl	811	4	44.4	390	4	US-08-392-542-3	Sequence 3, Appl1
739	4	44.4	356	2	US-08-602-713-12	Sequence 12, Appl	812	4	44.4	390	4	US-08-894-327-3	Sequence 3, Appl1
740	4	44.4	356	2	US-08-903-851-2	Sequence 2, Appl1	813	4	44.4	390	5	PCT-US95-15353-15	Sequence 15, Appl
741	4	44.4	356	4	US-08-989-493-12	Sequence 12, Appl	814	4	44.4	393	1	US-08-047-041A-25	Sequence 25, Appl
742	4	44.4	353	2	US-08-697-221-18	Sequence 18, Appl	815	4	44.4	393	1	US-08-047-041A-27	Sequence 27, Appl
743	4	44.4	353	2	US-08-697-221-19	Sequence 19, Appl	816	4	44.4	393	1	US-08-347-792-2	Sequence 2, Appl1
744	4	44.4	353	2	US-08-697-221-21	Sequence 21, Appl	817	4	44.4	393	1	US-08-390-516C-6	Sequence 6, Appl1
745	4	44.4	353	2	US-08-697-221-20	Sequence 20, Appl	818	4	44.4	393	1	US-08-390-516C-8	Sequence 8, Appl1
746	4	44.4	353	2	US-08-697-221-21	Sequence 21, Appl	819	4	44.4	393	1	US-08-431-357-2	Sequence 2, Appl1
747	4	44.4	353	2	US-08-697-221-22	Sequence 22, Appl	820	4	44.4	393	1	US-08-390-515A-6	Sequence 6, Appl1
748	4	44.4	353	2	US-08-697-221-23	Sequence 23, Appl	821	4	44.4	393	1	US-08-390-515A-8	Sequence 8, Appl1
749	4	44.4	353	2	US-08-697-221-24	Sequence 24, Appl	822	4	44.4	393	2	US-08-795-006A-32	Sequence 32, Appl
750	4	44.4	354	1	US-08-447-500-12	Sequence 12, Appl	823	4	44.4	393	2	US-08-697-221-2	Sequence 2, Appl1
751	4	44.4	354	1	US-08-454-097-10	Sequence 10, Appl	824	4	44.4	393	2	US-08-697-221-3	Sequence 3, Appl1
752	4	44.4	354	1	US-08-453-866-12	Sequence 12, Appl	825	4	44.4	393	2	US-08-697-221-4	Sequence 4, Appl1
753	4	44.4	354	2	US-08-204-288-2	Sequence 2, Appl1	826	4	44.4	393	2	US-08-697-221-11	Sequence 11, Appl
754	4	44.4	354	2	US-08-185-359-10	Sequence 10, Appl	827	4	44.4	393	2	US-08-697-221-12	Sequence 12, Appl
755	4	44.4	354	4	US-09-338-671-2	Sequence 2, Appl1	828	4	44.4	393	2	US-08-697-221-13	Sequence 13, Appl
756	4	44.4	365	4	US-08-715-325-2	Sequence 2, Appl1	829	4	44.4	393	2	US-08-697-221-14	Sequence 14, Appl
757	4	44.4	367	2	US-08-514-451A-7	Sequence 7, Appl1	830	4	44.4	393	2	US-08-697-221-15	Sequence 15, Appl

831	4	44.4	393	2	US-08-697-221-16	Sequence 16, Appl	904	4	44.4	430	1	US-08-643-763A-19	Sequence 19, Appl
832	4	44.4	393	2	US-08-697-221-25	Sequence 25, Appl	905	4	44.4	430	1	US-08-462-923-19	Sequence 19, Appl
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834	4	44.4	393	2	US-08-697-221-27	Sequence 27, Appl	907	4	44.4	430	2	US-08-459-346-4	Sequence 4, Appl
835	4	44.4	393	2	US-08-697-221-28	Sequence 28, Appl	908	4	44.4	430	2	US-08-445-468A-19	Sequence 19, Appl
836	4	44.4	393	2	US-08-801-718-6	Sequence 6, Appl	909	4	44.4	430	2	US-08-901-200A-6	Sequence 6, Appl
837	4	44.4	393	2	US-08-801-718-8	Sequence 8, Appl	910	4	44.4	430	2	US-08-449-700-25	Sequence 25, Appl
838	4	44.4	393	2	US-08-247-904B-12	Sequence 12, Appl	911	4	44.4	430	2	US-08-449-699A-25	Sequence 25, Appl
839	4	44.4	393	3	US-08-767-942A-23	Sequence 23, Appl	912	4	44.4	430	2	US-08-461-397A-19	Sequence 19, Appl
840	4	44.4	393	4	US-08-392-542-2	Sequence 2, Appl	913	4	44.4	430	2	US-08-912-088-19	Sequence 19, Appl
841	4	44.4	393	4	US-09-184-073-32	Sequence 32, Appl	914	4	44.4	430	3	US-08-278-730A-19	Sequence 19, Appl
842	4	44.4	393	4	US-08-328-673A-9	Sequence 9, Appl	915	4	44.4	430	3	US-08-889-419-4	Sequence 4, Appl
843	4	44.4	393	4	US-08-894-327-2	Sequence 2, Appl	916	4	44.4	430	3	US-08-445-467-19	Sequence 19, Appl
844	4	44.4	393	5	PCT-US95-15353-2	Sequence 2, Appl	917	4	44.4	430	3	US-08-480-515A-19	Sequence 19, Appl
845	4	44.4	394	3	US-08-466-366-2	Sequence 2, Appl	918	4	44.4	430	4	US-09-219-391-6	Sequence 6, Appl
846	4	44.4	394	6	5223418-2	Patent No. 5223418	919	4	44.4	430	4	PCT-US90-07654-2	Sequence 2, Appl
847	4	44.4	396	2	US-08-926-253-2	Sequence 2, Appl	920	4	44.4	430	5	PCT-US92-01968-19	Sequence 19, Appl
848	4	44.4	396	3	US-09-120-074-2	Sequence 2, Appl	921	4	44.4	430	5	PCT-US93-05446-9	Sequence 9, Appl
849	4	44.4	396	4	US-09-330-611-12	Sequence 12, Appl	922	4	44.4	430	5	PCT-US93-07189-4	Sequence 4, Appl
850	4	44.4	398	1	US-08-446-777-2	Sequence 2, Appl	923	4	44.4	430	5	PCT-US93-07190-19	Sequence 19, Appl
851	4	44.4	398	2	US-08-599-171A-29	Sequence 29, Appl	924	4	44.4	430	5	PCT-US93-07221-19	Sequence 19, Appl
852	4	44.4	398	2	US-08-284-391B-29	Sequence 29, Appl	925	4	44.4	430	5	PCT-US93-08742-19	Sequence 19, Appl
853	4	44.4	398	2	US-08-646-590B-29	Sequence 29, Appl	926	4	44.4	430	5	PCT-US93-08808-19	Sequence 19, Appl
854	4	44.4	398	3	US-09-069-226-29	Sequence 29, Appl	927	4	44.4	430	5	PCT-US93-08885-19	Sequence 19, Appl
855	4	44.4	398	4	US-09-412-184-29	Sequence 29, Appl	928	4	44.4	430	5	PCT-US93-10520-6	Sequence 6, Appl
856	4	44.4	399	2	US-08-839-581A-2	Sequence 2, Appl	929	4	44.4	431	1	US-07-841-646-2	Sequence 2, Appl
857	4	44.4	400	1	US-09-023-591A-2	Sequence 2, Appl	930	4	44.4	431	1	US-07-901-703-2	Sequence 2, Appl
858	4	44.4	400	1	US-07-764-731B-10	Sequence 10, Appl	931	4	44.4	431	1	US-07-539-736-4	Sequence 4, Appl
859	4	44.4	401	2	US-08-591-079-4	Sequence 4, Appl	932	4	44.4	431	1	US-08-147-023-2	Sequence 2, Appl
860	4	44.4	401	2	US-08-591-079-6	Sequence 6, Appl	933	4	44.4	431	1	US-08-206-864-2	Sequence 2, Appl
861	4	44.4	405	1	US-08-370-193A-9	Sequence 9, Appl	934	4	44.4	431	1	US-08-278-729A-17	Sequence 17, Appl
862	4	44.4	405	1	US-09-413-574-2	Sequence 2, Appl	935	4	44.4	431	1	US-08-480-528A-4	Sequence 4, Appl
863	4	44.4	406	1	US-07-978-687-38	Sequence 38, Appl	936	4	44.4	431	1	US-08-479-666-4	Sequence 4, Appl
864	4	44.4	406	5	PCT-US91-05801-38	Sequence 38, Appl	937	4	44.4	431	1	US-08-155-343A-17	Sequence 17, Appl
865	4	44.4	408	1	US-07-841-646-15	Sequence 15, Appl	938	4	44.4	431	1	US-08-406-672-17	Sequence 17, Appl
866	4	44.4	408	1	US-08-147-023-15	Sequence 15, Appl	939	4	44.4	431	1	US-08-643-468A-17	Sequence 17, Appl
867	4	44.4	408	1	US-08-447-570-15	Sequence 15, Appl	940	4	44.4	431	1	US-08-447-570-2	Sequence 2, Appl
868	4	44.4	408	2	US-08-449-700-15	Sequence 15, Appl	941	4	44.4	431	1	US-08-643-763A-17	Sequence 17, Appl
869	4	44.4	408	2	US-08-449-699A-15	Sequence 15, Appl	942	4	44.4	431	1	US-08-462-623-17	Sequence 17, Appl
870	4	44.4	409	2	US-08-809-740A-5	Sequence 5, Appl	943	4	44.4	431	1	US-08-451-953A-17	Sequence 17, Appl
871	4	44.4	410	1	US-08-123-345A-7	Sequence 7, Appl	944	4	44.4	431	2	US-08-459-346-2	Sequence 2, Appl
872	4	44.4	410	1	US-08-123-343A-7	Sequence 7, Appl	945	4	44.4	431	2	US-08-445-468A-17	Sequence 17, Appl
873	4	44.4	410	1	US-08-073-807A-16	Sequence 16, Appl	946	4	44.4	431	2	US-08-901-200A-4	Sequence 4, Appl
874	4	44.4	410	2	US-08-472-666-2	Sequence 2, Appl	947	4	44.4	431	2	US-08-481-337A-10	Sequence 10, Appl
875	4	44.4	410	4	US-09-431-573-4	Sequence 4, Appl	948	4	44.4	431	2	US-08-449-700-2	Sequence 2, Appl
876	4	44.4	410	4	US-09-431-573-5	Sequence 5, Appl	949	4	44.4	431	2	US-07-989-847-6	Sequence 6, Appl
877	4	44.4	410	5	PCT-US96-07615-2	Sequence 2, Appl	950	4	44.4	431	2	US-08-449-699A-2	Sequence 2, Appl
878	4	44.4	413	2	US-08-481-814A-8	Sequence 8, Appl	951	4	44.4	431	2	US-08-696-268B-4	Sequence 4, Appl
879	4	44.4	413	2	US-08-282-197C-49	Sequence 49, Appl	952	4	44.4	431	2	US-08-461-397A-17	Sequence 17, Appl
880	4	44.4	413	3	US-08-836-583-2	Sequence 2, Appl	953	4	44.4	431	2	US-08-912-088-17	Sequence 17, Appl
881	4	44.4	415	1	US-08-381-936-2	Sequence 2, Appl	954	4	44.4	431	3	US-08-278-730A-17	Sequence 17, Appl
882	4	44.4	415	3	US-08-943-374-2	Sequence 2, Appl	955	4	44.4	431	3	US-08-458-811-2	Sequence 2, Appl
883	4	44.4	415	4	US-08-927-219-8	Sequence 8, Appl	956	4	44.4	431	3	US-08-889-419-2	Sequence 2, Appl
884	4	44.4	417	2	US-08-672-564-9	Sequence 9, Appl	957	4	44.4	431	3	US-08-445-467-17	Sequence 17, Appl
885	4	44.4	418	5	PCT-US94-01321-72	Sequence 72, Appl	958	4	44.4	431	3	US-08-480-515A-17	Sequence 17, Appl
886	4	44.4	420	1	US-07-700-526-1	Sequence 1, Appl	959	4	44.4	431	3	US-08-459-129-2	Sequence 2, Appl
887	4	44.4	420	5	PCT-US92-03132-1	Sequence 1, Appl	960	4	44.4	431	4	US-09-219-391-4	Sequence 4, Appl
888	4	44.4	425	4	US-08-867-611-22	Sequence 22, Appl	961	4	44.4	431	4	US-08-469-411-6	Sequence 6, Appl
889	4	44.4	425	5	PCT-US92-06965A-27	Sequence 27, Appl	962	4	44.4	431	5	PCT-US90-07654-4	Sequence 4, Appl
890	4	44.4	426	1	US-08-455-550-21	Sequence 21, Appl	963	4	44.4	431	5	PCT-US91-07635-2	Sequence 2, Appl
891	4	44.4	429	1	US-08-234-783-4	Sequence 4, Appl	964	4	44.4	431	5	PCT-US92-01968-17	Sequence 17, Appl
892	4	44.4	429	1	US-08-456-907-4	Sequence 4, Appl	965	4	44.4	431	5	PCT-US93-05446-2	Sequence 2, Appl
893	4	44.4	429	5	PCT-US95-05523-4	Sequence 4, Appl	966	4	44.4	431	5	PCT-US93-07189-2	Sequence 2, Appl
894	4	44.4	430	1	US-07-841-646-25	Sequence 25, Appl	967	4	44.4	431	5	PCT-US93-07190-17	Sequence 17, Appl
895	4	44.4	430	1	US-07-901-703-9	Sequence 9, Appl	968	4	44.4	431	5	PCT-US93-07231-17	Sequence 17, Appl
896	4	44.4	430	1	US-08-147-023-25	Sequence 25, Appl	969	4	44.4	431	5	PCT-US93-08742-17	Sequence 17, Appl
897	4	44.4	430	1	US-08-278-729A-19	Sequence 19, Appl	970	4	44.4	431	5	PCT-US93-08808-17	Sequence 17, Appl
898	4	44.4	430	1	US-08-480-528A-6	Sequence 6, Appl	971	4	44.4	431	5	PCT-US93-08885-17	Sequence 17, Appl
899	4	44.4	430	1	US-08-479-666-6	Sequence 6, Appl	972	4	44.4	431	5	PCT-US93-10520-4	Sequence 4, Appl
900	4	44.4	430	1	US-08-155-343A-19	Sequence 19, Appl	973	4	44.4	431	5	PCT-US95-05467-10	Sequence 10, Appl
901	4	44.4	430	1	US-08-406-672-19	Sequence 19, Appl	974	4	44.4	431	5	PCT-US95-06724-2	Sequence 2, Appl
902	4	44.4	430	1	US-08-643-563A-19	Sequence 19, Appl	975	4	44.4	432	5	US-08-411-607A-3	Sequence 3, Appl
903	4	44.4	430	1	US-08-447-570-25	Sequence 25, Appl	976	4	44.4	433	2	US-08-867-149-1	Sequence 1, Appl

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577 4 44.4 433 2 US-08-808-374-1 Sequence 1, Appli
978 4 44.4 433 3 US-09-100-409A-1 Sequence 1, Appli
979 4 44.4 433 6 5171838-13 Patent No. 5171838
980 4 44.4 437 2 US-08-883-515-4 Sequence 4, Appli
981 4 44.4 437 3 US-08-486-099-91 Sequence 91, Appli
982 4 44.4 437 3 US-08-360-107A-101 Sequence 101, Appli
983 4 44.4 437 3 US-08-484-223B-91 Sequence 91, Appli
984 4 44.4 437 3 US-08-919-597-91 Sequence 91, Appli
985 4 44.4 437 3 US-08-475-668A-91 Sequence 91, Appli
986 4 44.4 437 3 US-08-485-551A-91 Sequence 91, Appli
987 4 44.4 437 3 US-08-471-913A-91 Sequence 91, Appli
988 4 44.4 437 4 US-08-485-264A-91 Sequence 91, Appli
989 4 44.4 438 2 US-08-282-197C-59 Sequence 59, Appli
990 4 44.4 439 1 US-08-553-999B-2 Sequence 2, Appli
991 4 44.4 439 1 US-08-959-638-9 Sequence 9, Appli
992 4 44.4 445 1 US-08-447-925-6 Sequence 6, Appli
993 4 44.4 446 2 US-08-244-205-5 Sequence 5, Appli
994 4 44.4 446 5 PCT-US92-10284-5 Sequence 5, Appli
995 4 44.4 446 5 PCT-US94-01321-10 Sequence 10, Appli
996 4 44.4 448 2 US-08-959-749-2 Sequence 2, Appli
997 4 44.4 449 1 US-08-102-942A-6 Sequence 6, Appli
998 4 44.4 449 1 US-08-102-942A-6 Sequence 6, Appli
999 4 44.4 453 1 US-08-417-330A-18 Sequence 18, Appli
1000 4 44.4 453 1 US-08-570-157-7 Sequence 7, Appli
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ALIGNMENTS

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RESULT 1
US-08-456-670B-26
; Sequence 26, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, STEFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINKEWILLER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLER, WHITE, ZELANO & BRANTGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456.670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: A35
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412.227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075.248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
```

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; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
; US-08-456-670B-26
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Query Match 100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No.1.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 VSTPVAPTO 9
Db 1 VSTPVAPTO 9
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RESULT 2
US-08-127-499A-27
; Sequence 27, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-127-499A-27
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Query Match 100.0%; Score 9; DB 1; Length 21;
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Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
|||||
DB 2 VSTPVAPTQ 10

RESULT 3

US-08-482-847-27
; Sequence 27, Application US/08482847
; Patent No. 5556757

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane

TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR

TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: unknown

US-08-482-847-27

Query Match 100.0%; Score 9; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
|||||
DB 2 VSTPVAPTQ 10

RESULT 4

US-08-456-670B-39
; Sequence 39, Application US/08456670B
; Patent No. 5932415

GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA

APPLICANT: LINXWEILER, WINFRIED

APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED

APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER

APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: US

ZIP: 22201
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248

FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4

FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1694DI
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

TELEX: 64191
INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
ORIGINAL SOURCE:

ORGANISM: Listeria monocytogenes
STRAIN: EGD

US-08-456-670B-39

Query Match 100.0%; Score 9; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
|||||
DB 76 VSTPVAPTQ 84

RESULT 5
US-08-456-670B-40
; Sequence 40, Application US/08456670B
; Patent No. 5932415

GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA

APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-40

Query Match 100.0%; Score 9; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPTQ 9
Db 145 VSTPVAPTQ 153

RESULT 6
US-08-127-499A-26
Sequence 26, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra

TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-26

Query Match 100.0%; Score 9; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPTQ 9
Db 145 VSTPVAPTQ 153

RESULT 7
US-08-482-847-26
Sequence 26, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499

FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-26

Query Match 100.0%; Score 9; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
|||||
Db 145 VSTPVAPTQ 153

RESULT 8
US-08-456-670B-30
Sequence 30, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINWELLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-30

Query Match 88.9%; Score 8; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVAPTQ 9
|||||
Db 1 STPVAPTQ 8

RESULT 9
US-08-456-670B-31
Sequence 31, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINWELLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

Query Match 66.7%; Score 6; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPQ 9
11111
Db 1 PVAPQ 6

RESULT 10
US-08-456-670B-17
Sequence 17, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4

FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note="SOME OR ALL XAA AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14-20
OTHER INFORMATION: /note="SOME OR ALL XAA AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-17

Query Match 66.7%; Score 6; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPQ 9
11111
Db 8 PVAPQ 13

RESULT 11
US-09-001-984C-55
Sequence 55, Application US/09001984C
Patent No. 6245331
GENERAL INFORMATION:
APPLICANT: Laal, Suman
APPLICANT: Bellisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: NYU-011
CURRENT APPLICATION NUMBER: US/09/001,984C
CURRENT FILING DATE: 1997-12-31
PRIOR APPLICATION NUMBER: 60/034,003
PRIOR FILING DATE: 1996-12-31
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 55
LENGTH: 11
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis strain H37rv
US-09-001-984C-55

Query Match 55.6%; Score 5; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
11111
Db 1 TPVAP 5

RESULT 12

US-07-899-535A-1
; Sequence 1, Application US/07899535A
; Patent No. 5428011
; GENERAL INFORMATION:
; APPLICANT: Sheth, Anil R.
; APPLICANT: Garde, Seema
; TITLE OF INVENTION: Pharmaceutical Preparations For
; TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
; TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mr. George Loud
; STREET: 2001 Jefferson Davis Highway, Suite 306
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/899,535A
; FILING DATE: 16-JUN-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Loud, George A.
; REGISTRATION NUMBER: 25,814
; REFERENCE/DOCKET NUMBER: S&B-A835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-0960
; TELEFAX: 703-415-0962
; TELEX: 24 8614
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; US-07-899-535A-1

Query Match 55.6%; Score 5; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
DB 53 VSTPV 57

RESULT 13
US-08-086-428B-57
; Sequence 57, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK

COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
US-08-086-428B-57

Query Match 55.6%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
DB 50 PVAPT 54

RESULT 14
US-08-440-103-44
; Sequence 44, Application US/08440103
; Patent No. 5670152
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,103
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113

REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-103-44

Query Match 55.6%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
Db 50 PVAPT 54

RESULT 15
US-08-440-542-44
Sequence 44, Application US/08440542
Patent No. 5670153
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
TITLE OF INVENTION: Immunoactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,542
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-542-44

Query Match 55.6%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
Db 50 PVAPT 54

RESULT 16
US-08-231-368-44
Sequence 44, Application US/08231368
Patent No. 5756312
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
TITLE OF INVENTION: Immunoactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-368-44

Query Match 55.6%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
Db 50 PVAPT 54

RESULT 17
US-08-440-210-44
Sequence 44, Application US/08440210
Patent No. 5766845
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
TITLE OF INVENTION: Immunoactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville

STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,210
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205,001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-210-44

Query Match 55.6%; Score 5; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
|||||
DB 50 PVAPT 54

RESULT 18
US-08-468-570-57
Sequence 57, Application US/08468570
Patent No. 5871962
GENERAL INFORMATION:
APPLICANT: BURK, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
US-08-468-570-57

Query Match 55.6%; Score 5; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
|||||
DB 50 PVAPT 54

RESULT 19
US-08-290-665A-57
Sequence 57, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BURK, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid

STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
US-08-290-665A-57

Query Match 55.6%; Score 5; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
|||||
DB 50 PVAPT 54

RESULT 20
US-08-444-818-167
Sequence 167, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
City: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: JH27
US-08-444-818-167

Query Match 55.6%; Score 5; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
|||||
DB 125 PVAPT 129

RESULT 21
PCT-US95-10398-57
Sequence 57, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R. H. AND
APPLICANT: PURCELL, R. H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
City: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
PCT-US95-10398-57

Query Match 55.6%; Score 5; DB 5; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPT 8
|||||
DB 50 PVAPT 54

RESULT 22
US-08-969-644-12
Sequence 12, Application US/08969644
Patent No. 6096519
GENERAL INFORMATION:
APPLICANT: Rattli, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA

TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,152
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-969-644-12

Query Match 55.6%; Score 5; DB 3; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
|||||
DB 40 STPVA 44

RESULT 23
US-08-444-189-12
Sequence 12, Application US/08444189
Patent No. 6110705
GENERAL INFORMATION:
APPLICANT: Rattl, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCID PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA

ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:
APPLICATION NUMBER: US/07/991,512
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-189-12

Query Match 55.6%; Score 5; DB 3; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
|||||
DB 40 STPVA 44

RESULT 24
US-08-465-465-2
Sequence 2, Application US/08465465
Patent No. 6210968
GENERAL INFORMATION:
APPLICANT: Giulio Rattl
TITLE OF INVENTION: RECOMBINANT CHLAMYDIA TRACHOMATIS PCP3
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6210968rirs
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 KB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,465
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,980
FILING DATE: 19-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Leggaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: CHIR-0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-465-2

Query Match 55.6%; Score 5; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
|||||
Db 40 STPVA 44

RESULT 25
US-08-468-544-12
Sequence 12, Application US/08468544
Patent No. 6248563
GENERAL INFORMATION:
APPLICANT: Ratti, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-468-544-12

Query Match 55.6%; Score 5; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
|||||
Db 40 STPVA 44

RESULT 26
US-08-382-184-3
Sequence 3, Application US/08382184
Patent No. 5714593
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-08-382-184-3

Query Match 55.6%; Score 5; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
|||||
Db 27 TPVAP 31

RESULT 27
US-08-641-356-3
Sequence 3, Application US/08641356
Patent No. 5865130
GENERAL INFORMATION:
APPLICANT:

;; TITLE OF INVENTION: MICROBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
;; TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
;; NUMBER OF SEQUENCES: 3
;; CORRESPONDENCE ADDRESS: 3
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER &
;; ADDRESSEE: NEUSTADT, P.C.
;; STREET: 1755 S. Jefferson Davis Highway, Suite 400
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/641,356
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/382,184
;; FILING DATE: 01-FEB-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 22640720
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2220
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; US-08-641-356-3

Query Match 55.6%; Score 5; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
DB 27 TPVAP 31

RESULT 28
US-09-132-528-4
; Sequence 4, Application US/09132528A
; Patent No. 6221353
; GENERAL INFORMATION:
; APPLICANT: LAQUEYERIE, ANNE
; APPLICANT: MARCHAL, GILLES
; APPLICANT: PESCHER, PASCALE
; APPLICANT: ROMAIN, FELIX
; TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
; TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 0660-0138-0DIY
; CURRENT APPLICATION NUMBER: US/09/132,528A
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/641,356
; EARLIER FILING DATE: 1996-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 286
; TYPE: PRT

;; ORGANISM: Mycobacterium tuberculosis
;; US-09-132-528-4

Query Match 55.6%; Score 5; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
DB 27 TPVAP 31

RESULT 29
US-08-875-494-3
; Sequence 3, Application US/08875494
; Patent No. 6221610
; GENERAL INFORMATION:
; APPLICANT: LAQUEYERIE, ANNE
; APPLICANT: MARCHAL, GILLES
; APPLICANT: PESCHER, PASCALE
; APPLICANT: ROMAIN, FELIX
; TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
; TITLE OF INVENTION: AND THEIR USES FOR VACCINES AND FOR THE DETECTION OF
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 0660-0122-0 PCT
; CURRENT APPLICATION NUMBER: US/08/875,494
; CURRENT FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: PCT/FR96/00166
; EARLIER FILING DATE: 1996-02-01
; EARLIER APPLICATION NUMBER: 382184
; EARLIER FILING DATE: 1995-02-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
;; US-08-875-494-3

Query Match 55.6%; Score 5; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
DB 27 TPVAP 31

RESULT 30
US-08-382-184-2
; Sequence 2, Application US/08382184
; Patent No. 5714593
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
; TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
; TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-382-184-2

Query Match 55.6%; Score 5; DB 1; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
Db 66 TPVAP 70

RESULT 31
US-08-641-356-2
Sequence 2, Application US/08641356
Patent No. 5866130

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBACTERIAL PROTEINS, THEM AND THEIR USE FOR VACCINES
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/641,356

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/382,184

FILING DATE: 01-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 22640720

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 55.6%; Score 5; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
Db 66 TPVAP 70

RESULT 32
US-09-132-528-2
Sequence 2, Application US/09132528A
Patent No. 6221353

GENERAL INFORMATION:

APPLICANT: LAQUEYERIE, Anne

APPLICANT: MARCHAL, Gilles

APPLICANT: PESCHER, Pascale

APPLICANT: ROMAIN, Felix

TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM

TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 0660-0138-0D1V

CURRENT APPLICATION NUMBER: US/09/132,528A

CURRENT FILING DATE: 1998-08-11

EARLIER APPLICATION NUMBER: 08/641,356

EARLIER FILING DATE: 1996-04-30

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 325

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis

US-09-132-528-2

Query Match 55.6%; Score 5; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
|||||
Db 66 TPVAP 70

RESULT 33
US-09-132-528-3
Sequence 3, Application US/09132528A
Patent No. 6221353

GENERAL INFORMATION:

APPLICANT: LAQUEYERIE, Anne

APPLICANT: MARCHAL, Gilles

APPLICANT: PESCHER, Pascale

APPLICANT: ROMAIN, Felix

TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM

TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 0660-0138-0D1V

CURRENT APPLICATION NUMBER: US/09/132,528A

CURRENT FILING DATE: 1998-08-11

EARLIER APPLICATION NUMBER: 08/641,356

EARLIER FILING DATE: 1996-04-30

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 325

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis

US-09-132-528-3

Query Match 55.6%; Score 5; DB 4; Length 325;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
|||||

DB 66 TPVAP 70

RESULT 34

US-08-875-494-2
; Sequence 2, Application US/08875494
; Patent No. 6221610
; GENERAL INFORMATION:
; APPLICANT: LAOUEYERIE, ANNE
; APPLICANT: MARCHEL, GILLES
; APPLICANT: PESCHER, PASCAL
; APPLICANT: ROMAIN, FELIX
; TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
; TITLE OF INVENTION: AND THEIR USES FOR VACCINES AND FOR THE DETECTION OF
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 0660-0122-0 PCT
; CURRENT APPLICATION NUMBER: US/08/875,494
; CURRENT FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: PCT/FR96/00166
; EARLIER FILING DATE: 1996-02-01
; EARLIER APPLICATION NUMBER: 382184
; EARLIER FILING DATE: 1995-02-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-08-875-494-2

Query Match 55.6%; Score 5; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAP 7
|||||

DB 66 TPVAP 70

RESULT 35

US-08-444-818-152
; Sequence 152, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.

REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885

INFORMATION FOR SEQ ID NO: 152:

SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-444-818-152

Query Match 55.6%; Score 5; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
|||||

DB 113 PVAPT 117

RESULT 36

US-08-444-818-156
; Sequence 156, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human 27
US-08-444-818-156

Query Match 55.6%; Score 5; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVAPT 8
11111
Db 113 PVAPT 117

RESULT 37
US-08-137-627-4
; Sequence 4, Application US/08137627
; Patent No. 5681737
; GENERAL INFORMATION:
; APPLICANT: Gee, Pauline
; APPLICANT: Maion, Dorothy M.
; APPLICANT: Ames, Bruce N.
; TITLE OF INVENTION: A DETECTION SYSTEM FOR MUTAGENS THAT
; TITLE OF INVENTION: IDENTIFIES MUTAGENIC CHANGES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: Karen S. Smith
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,627
; FILING DATE: 15-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Karen S.
; REGISTRATION NUMBER: 31,426
; REFERENCE/DOCKET NUMBER: A-58312/KSS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-137-627-4

Query Match 55.6%; Score 5; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
11111
Db 249 STPVA 253

RESULT 38
US-08-865-348-4
; Sequence 4, Application US/08865348
; Patent No. 5869258
; GENERAL INFORMATION:
; APPLICANT: Gee, Pauline
; APPLICANT: Maion, Dorothy M.
; APPLICANT: Ames, Bruce N.
; TITLE OF INVENTION: A DETECTION SYSTEM FOR MUTAGENS THAT
; TITLE OF INVENTION: ALSO IDENTIFIES MUTAGENIC CHANGES
; NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: Karen S. Smith
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,348
; FILING DATE: 28-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/137,627
; FILING DATE: 15-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Karen S.
; REGISTRATION NUMBER: 31,426
; REFERENCE/DOCKET NUMBER: A-58312-1/KSS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-865-348-4

Query Match 55.6%; Score 5; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
11111
Db 249 STPVA 253

RESULT 39
US-08-969-644-23
; Sequence 23, Application US/08969644
; Patent No. 6096519
; GENERAL INFORMATION:
; APPLICANT: Rattli, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tece, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,152
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
STRAIN: E. coli ATCC 68315
IMMEDIATE SOURCE:
CLONE: plasmid p03/GO/MC1
FEATURE:
NAME/KEY: Region
LOCATION: 1..370
OTHER INFORMATION: /label= polypeptide
OTHER INFORMATION: /note= "polypeptide is a fusion protein of the
OTHER INFORMATION: RNA polymerase from bacteriophage MS2 and the
OTHER INFORMATION: protein encoded by the ORF3D gene of C.
FEATURE:
NAME/KEY: Region
LOCATION: 107..370
OTHER INFORMATION: /label= region
OTHER INFORMATION: /note= "this portion of the fusion protein is the
OTHER INFORMATION: protein encoded by the ORF3D gene."
FEATURE:
NAME/KEY: Region
LOCATION: 1..106
OTHER INFORMATION: /label= region
OTHER INFORMATION: /note= "this portion of the fusion protein is a
OTHER INFORMATION: fragment of the RNA polymerase gene from the
OTHER INFORMATION: bacteriophage MS2."
US-08-969-644-23
Query Match 55.6%; Score 5; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 STPVA 6
|||||
DB 146 STPVA 150
RESULT 40
US-08-444-189-23
Sequence 23, Application US/08444189
Patent No. 6110705
GENERAL INFORMATION:
APPLICANT: Ratelli, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:
APPLICATION NUMBER: US/07/991,512
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
STRAIN: E. coli ATCC 68315
IMMEDIATE SOURCE:
CLONE: plasmid p03/GO/MC1
FEATURE:
NAME/KEY: Region
LOCATION: 1..370
OTHER INFORMATION: /label= polypeptide
OTHER INFORMATION: /note= "polypeptide is a fusion protein of the
OTHER INFORMATION: RNA polymerase from bacteriophage MS2 and the
OTHER INFORMATION: protein encoded by the ORF3D gene of C.
FEATURE:
NAME/KEY: Region
LOCATION: 107..370
OTHER INFORMATION: /label= region
OTHER INFORMATION: /note= "this portion of the fusion protein is the
OTHER INFORMATION: protein encoded by the ORF3D gene."
FEATURE:
NAME/KEY: Region
LOCATION: 1..106
OTHER INFORMATION: /label= region
OTHER INFORMATION: /note= "this portion of the fusion protein is a
OTHER INFORMATION: fragment of the RNA polymerase gene from the
OTHER INFORMATION: bacteriophage MS2."
US-08-444-189-23
Query Match 55.6%; Score 5; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 STPVA 6
|||||

Db 146 STPVA 150

RESULT 41
US-08-468-544-23
Sequence 23, Application US/08468544
Patent No. 6248563
GENERAL INFORMATION:
APPLICANT: Ratelli, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tece, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
ORIGINAL SOURCE:
STRAIN: E. coli ATCC 68315
IMMEDIATE SOURCE:
CLONE: plasmid P03/GO/MC1
FEATURE:
NAME/KEY: Region
LOCATION: 1..370
OTHER INFORMATION: /label- polypeptide is a fusion protein of the
OTHER INFORMATION: /note- "polymerase from bacteriophage MS2 and the
OTHER INFORMATION: protein encoded by the ORF3D gene of C.
FEATURE:
NAME/KEY: Region
LOCATION: 107..370
OTHER INFORMATION: /label- region
OTHER INFORMATION: /note- "this portion of the fusion protein is the
OTHER INFORMATION: protein encoded by the ORF3D gene."
NAME/KEY: Region
LOCATION: 1..106
OTHER INFORMATION: /label- region

OTHER INFORMATION: /note- "this portion of the fusion protein is a
OTHER INFORMATION: fragment of the RNA polymerase gene from the
OTHER INFORMATION: bacteriophage MS2."
US-08-468-544-23

Query Match 55.6%; Score 5; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVA 6
Db 146 STPVA 150

RESULT 42
US-08-853-659A-41
Sequence 41, Application US/08853659A
Patent No. 5925522
GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saifer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: OF A
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
STREET: P.O. Box 999
CITY: Washington Way
STATE: Washington
COUNTRY: U.S.A.
ZIP: 99352
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 MB storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
FILING DATE: Unknown
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: n/a
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-853-659A-41

Query Match 55.6%; Score 5; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPV 5
Db 294 VSTPV 298

RESULT 43
US-08-852-824-4
Sequence 4, Application US/08852824C
Patent No. 6060272
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Human G-protein Coupled Receptors
FILE REFERENCE: 1488.1220000
CURRENT APPLICATION NUMBER: US/08/852,824C

; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 384
; TYPE: PRT
; ORGANISM: genomic
US-08-853-824-4

Query Match 55.6%; Score 5; DB 3; Length 384;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
| | | | |
DB 6 TPVAP 10

RESULT 44

US-08-769-309A-15
; Sequence 15, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Knauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,309A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5741890and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-769-309A-15

Query Match 55.6%; Score 5; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
| | | | |
DB 44 STPVA 48

RESULT 45
US-08-994-570-15

; Sequence 15, Application US/08994570
; Patent No. 6090929
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Knauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,570
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090929and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-994-570-15

Query Match 55.6%; Score 5; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 STPVA 6
| | | | |
DB 44 STPVA 48

RESULT 46
US-08-839-008-5
; Sequence 5, Application US/08839008
; Patent No. 5916758
; GENERAL INFORMATION:
; APPLICANT: Hurle, Mark R
; APPLICANT: McDonnell, Peter C
; APPLICANT: McNulty, Dean E
; APPLICANT: Rosen, Craig A
; APPLICANT: Siemens, Ivo R
; APPLICANT: Young, Peter R
; APPLICANT: Yue, Tian-Li
; TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,008
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/563,697
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50384
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-008-5

Query Match 55.6%; Score 5; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAP 7
Db 330 TPVAP 334

RESULT 47
US-08-403-545-4
Sequence 4, Application US/08403545
Patent No. 5656483
GENERAL INFORMATION:
APPLICANT: Sokatch, John R.
APPLICANT: Sykes, Pamela Joy
APPLICANT: Madhusudhan, K.T.
TITLE OF INVENTION: Genes Encoding Operon and Promoter for
TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putida
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn D. Moon
ADDRESSEE: Dunlap, Coddling, Peterson and Lee
STREET: 9400 N. Broadway, Suite 420
CITY: Oklahoma City
STATE: Oklahoma
COUNTRY: USA
ZIP: 73114
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 Kb Storage
COMPUTER: IBM AT
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Professional Write 2.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,545
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7/603/781
APPLICATION NUMBER: 07/172,148
FILING DATE: 23-003-1988
ATTORNEY/AGENT INFORMATION:
NAME: Carolyn D. Moon
REGISTRATION NUMBER: 33,022
REFERENCE/DOCKET NUMBER: 5820.101

TELECOMMUNICATION INFORMATION:
TELEPHONE: Attorney, (405) 478-5344
TELEFAX: Attorney, (405) 478-5349
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 Amino acids
TYPE: Amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E2 component
LOCATION: 3098-4363, does not include initiating methionine
IDENTIFICATION METHOD: N-terminal sequence
PUBLICATION INFORMATION:
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Comparison of the amion acid sequences of the
TITLE: transacylase components of branched-chain oxoacid
TITLE: dehydrogenase of Pseudomonas putida, and the pyruvate and
TITLE: 2-oxoglutarate dehydrogenases of Escherichia coli
JOURNAL: European Journal of Biochemistry
VOLUME: 176
PAGES: 165-169
DATE: 1988
US-08-403-545-4

Query Match 55.6%; Score 5; DB 1; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPV 5
Db 351 VSTPV 355

RESULT 48
US-08-404-381-4
Sequence 4, Application US/08404381
Patent No. 6168945
GENERAL INFORMATION:
APPLICANT: Sokatch, John R.
APPLICANT: Sykes, Pamela Joy
APPLICANT: Madhusudhan, K.T.
TITLE OF INVENTION: Genes Encoding Operon and Promoter for
TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putid
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn D. Moon
ADDRESSEE: Dunlap, Coddling, Peterson and Lee
STREET: 9400 N. Broadway, Suite 420
CITY: Oklahoma City
STATE: Oklahoma
COUNTRY: USA
ZIP: 73114
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 kb Storage
COMPUTER: IBM AT
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Professional Write 2.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,381
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,781
APPLICATION NUMBER: 07/172,148
FILING DATE: 23-003-1988

ATTORNEY/AGENT INFORMATION:
NAME: Carolyn D. Moon
REGISTRATION NUMBER: 33,022
REFERENCE/DOCKET NUMBER: 5820.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: Attorney, (405) 478-5344
TELEFAX: Attorney, (405) 478-5349
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: E2 component
LOCATION: 3098-4363, does not include initiating methionine
IDENTIFICATION METHOD: N-terminal sequence
PUBLICATION INFORMATION:
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Walter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Comparison of the amion acid sequences of the
TITLE: transacylase components of branched-chain oxoacid
TITLE: dehydrogenase of Pseudomonas putida, and the pyruvate and
TITLE: 2-oxoglutarate dehydrogenases of Escherichia coli
JOURNAL: European Journal of Biochemistry
VOLUME: 176
PAGES: 165-169
DATE: 1988
US-08-404-381-4

Query Match 55.6%; Score 5; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VSTPV 5
|||||
DB 351 VSTPV 355

RESULT 49
US-08-353-550-1
Sequence 1, Application US/08353550
Patent No. 5744313
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Cavanaugh, William M.
TITLE OF INVENTION: No. 5744313el Protein Domain Which Binds
TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,550
FILING DATE: 09-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 02307K-057300

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-550-1

Query Match 55.6%; Score 5; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PVAPT 8
|||||
DB 361 PVAPT 365

RESULT 50
US-08-551-687-1
Sequence 1, Application US/08551687
Patent No. 5925547
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Cavanaugh, William M.
TITLE OF INVENTION: No. 5925547el Protein Domain Which Binds
TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,687
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,550
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: P39,787
REFERENCE/DOCKET NUMBER: 2307K-5731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-687-1

Query Match 55.6%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PVAPT 8

Wed Aug 15 13:34:53 2001

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Db 361 PVAPT 365

Search completed: August 15, 2001, 12:33:43
Job time: 48 sec
